

Access DB# 87364

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Jan Delaval
 Reference Librarian
 Biotechnology & Chemical Library
 CM1 1E07 - 703-308-4498
 jan.delaval@uspto.gov

STAFF USE ONLY

Searcher: <u>Ja</u>	Type of Search	Vendors and cost where applicable
Searcher Phone #: <u>4498</u>	NA Sequence (#) <u>✓1</u>	STN _____
Searcher Location: _____	AA Sequence (#) <u>✓13</u>	Dialog _____
Date Searcher Picked Up: <u>2/25/03</u>	Structure (#) _____	Questel/Orbit _____
Date Completed: <u>3/11/03</u>	Bibliographic _____	Dr.Link _____
Searcher Prep & Review Time: _____	Litigation _____	Lexis/Nexis _____
clerical Prep Time: <u>15</u>	Fulltext _____	Sequence Systems <u>✓</u>
Online Time: <u>✓10</u>	Patent Family _____	WWW/Internet _____
	Other _____	Other (specify) _____

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 : Search time 1.005 Seconds
(without alignments)
263.489 Million cell updates/sec

Title: US-09-743-482A-6
Perfect score: 49
Sequence: 1 LQRYSNPNT 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	67.3	1186	1	US-08-485-568A-4	Sequence 4, Appli
2	33	67.3	1186	1	US-08-357-698-6	Sequence 6, Appli
3	33	67.3	1186	2	US-08-590-554A-4	Sequence 4, Appli
4	33	67.3	1186	2	US-09-184-223-4	Sequence 4, Appli
5	33	67.3	1186	5	PCT-US93-12682-6	Sequence 6, Appli
6	32	65.3	87	2	US-07-885-0898-14	Sequence 14, Appli
7	32	65.3	119	2	US-08-800-198-2	Sequence 2, Appli
8	32	65.3	119	3	US-09-286-595-2	Sequence 2, Appli
9	32	65.3	240	2	US-08-800-198-8	Sequence 8, Appli
10	32	65.3	240	3	US-09-296-595-8	Sequence 8, Appli
11	32	65.3	254	2	US-08-948-616-9	Sequence 9, Appli
12	32	65.3	254	2	US-09-193-510-9	Sequence 9, Appli
13	32	65.3	254	4	US-08-368-402-9	Sequence 9, Appli
14	32	65.3	307	2	US-08-948-616-3	Sequence 3, Appli
15	32	65.3	307	2	US-09-193-510-3	Sequence 3, Appli
16	32	65.3	307	3	US-09-368-402-3	Sequence 3, Appli
17	32	65.3	600	4	US-09-134-001C-5293	Sequence 5293, Ap
18	31	63.3	262	2	US-07-857-224B-62	Sequence 62, Appli
19	31	63.3	262	2	US-07-857-224B-62	Sequence 62, Appli
20	31	63.3	275	2	US-08-701-181A-38	Sequence 38, Appli
21	31	63.3	521	5	PCT-US93-08386-10	Sequence 10, Appli
22	31	63.3	752	4	US-09-817-180-2	Sequence 2, Appli
23	31	63.3	822	4	US-09-817-180-4	Sequence 4, Appli
24	31	63.3	1404	2	US-08-400-159-2	Sequence 2, Appli
25	31	63.3	1404	3	US-08-611-729A-2	Sequence 2, Appli
26	30	61.2	19	2	US-07-921-447-6	Sequence 6, Appli
27	30	61.2	29	2	US-08-143-311B-15	Sequence 15, Appli

28	30	61.2	34	3	US-08-564-225-8	Sequence 8, Appli
29	30	61.2	78	3	US-08-564-225-9	Sequence 9, Appli
30	30	61.2	191	3	US-08-737-228-22	Sequence 22, Appli
31	30	61.2	237	4	US-09-326-643A-25	Sequence 25, Appli
32	30	61.2	236	6	5175255-9	Patent No. 5175255
33	30	61.2	338	2	US-08-359-850-2	Sequence 2, Appli
34	30	61.2	354	1	US-07-946-497-4	Sequence 4, Appli
35	30	61.2	354	1	US-08-483-322-4	Sequence 4, Appli
36	30	61.2	354	2	US-08-478-882-4	Sequence 4, Appli
37	30	61.2	432	2	US-08-904-278-6	Sequence 6, Appli
38	30	61.2	432	4	US-09-222-594-6	Sequence 6, Appli
39	30	61.2	457	4	US-09-134-001C-3013	Sequence 3013, Ap
40	30	61.2	475	1	US-07-715-184-4	Sequence 4, Appli
41	30	61.2	475	1	US-07-876-280-7	Sequence 7, Appli
42	30	61.2	475	1	US-07-876-280-28	Sequence 28, Appli
43	30	61.2	475	1	US-07-935-310A-2	Sequence 2, Appli
44	30	61.2	475	1	US-07-828-788A-2	Sequence 2, Appli
45	30	61.2	475	1	US-08-049-783-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-485-568A-4
Sequence 4, Application US/08485568A
Patent No. 5589382
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: No. 5589382a1 Bacillus thuringiensis Genes Encoding
TITLE OF INVENTION: Nematode-Active Toxins
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,568A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,197
FILING DATE: 21-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,345
FILING DATE: 21-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/558,738
FILING DATE: 27-JUL-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357,698
FILING DATE: 16-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,403
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/999,053
FILING DATE: 14-JUL-1993

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA48DD2.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-568A-4

Query Match 67.3%; Score 33; DB 1; Length 1186;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RYSNPT 9
DB 587 RYANPNS 593

RESULT 2
US-08-357-698-6
Sequence 6, Application US/08357698
Patent No. 5632987
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
TITLE OF INVENTION: No. 5632987e1 Bacillus thuringiensis Toxins Active
TITLE OF INVENTION: Against Corn Rootworm Larvae
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357,698
FILING DATE: 16-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/176,403
FILING DATE: 30-DEC-1993
APPLICATION NUMBER: US 07/999,186
FILING DATE: 31-DEC-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA82
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-357-698-6

Query Match 67.3%; Score 33; DB 1; Length 1186;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RYSNPT 9
DB 587 RYANPNS 593

RESULT 3
US-08-590-554A-4
Sequence 4, Application US/08590554A
Patent No. 5831011
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
TITLE OF INVENTION: No. 5831011e1 Bacillus thuringiensis Genes Encoding
TITLE OF INVENTION: Nematode-Active Toxins
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,554A
FILING DATE: 21-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,568
FILING DATE: 7-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,197
FILING DATE: 21-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,345
FILING DATE: 21-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/558,738
FILING DATE: 27-JUL-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357,698
FILING DATE: 16-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,403
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/999,053
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA48DD2.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 1186 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-590-554A-4

Query Match 67.3%; Score 33; DB 2; Length 1186;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RYSNPT 9
DB 587 RYANPNS 593

RESULT 4
US-09-184-223-4
Sequence 4, Application US/09184223
Patent No. 5959080
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Narva, Kenneth E.
APPLICANT: Fu, Jenny M.
TITLE OF INVENTION: No. 5959080e1 Bacillus thuringiensis Genes Encoding
TITLE OF INVENTION: Nematode-Active Toxins
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,223
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/590,554
FILING DATE: 21-MAR-1996
APPLICATION NUMBER: US 08/485,568
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,197
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,345
FILING DATE: 21-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/558,738
FILING DATE: 27-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357,698
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,403
FILING DATE: 30-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/999,053
FILING DATE: 14-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA48DD2.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-184-223-4

Query Match 67.3%; Score 33; DB 2; Length 1186;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RYSNPT 9
DB 587 RYANPNS 593

RESULT 5
PCT-US93-12682-6
Sequence 6, Application PC/TUS9312682
GENERAL INFORMATION:
APPLICANT: MCGOGEN CORPORATION
TITLE OF INVENTION: Novel Bacillus thuringiensis Toxins Active
TITLE OF INVENTION: Against Corn Rootworm Larvae
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SALIWANCHIK, DAVID R.
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12682
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/999,186
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA82
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-12682-6
Query Match 67.3%; Score 33; DB 5; Length 1186;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RYSNPT 9
DB 587 RYANPNS 593

RESULT 6
US-07-885-089B-14

Sequence 14, Application US/07885089B
Patent No. 5830995
GENERAL INFORMATION:
APPLICANT: SHOYAB, Mohammed
APPLICANT: McDONALD, VICKI L.
APPLICANT: BRADLEY, James G.
APPLICANT: PLOMAN, Gregory D.
TITLE OF INVENTION: AMPHIREGULINS: A FAMILY OF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,089B
FILING DATE: 18-MAY-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5624-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-885-089B-14

Query Match 65.3%; Score 32; DB 2; Length 87;
Best Local Similarity 75.0%; Pred. NO. 53;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSNPNT 9
11 11111
Db 45 QYSENPT 52

RESULT 7
US-08-800-198-2
Sequence 2, Application US/08800198
Patent No. 5942602
GENERAL INFORMATION:
APPLICANT: WELS, WINFRIED S.
APPLICANT: SCHMIDT, MATTHIAS
APPLICANT: VAKALOPOULOU, EVANGELIA
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,198
FILING DATE: 13-FEB-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: SCH 1576
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-800-198-2

Query Match 65.3%; Score 32; DB 2; Length 119;
Best Local Similarity 83.3%; Pred. NO. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSNPNT 9
11 11111
Db 50 YTNPT 55

RESULT 8
US-09-296-595-2
Sequence 2, Application US/09296595A
Patent No. 6129915
GENERAL INFORMATION:
APPLICANT: WELS, WINFRIED S.
APPLICANT: SCHMIDT, MATTHIAS
APPLICANT: VAKALOPOULOU, EVANGELIA
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
FILE REFERENCE: SCH-1576 D1
CURRENT APPLICATION NUMBER: US/09/296,595A
CURRENT FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: 08/800,198
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 2
LENGTH: 119
TYPE: PRT
ORGANISM: Murine sp.
US-09-296-595-2

Query Match 65.3%; Score 32; DB 3; Length 119;
Best Local Similarity 83.3%; Pred. NO. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSNPNT 9
11 11111
Db 50 YTNPT 55

RESULT 9
US-08-800-198-8
Sequence 8, Application US/08800198
Patent No. 5942602
GENERAL INFORMATION:
APPLICANT: WELS, WINFRIED S.
APPLICANT: SCHMIDT, MATTHIAS

APPLICANT: VAKALOPOULOU, EVANGELIA
APPLICANT: SCHNEIDER, DOUGLAS
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,198
FILING DATE: 13-FEB-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: SCH 1576
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
US-08-800-198-8
Query Match
Best Local Similarity 65.3%; Score 32; DB 2; Length 240;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 YSNPNT 9
|:|||||
Db 50 YTNPNT 55
RESULT 10
US-09-296-595-8
Sequence 8, Application US/09296595A
Patent No. 6129915
GENERAL INFORMATION:
APPLICANT: WIESS, WINFRIED S.
APPLICANT: SCHMIDT, MATTHIAS
APPLICANT: VAKALOPOULOU, EVANGELIA
APPLICANT: SCHNEIDER, DOUGLAS
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
FILE REFERENCE: SCH-1576 D1
CURRENT APPLICATION NUMBER: US/09/296,595A
CURRENT FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: 08/800,198
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 240
TYPE: PPT
ORGANISM: Murine sp.
US-09-296-595-8
Query Match
Best Local Similarity 65.3%; Score 32; DB 3; Length 240;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSNPNT 9
|:|||||
Db 50 YTNPNT 55
RESULT 11
US-08-948-616-9
Sequence 9, Application US/08948616
Patent No. 5840539
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: VESICLE TRANSPORT ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,616
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0409 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1223894
US-08-948-616-9
Query Match
Best Local Similarity 65.3%; Score 32; DB 2; Length 254;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 QRYSNPNT 9
|:|||||
Db 124 QRYNPNRS 131
RESULT 12
US-09-193-510-9
Sequence 9, Application US/09193510
Patent No. 5981226
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.

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: TITLE OF INVENTION: VESICLE TRANSPORT ASSOCIATED PROTEINS
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/193,510
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/948,616
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0409 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-855-0555
: TELEFAX: 650-845-4166
: TELEX:
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 254 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: GenBank
: CLONE: 1223894
: US-09-193-510-9

Query Match
Best Local Similarity 65.3%; Score 32; DB 2; Length 254;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRSNPNT 9
Db 124 QRYNNPRS 131

RESULT 13
US-09-368-402-9
: Sequence 9, Application US/09368402
: Patent No. 6200790
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Lal, Preeti
: APPLICANT: Shah, Purvi
: APPLICANT: Corley, Neil C.
: TITLE OF INVENTION: VESICLE TRANSPORT ASSOCIATED PROTEINS
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 08/948,616
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/948,616
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0409 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-855-0555
: TELEFAX: 650-845-4166
: TELEX:
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 254 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: GenBank
: CLONE: 1223894
: US-09-368-402-9

Query Match
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRSNPNT 9
Db 124 QRYNNPRS 131

RESULT 14
US-08-948-616-3
: Sequence 3, Application US/08948616
: Patent No. 5840539
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Lal, Preeti
: APPLICANT: Shah, Purvi
: APPLICANT: Corley, Neil C.
: TITLE OF INVENTION: VESICLE TRANSPORT ASSOCIATED PROTEINS
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/948,616
: FILING DATE: Herewith
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0409 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-855-0555
: TELEFAX: 650-845-4166
: TELEX:
: INFORMATION FOR SEQ ID NO: 3:

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: APPLICATION NUMBER: US/09/368,402
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/193,510
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0409 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-855-0555
: TELEFAX: 650-845-4166
: TELEX:
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 254 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: GenBank
: CLONE: 1223894
: US-09-368-402-9

Query Match
Best Local Similarity 65.3%; Score 32; DB 4; Length 254;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRSNPNT 9
Db 124 QRYNNPRS 131

RESULT 14
US-08-948-616-3
: Sequence 3, Application US/08948616
: Patent No. 5840539
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Lal, Preeti
: APPLICANT: Shah, Purvi
: APPLICANT: Corley, Neil C.
: TITLE OF INVENTION: VESICLE TRANSPORT ASSOCIATED PROTEINS
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/948,616
: FILING DATE: Herewith
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0409 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-855-0555
: TELEFAX: 650-845-4166
: TELEX:
: INFORMATION FOR SEQ ID NO: 3:

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SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

IMMEDIATE SOURCE:
LIBRARY: LUNGTUT07
CLONE: 2607662

US-08-948-616-3

Query Match

Best Local Similarity 65.3%; Score 32; DB 2; Length 307;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ORYSNPNT 9

DB 124 QRYNNPRS 131

RESULT 15

US-09-193-510-3

Sequence 3, Application US/09193510
Patent No. 5981226

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Shah, Purni

APPLICANT: Corley, Neil C.

TITLE OF INVENTION: VESICLE TRANSPORT ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/193,510

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/948,616

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0409 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 307 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: LUNGTUT07

CLONE: 2607662

US-09-193-510-3

DB 124 QRYNNPRS 131

Search completed: February 25, 2003, 10:38:41
Job time: 2.005 secs

Query Match 65.3%; Score 32; DB 2; Length 307;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ORYSNPNT 9

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 2.53333 Seconds
(without alignments)
813.344 Million cell updates/sec

Title: US-09-743-482A-8
Perfect score: 59
Sequence: 1 GYFTSYDMH 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL.21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.todent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	84.7	109	11	09JL75 mus musculu
2	49	83.1	102	11	09JL79 mus musculu
3	49	83.1	137	11	092AR6 mus musculu
4	49	83.1	139	11	092AR5 mus musculu
5	49	83.1	140	11	092AR2 mus musculu
6	49	83.1	140	11	092AP8 mus musculu
7	49	83.1	141	11	092A04 mus musculu
8	49	83.1	142	11	092A01 mus musculu
9	49	83.1	143	11	092AR7 mus musculu
10	49	83.1	143	11	092AR0 mus musculu
11	49	83.1	143	11	092A05 mus musculu
12	49	83.1	143	11	092AP6 mus musculu
13	49	83.1	143	11	091VA2 mus musculu
14	49	83.1	143	11	091V67 mus musculu
15	49	83.1	144	11	092AP5 mus musculu
16	49	83.1	145	11	092AR4 mus musculu

17	49	83.1	145	11	092AR3 mus musculu
18	49	83.1	145	11	092AR1 mus musculu
19	49	83.1	145	11	092A09 mus musculu
20	49	83.1	145	11	092A07 mus musculu
21	49	83.1	145	11	092A06 mus musculu
22	49	83.1	145	11	092AP7 mus musculu
23	49	83.1	146	11	092AR8 mus musculu
24	49	83.1	146	11	092A03 mus musculu
25	49	83.1	170	11	092552 mus musculu
26	49	83.1	278	11	0921K1 mus musculu
27	49	83.1	484	11	099LA6 mus musculu
28	46	78.0	119	4	090L94 mus sapien
29	46	78.0	124	4	090L92 mus sapien
30	46	78.0	125	4	090L95 mus sapien
31	46	78.0	481	11	091WT1 mus musculu
32	45	76.3	114	11	091L81 mus musculu
33	45	76.3	117	11	092L6 mus musculu
34	44	74.6	113	4	090L90 mus sapien
35	44	74.6	613	4	08W0K1 mus sapien
36	43	72.9	116	4	090L93 mus sapien
37	43	72.9	486	11	091Z07 mus musculu
38	41	69.5	142	11	092A02 mus musculu
39	41	69.5	143	11	092AP9 mus musculu
40	41	69.5	146	11	092A08 mus musculu
41	41	69.5	147	11	0925S3 mus musculu
42	41	69.5	157	4	095978 mus musculu
43	41	69.5	241	11	0921A6 mus musculu
44	40	67.8	110	11	090L77 mus musculu
45	40	67.8	143	11	092A00 mus musculu

ALIGNMENTS

RESULT 1

ID	Q9JL75	PRELIMINARY:	PRT:	109 AA.
AC	Q9JL75;			
DT	01-OCT-2000 (TREMUR1.15, Created)			
DT	01-OCT-2000 (TREMUR1.15, Last sequence update)			
DT	01-DEC-2001 (TREMUR1.19, Last annotation update)			
DE	Anti-mysin immunoglobulin heavy chain variable region			
DE	(Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/C.			
RX	MEDLINE=2044942; PubMed=10992488.			
RA	Maikael S., Liao L., Cunningham M.W., Diamond B.			
RT	"T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-galactosamine, is cross-reactive with cardiac myosin."			
RL	Infect. Immun. 68:5803-5808(2000).			
DR	EMBL; AF206031; AAF6329.1; ..			
DR	HSSP; P01810; 2EBU.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG-V.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IGV; 1.			
FT	NON_TER			
FT	NON_TER			
FT	NON_TER			
EQ	SEQUENCE			
EQ	109 AA; 12118 MW; FFG5E441BFP36A6 CRC64;			

Query Match 84.7%; Score 50; DB 11; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
DB 17 GYFTSYDMH 26

RESULT 2

09JUL79

ID 09JUL79 PRELIMINARY: PRT: 102 AA.

AC 09JUL79;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Anti-mycosin immunoglobulin heavy chain variable region

(Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A.CA;

RX MEDLINE=20448942; PubMed=10992486;

RA Makiel S., Liao L., Cunningham M.W., Diamond B.;

RT "T-cell-dependent antibody response to the dominant epitope of

streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive

with cardiac myosin.";

RL Infect. Immun. 68:5803-5808(2000).

DR EMBL: AF206027; AAF69325.1; -

DR HSSP: P01772; 2F8A.

DR InterPro: IPR003006; I9_MHC.

DR InterPro: IPR003596; I9_V.

DR Pfam: PF00047; I9; 1.

DR SMART: SM00406; IGV; 1.

FT NON_TER 1

FT NON_TER 102

SQ SEQUENCE 102 AA: 11543 MW; E590C292093F6711 CRC64;

Query Match

Best Local Similarity 83.1%; Score 49; DB 11; Length 102;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10

DB 11 GYFTSYDMH 20

RESULT 3

0924R6

ID 0924R6 PRELIMINARY: PRT: 137 AA.

AC 0924R6;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE VH186.2-D-J-C mu protein (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RA Kozono Y., Kozono H., Azuma T.;

RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Hydroxy-3-Nitrophenyl)Acetyl (NP).";

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB067783; BAB63268.1; -

DR InterPro: IPR003006; I9_MHC.

DR Pfam: PF00047; I9; 1.

FT NON_TER 1

FT NON_TER 137

SQ SEQUENCE 137 AA: 15171 MW; 5C38D966DC6A4124 CRC64;

Query Match

Best Local Similarity 83.1%; Score 49; DB 11; Length 137;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10

DB 26 GYFTSYDMH 35

RESULT 4

0924R5

ID 0924R5 PRELIMINARY: PRT: 139 AA.

AC 0924R5;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE VH186.2-D-J-C mu protein (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RA Kozono Y., Kozono H., Azuma T.;

RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Hydroxy-3-Nitrophenyl)Acetyl (NP).";

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB067784; BAB63269.1; -

DR InterPro: IPR003006; I9_MHC.

DR Pfam: PF00047; I9; 1.

FT NON_TER 1

FT NON_TER 139

SQ SEQUENCE 139 AA: 15221 MW; 8491E2F85614736A CRC64;

Query Match

Best Local Similarity 83.1%; Score 49; DB 11; Length 139;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10

DB 26 GYFTSYDMH 35

RESULT 5

0924R2

ID 0924R2 PRELIMINARY: PRT: 140 AA.

AC 0924R2;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE VH186.2-D-J-C mu protein (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RA Kozono Y., Kozono H., Azuma T.;

RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Hydroxy-3-Nitrophenyl)Acetyl (NP).";

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB067788; BAB63273.1; -

DR InterPro: IPR003006; I9_MHC.

DR Pfam: PF00047; I9; 1.

FT NON_TER 1

FT NON_TER 140

SQ SEQUENCE 140 AA: 15361 MW; 60739B790FC6AF24 CRC64;

Query Match

Best Local Similarity 83.1%; Score 49; DB 11; Length 140;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
 111111 11
 DB 26 GYFTSYWMH 35

RESULT 6

Q924P8 PRELIMINARY: PRT: 140 AA.
 AC Q924P8:
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE V23-D-J-C mu protein (Fragment).
 GN V23-D-J-C MU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB069917; BAB63933.1; -;
 DR InterPro: IPR003006; I9_MHC.
 DR Pfam: PF00047; I9; 1.
 FT NON_TER 1 1
 FT NON_TER 140 140
 SQ SEQUENCE 140 AA; 15392 MW; 904C80C82548C936 CRC64;

Query Match 83.1%; Score 49; DB 11; Length 140;
 Best Local Similarity 90.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
 111111 11
 DB 26 GYFTSYWMH 35

RESULT 7

Q924Q4 PRELIMINARY: PRT: 141 AA.
 AC Q924Q4:
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE VHL86.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB067796; BAB63281.1; -;
 DR InterPro: IPR003006; I9_MHC.
 DR Pfam: PF00047; I9; 1.
 FT NON_TER 1 1
 FT NON_TER 141 141
 SQ SEQUENCE 141 AA; 15561 MW; DDD80482D66B76A0 CRC64;

Query Match 83.1%; Score 49; DB 11; Length 141;
 Best Local Similarity 90.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
 111111 11
 DB 26 GYFTSYWMH 35

RESULT 8

Q924Q1 PRELIMINARY: PRT: 142 AA.
 AC Q924Q1:
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE V23-D-J-C mu protein (Fragment).
 GN V23-D-J-C MU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB069913; BAB63929.1; -;
 DR InterPro: IPR003006; I9_MHC.
 DR Pfam: PF00047; I9; 1.
 FT NON_TER 1 1
 FT NON_TER 142 142
 SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;

Query Match 83.1%; Score 49; DB 11; Length 142;
 Best Local Similarity 90.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
 111111 11
 DB 26 GYFTSYWMH 35

RESULT 9

Q924R7 PRELIMINARY: PRT: 143 AA.
 AC Q924R7:
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE VHL86.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB067782; BAB63267.1; -;
 DR InterPro: IPR003006; I9_MHC.
 DR Pfam: PF00047; I9; 1.
 FT NON_TER 1 1
 FT NON_TER 143 143
 SQ SEQUENCE 143 AA; 15648 MW; 51894D22EA9FDD47 CRC64;

Query Match 83.1%; Score 49; DB 11; Length 143;
 Best Local Similarity 90.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
||||||| 11
Db 26 GYFTSYWMH 35

RESULT 10

O924R0 PRELIMINARY: PRT: 143 AA.

AC O924R0: 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE VHI86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB067790; BAB63275.1; -
DR InterPro: IPR003598; 19_c2.
DR Pfam: PF00047; 19; 1.
DR SMART: SM00408; IGC2; 1.
DR Immunoglobulin domain.
KM NON_TER 1
FT NON_TER 1
SQ SEQUENCE 143 AA: 15868 MW: 1398296681E07F CRC64;

Query Match 83.1%; Score 49; DB 11: Length 143;
Best Local Similarity 90.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GYFTSYDMH 10
||||||| 11
Db 26 GYFTSYWMH 35

RESULT 11

O924O5 PRELIMINARY: PRT: 143 AA.

AC O924O5: 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE VHI86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB067795; BAB63280.1; -
DR InterPro: IPR003006; 19_MHC.
DR Pfam: PF00047; 19; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 143 AA: 15908 MW: 55A2372870F0D568 CRC64;

Query Match 83.1%; Score 49; DB 11: Length 143;
Best Local Similarity 90.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GYFTSYDMH 10
||||||| 11
Db 26 GYFTSYWMH 35

RESULT 12

O924P6 PRELIMINARY: PRT: 143 AA.

AC O924P6: 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE VHI86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB069919; BAB63935.1; -
DR InterPro: IPR003006; 19_MHC.
DR Pfam: PF00047; 19; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 143 AA: 15714 MW: 523385316C345A93 CRC64;

Query Match 83.1%; Score 49; DB 11: Length 143;
Best Local Similarity 90.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GYFTSYDMH 10
||||||| 11
Db 26 GYFTSYWMH 35

RESULT 13

O91VA2 PRELIMINARY: PRT: 143 AA.

AC O91VA2: 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE VHI86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB067786; BAB63271.1; -
DR EMBL: AB069911; BAB63927.1; -
DR InterPro: IPR003006; 19_MHC.
DR Pfam: PF00047; 19; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 143 AA: 15617 MW: 51952152F6F3AD47 CRC64;

Query Match 83.1%; Score 49; DB 11: Length 143;
Best Local Similarity 90.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
 ||||| 11

Db 26 GYFTSYDMH 35

RESULT 14

Q91V67 PRELIMINARY; PRT; 143 AA.

AC Q91V67;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE V186-2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
 GN V304-D-J-C MU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB069912; BAB63928.1; -;
 DR EMBL; AB069914; BAB63930.1; -;
 DR InterPro: IPR003006; I9_MHC.
 DR Pfam: PF00047; I9; 1.
 FT NON_TER 1 1
 FT NON_TER 143 143
 SQ SEQUENCE 143 AA: 15775 MW; 91BC6012B4FEFEBF CRC64;

Query Match 83.1%; Score 49; DB 11; Length 143;
 Best Local Similarity 90.0%; Pred. NO. 0.16;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
 ||||| 11

Db 26 GYFTSYDMH 35

RESULT 15

Q924P5 PRELIMINARY; PRT; 144 AA.

AC Q924P5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE V186-2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB069920; BAB63936.1; -;
 DR InterPro: IPR003006; I9_MHC.
 DR Pfam: PF00047; I9; 1.
 FT NON_TER 1 1
 FT NON_TER 144 144
 SQ SEQUENCE 144 AA: 15865 MW; CD07BE97E95C1B27 CRC64;

Query Match

83.1%; Score 49; DB 11; Length 144;

Best Local Similarity 90.0%; Pred. NO. 0.16;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
 ||||| 11

Db 26 GYFTSYDMH 35

Search completed: February 25, 2003, 10:36:31
 Job time : 3.53333 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 0.883333 Seconds
(without alignments)
469.543 Million cell updates/sec

Title: US-09-743-482a-8
Perfect score: 59
Sequence: 1 GYFTSYDMH 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	84.7	117	1 HV14_MOUSE	P01758 mus musculu
2	49	83.1	117	1 HV04_MOUSE	P01748 mus musculu
3	49	83.1	117	1 HV06_MOUSE	P01750 mus musculu
4	49	83.1	117	1 HV09_MOUSE	P01753 mus musculu
5	49	83.1	117	1 HV10_MOUSE	P01754 mus musculu
6	49	83.1	117	1 HV49_MOUSE	P06328 mus musculu
7	49	83.1	120	1 HV50_MOUSE	P06329 mus musculu
8	49	83.1	137	1 HV11_MOUSE	P01755 mus musculu
9	49	83.1	139	1 HV07_MOUSE	P01751 mus musculu
10	48	81.4	117	1 HV52_MOUSE	P06327 mus musculu
11	47	79.7	136	1 HV15_MOUSE	P01759 mus musculu
12	46	78.0	117	1 HV1G_HUMAN	P23083 homo sapien
13	45	76.3	117	1 HV1B_HUMAN	P01743 homo sapien
14	42	71.2	114	1 HV00_MOUSE	P01741 mus musculu
15	41	69.5	117	1 HV05_MOUSE	P01749 mus musculu
16	41	69.5	120	1 HV03_MOUSE	P01747 mus musculu
17	41	69.5	121	1 HV3J_HUMAN	P01771 homo sapien
18	41	69.5	140	1 HV02_MOUSE	P01745 mus musculu
19	40	67.8	122	1 HV3G_HUMAN	P01768 homo sapien
20	40	67.8	136	1 HV16_MOUSE	P01783 mus musculu
21	39	66.1	118	1 HV51_MOUSE	P06330 mus musculu
22	38	64.4	117	1 HV03_CARAU	P19180 carassius a
23	38	64.4	117	1 HV12_MOUSE	P01756 mus musculu
24	38	64.4	117	1 HV13_MOUSE	P01757 mus musculu
25	38	64.4	117	1 HV55_MOUSE	P18526 mus musculu
26	38	64.4	492	1 TR11_FUSSP	O13317 fusarium sp
27	38	64.4	533	1 TIV_DEBOC	P24133 debruyomyce
28	38	64.4	1256	1 MRP_STRSU	P32653 streptococc
29	37	62.7	121	1 HV01_MOUSE	P01748 mus musculu
30	37	62.7	138	1 HV48_MOUSE	P03980 mus musculu
31	37	62.7	477	1 GIGA_CIOAB	O979x6 clostridium
32	36	61.0	117	1 HV54_MOUSE	P16525 mus musculu
33	36	61.0	122	1 HV3H_HUMAN	P01769 homo sapien

34	36	61.0	217	1 COAT_PSVJ	P22116 peanut stun
35	36	61.0	229	1 COAT_TAV	P23627 tomato aspe
36	36	61.0	532	1 INV1_YEAST	P10594 saccharomyc
37	36	61.0	532	1 INV2_YEAST	P10596 saccharomyc
38	36	61.0	532	1 INV4_YEAST	P10596 saccharomyc
39	35	59.3	97	1 HV56_MOUSE	P18527 mus musculu
40	35	59.3	114	1 HV01_CANFA	P01784 canis fami
41	35	59.3	117	1 HV3C_HUMAN	P01764 homo sapien
42	35	59.3	119	1 HV3I_HUMAN	P01770 homo sapien
43	35	59.3	326	1 YORO_BACSU	P45950 bacillus su
44	35	59.3	465	1 EGIC_RHIME	O929q2 rhizobium m
45	35	59.3	476	1 GIGA_BACHD	O9K0x6 bacillus ha

ALIGNMENTS

RESULT 1
ID HV14_MOUSE STANDARD: PRT: 117 AA.
AC P01758:
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 108A precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.:
RT "Diversity of germ-line immunoglobulin Vh genes."
RL Nature 292:426-430(1981).

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CC or send an email to license@sib-sib.ch).

CC PIR: J00488; AAA38519.1; -
DR EMBL: A02041; HVMS8A.
DR HSP: P01810; 2FRT.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
FT SIGNAL 1 19
FT CHAIN 1 19 IG HEAVY CHAIN V REGION 108A.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44F25D1BC2 CRC64;

Query Match 84.7% Score 50; DB 1; Length 117;
Best Local Similarity 80.0% Pred. No. 0.013;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
DB 45 GYFTSYDMH 54

RESULT 2
ID HV04_MOUSE STANDARD: PRT: 117 AA.
AC P01748:
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Ig heavy chain V region 23 precursor.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC PIR: A02030; HVMS23.
DR HSSP; P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; Igv_1.
KM Immunoglobulin V region; Signal.
FT SIGNAL
FT CHAIN 1
FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 83.1%; Score 49; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
DB 45 GYFTSYWMH 54

RESULT 3
HVO6_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DR 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC PIR: A02032; HVMS02.
DR HSSP; P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; Igv_1.
KM Immunoglobulin V region; Signal.

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FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Query Match 83.1%; Score 49; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
DB 45 GYFTSYWMH 54

RESULT 4
HVO9_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DR 21-JUL-1986 (Rel. 01, Created)
DR 01-JUL-1989 (Rel. 11, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC PIR: B02034; HVMS61.
DR HSSP; P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; Igv_1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A08CB17F5A CRC64;

Query Match 83.1%; Score 49; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
DB 45 GYFTSYWMH 54

RESULT 5
HVO10_MOUSE STANDARD; PRT; 117 AA.

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AC P06754: P11270:
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 145 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NDb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1 MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT CODE ENCODE V REGIONS OF NDb ANTIBODIES.
CC -----
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CC -----
CC EMBL: J00533; AAA38602.1; -.
CC PIR: C02034; HVM545.
CC HSSP: P01810; 2FBJ.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam: PF00047; 1g_1.
CC SMART: SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC NON_TER 117
CC SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 83.1%; Score 49; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
DB 45 GYFTSYDMH 54

RESULT 6
HVS_MOUSE STANDARD; PRT; 117 AA.
ID HVS_MOUSE
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH55 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RX Vancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of

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RT unarranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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CC -----
CC EMBL: M13788; AAA38506.1; -.
CC PIR: A02035; MHMSB4.
CC HSSP: P01810; 2FBJ.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam: PF00047; 1g_1.
CC SMART: SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V REGION VH55 B4.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DISULFID 41 115 BY SIMILARITY.
CC NON_TER 117
CC SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 83.1%; Score 49; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
DB 45 GYFTSYDMH 54

RESULT 7
HVS_MOUSE STANDARD; PRT; 120 AA.
ID HVS_MOUSE
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RX Dildrop R., Bovens J., Stekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02037; MHMS15.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g_1.
DR SMART: SM00406; IGV; 1.
CC Immunoglobulin V region.
CC SIGNAL 1 98 V SEGMENT.
CC CHAIN 99 105 D SEGMENT.
CC DOMAIN 106 120 J SEGMENT.
CC DISULFID 22 96 BY SIMILARITY.
CC NON_TER 120
CC SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 83.1%; Score 49; DB 1; Length 120;

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Best Local Similarity 90.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
DB 26 GYFTSYDMH 35

RESULT 8
HV1_MOUSE

ID HV1_MOUSE STANDARD; PRT: 137 AA.

AC P01755: 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
OS Ig heavy chain V region S43 precursor.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RT Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
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CC -----

DR EMBL; J00539; AAA38172.1; -
DR PIR; A02038; G2MS43.
DR HSSP; P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 122
FT DOMAIN 123 137
FT DISULFID 41 115
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 83.1%; Score 49; DB 1; Length 137;
Best Local Similarity 90.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
DB 45 GYFTSYDMH 54

RESULT 9
HV07_MOUSE STANDARD; PRT: 139 AA.
ID HV07_MOUSE

AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
OS Ig heavy chain V region B1-8/186-2 precursor.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RT Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
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DR EMBL; J00529; AAA38170.1; -
DR PIR; A02034; MEMS18.
DR HSSP; P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 124
FT DOMAIN 125 139
FT DISULFID 41 115
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC9F465 CRC64;

Query Match 83.1%; Score 49; DB 1; Length 139;
Best Local Similarity 90.0%; Pred. No. 0.025;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
DB 45 GYFTSYDMH 54

RESULT 10
HV52_MOUSE STANDARD; PRT: 117 AA.
ID HV52_MOUSE
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
OS Ig heavy chain V region VH58 A1/A4 precursor.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-85093340; PubMed-2578321;
 RA Yancopoulos G.D., Alt F.W.;
 RT "developmentally controlled and tissue-specific expression of
 RL unarranged VH gene segments.";
 CC Cell 40:271-281(1985).
 CC -----
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 CC -----
 CC EMBL: M13787; AAA849.1; .
 CC PIR: A02029; HVMSA1.
 CC HSSP: P01810; 2F8A.
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR003596; Ig_V.
 CC Pfam: PF00047; Ig; 1.
 CC SMART: SM00406; IgV; 1.
 CC Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 17 IG HEAVY CHAIN V REGION VH558 A1/A4.
 FT DOMAIN 20 49
 FT DOMAIN 50 54 FRAMEWORK-1.
 FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 69 85 FRAMEWORK-2.
 FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-2.
 FT DISULFID 41 115 FRAMEWORK-3.
 FT NON_TER 117 117 BY SIMILARITY.
 FT SEQUENCE 117 AA; 12971 MW; 8B0BC13856DFC9D CRC64;
 Query Match 81.4%; Score 48; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.031;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYFTSYDMM 10
 Db 45 GYFTSYDMM 54
 RESULT 11
 HV15_MOUSE STANDARD; PRT; 136 AA.
 ID HV15_MOUSE
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region BCL1 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX SEQUENCE FROM N.A.
 RX MEDLINE-8222262; PubMed-6806821;
 RA Knapp M.R., Liu G.-P., Newell N., Ward R.B., Tucker P.W., Stroder S.,
 RT Blattner F.R.;
 RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
 RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
 RT by two adjacent CH genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
 CC -----
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 CC -----

DR EMBL: J00494; AAA38130.1; .
 DR PIR: A02042; HVMSB1.
 DR HSSP: P01772; 2F8A.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
 FT NON_TER 136 136
 FT SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;
 Query Match 79.7%; Score 47; DB 1; Length 136;
 Best Local Similarity 80.0%; Pred. No. 0.057;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GYFTSYDMM 10
 Db 45 GYFTSYDMM 54
 RESULT 12
 HV1G_HUMAN STANDARD; PRT; 117 AA.
 ID HV1G_HUMAN
 AC P23083;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-I region V35 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 ON NCBI_TaxID=9606;
 RX SEQUENCE FROM N.A.
 RX MEDLINE-88296406; PubMed-2841108;
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
 RA Ohno H., Fukuhara S., Honjo T.;
 RT "Dispersed localization of D segments in the human immunoglobulin
 RT heavy-chain locus.";
 RL EMBO J. 7:1047-1051(1988).
 CC -----
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 CC -----
 CC EMBL: X07448; -; NOT_ANNOTATED_CDS.
 CC PIR: S00476; HVH035.
 CC HSSP: P01772; 2F8A.
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR003596; Ig_V.
 CC Pfam: PF00047; Ig; 1.
 CC SMART: SM00406; IgV; 1.
 CC Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
 FT NON_TER 117 117
 FT SEQUENCE 117 AA; 13009 MW; B61C63F8CE97BD CRC64;
 Query Match 78.0%; Score 46; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.074;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GYFTSYDMM 10
 Db 45 GYFTSYDMM 54

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RESULT 13
HV05_HUMAN STANDARD: PRT: 117 AA.
AC P01743:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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CC -----
DR EMBL: J00240; AAA52988.1;
DR PIR: A02024; HVH0HG.
DR HSSP: P01772; 2F84.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 203F92FC60C01FE7 CRC64;

Query Match
Best Local Similarity 76.3%; Score 45; DB 1; Length 117;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GYTFSTYDMH 10
Db 45 GTTNSYTMH 54

RESULT 14
HV00_MOUSE STANDARD: PRT: 114 AA.
AC P01741:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 21-JUL-1986 (Rel. 01, Last annotation update)
DE Ig heavy chain V region (Anti-arsenate antibody).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX STRAIN=A/J;
RX MEDLINE=79195438; PubMed=109536;
RA Capra J.D., Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idiotype.";
RL J. Immunol. 123:279-284(1979).
CC -!- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF

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CC THE IGH1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
DR PIR: A02022; GIMSAA.
DR HSSP: P01772; 2F84.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A69F4BE CRC64;

Query Match
Best Local Similarity 71.2%; Score 42; DB 1; Length 114;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYTFSTYDMH 10
Db 26 GYTFSTYELV 35

RESULT 15
HV05_MOUSE STANDARD: PRT: 117 AA.
AC P01749:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 3 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC -----
DR EMBL: J00536; AAA38605.1;
DR PIR: A02031; HVMS3.
DR HSSP: P01810; 2F8J.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFD 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C3975EDC CRC64;

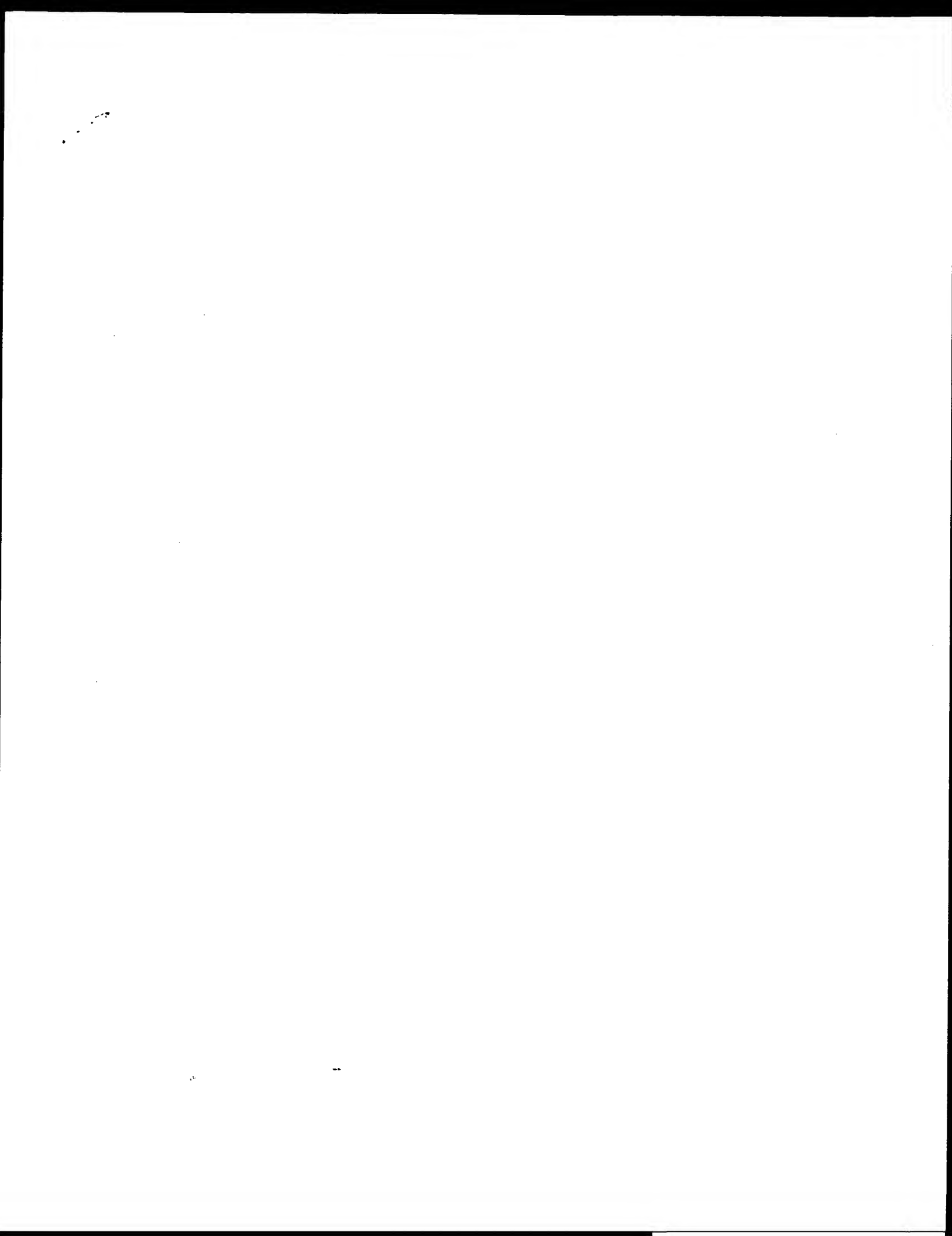
Query Match
Best Local Similarity 69.5%; Score 41; DB 1; Length 117;

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Best Local Similarity 88.9%, Pred. No. 0.64:
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDM 9
|||||
Db 45 GYFTSYWM 53

Search completed: February 25, 2003, 10:37:30
Job time : 0.883333 secs



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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 1.26667 Seconds

(without alignments)
758.956 Million cell updates/sec

Title: US-09-743-482a-8

Perfect score: 59

Sequence: 1 GYFTSYDMH 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	55	93.2	93	2 A37263	Ig heavy chain V r
2	55	93.2	101	2 I37262	Ig heavy chain V r
3	54	91.5	93	2 S42182	Ig gamma chain V r
4	54	91.5	94	2 S42177	Ig gamma chain V r
5	54	91.5	95	2 S42178	Ig gamma chain V r
6	54	91.5	97	2 S42181	Ig gamma chain V r
7	54	91.5	101	2 S42179	Ig gamma chain V r
8	54	91.5	101	2 S42184	Ig gamma chain V r
9	54	91.5	102	2 S42180	Ig gamma chain V r
10	52	88.1	96	2 S17230	Ig heavy chain V r
11	52	88.1	96	2 S17621	Ig heavy chain V r
12	52	88.1	96	2 S17620	Ig heavy chain V r
13	52	88.1	102	2 S26471	Ig heavy chain V r
14	51	86.4	96	2 S17609	Ig heavy chain V r
15	51	86.4	97	2 S26890	Ig heavy chain V r
16	51	86.4	104	2 PH1665	Ig heavy chain V r
17	51	86.4	114	2 PH1667	Ig heavy chain V r
18	51	86.4	117	2 S18553	Ig heavy chain V r
19	51	86.4	117	2 S18552	Ig heavy chain V r
20	51	86.4	118	2 PH1666	Ig heavy chain V r
21	50	84.7	94	2 PH0996	Ig heavy chain V r
22	50	84.7	96	2 S17618	Ig heavy chain V r
23	50	84.7	97	2 S17603	Ig heavy chain V r
24	50	84.7	98	2 S26313	Ig heavy chain V r
25	50	84.7	98	2 S26312	Ig heavy chain V r
26	50	84.7	98	2 S26920	Ig heavy chain V r
27	50	84.7	101	2 S26311	Ig heavy chain V r
28	50	84.7	101	2 S26310	Ig heavy chain V r
29	50	84.7	104	2 PH0991	Ig heavy chain V r

30	50	84.7	106	2 F32513	Ig heavy chain V r
31	50	84.7	109	2 PH1094	Ig heavy chain V r
32	50	84.7	109	2 PH1096	Ig heavy chain V r
33	50	84.7	109	2 PH0989	Ig heavy chain V r
34	50	84.7	110	2 PH0995	Ig heavy chain V r
35	50	84.7	111	2 PH0992	Ig heavy chain V r
36	50	84.7	111	2 PH0993	Ig heavy chain V r
37	50	84.7	111	2 PH0994	Ig heavy chain V r
38	50	84.7	117	1 HVM58A	Ig heavy chain pre
39	50	84.7	117	2 S31680	Ig heavy chain V r
40	50	84.7	121	2 S20783	Ig heavy chain V r
41	50	84.7	125	2 S20639	Ig heavy chain V r
42	50	84.7	131	2 S66537	Ig heavy chain V r
43	50	84.7	171	2 S23623	Ig heavy chain V r
44	49	83.1	69	2 D25150	Ig heavy chain V r
45	49	83.1	76	2 PH1153	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A37263
Ig heavy chain V region (4A9) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Aug-1991 #sequence_revision 03-Apr-1992 #text_change 16-Aug-1996

C:Accession: A37263

R:Goshorn, S.C.; Retzel, E.; Jemerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A:Title: Common structural features among monoclonal antibodies binding the same anti

A:Reference number: A38601; MUID:91115823; PMID:1703527

A:Accession: A37263

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-93 <GOS>

A:Cross-references: GB:M57996

A:Note: the authors translated the codon CAA for residue 38 as His, AGA for residue 3

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

Query Match

Best Local Similarity 93.2%; Score 55; DB 2; Length 93;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
||||| ||||
DB 10 GYFTSYDMH 19

RESULT 2

I37262

Ig heavy chain V region (1G1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999

C:Accession: I37262

R:Goshorn, S.C.; Retzel, E.; Jemerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A:Title: Common structural features among monoclonal antibodies binding the same anti

A:Reference number: A38601; MUID:91115823; PMID:1703527

A:Accession: I37262

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-101 <GOS>

A:Cross-references: GB:M57995; NID:g195375; PIDN:AA63334.1; PID:g195376

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

Query Match

Best Local Similarity 93.2%; Score 55; DB 2; Length 101;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
||||| ||||

Db 18 GYFTSYDMH 27

RESULT 3

19 gamma chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C:Accession: S42182
R:MO, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42182
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-93 <MOJ>
A:Cross-references: EMBL:Z25443; NID:9407822; PIDN:CA80940.1; PID:9407823
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:8-91/Domain: Immunoglobulin homology <IMM>

Query Match 91.5%; Score 54; DB 2; Length 93;
Best Local Similarity 90.0%; Pred. No. 0.0074; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0;

OY 1 GYFTSYDMH 10
|||||:|
Db 19 GYFTSYNMH 28

RESULT 4

19 gamma chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C:Accession: S42177
R:MO, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42177
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-94 <MOJ>
A:Cross-references: EMBL:Z25443; NID:9407812; PIDN:CA80930.1; PID:9407813
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:8-91/Domain: Immunoglobulin homology <IMM>

Query Match 91.5%; Score 54; DB 2; Length 94;
Best Local Similarity 90.0%; Pred. No. 0.0075; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0;

OY 1 GYFTSYDMH 10
|||||:|
Db 19 GYFTSYNMH 28

RESULT 5

19 gamma chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C:Accession: S42178
R:MO, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42178
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-95 <MOJ>

A:Cross-references: EMBL:Z25445; NID:9407814; PIDN:CA80932.1; PID:9407815
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:8-91/Domain: Immunoglobulin homology <IMM>

Query Match 91.5%; Score 54; DB 2; Length 95;
Best Local Similarity 90.0%; Pred. No. 0.0076; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0;

OY 1 GYFTSYDMH 10
|||||:|
Db 19 GYFTSYNMH 28

RESULT 6

19 gamma chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C:Accession: S42181
R:MO, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42181
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <MOJ>
A:Cross-references: EMBL:Z25451; NID:9407820; PIDN:CA80938.1; PID:9407821
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:8-91/Domain: Immunoglobulin homology <IMM>

Query Match 91.5%; Score 54; DB 2; Length 97;
Best Local Similarity 90.0%; Pred. No. 0.0077; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0;

OY 1 GYFTSYDMH 10
|||||:|
Db 19 GYFTSYNMH 28

RESULT 7

19 gamma chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C:Accession: S42179
R:MO, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42179
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <MOJ>
A:Cross-references: EMBL:Z25447; NID:9407816; PIDN:CA80934.1; PID:9407817
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 91.5%; Score 54; DB 2; Length 101;
Best Local Similarity 90.0%; Pred. No. 0.0081; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0;

OY 1 GYFTSYDMH 10
|||||:|
Db 26 GYFTSYNMH 35

RESULT 8

19 gamma chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)
C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 06-Jun-1997
C:Accession: S42184
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42184
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <MOJ>
A:Cross-references: EMBL:225457
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 91.5%; Score 54; DB 2; Length 101;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
|||||:|
DB 26 GYFTSYNMH 35

RESULT 9
S42180
Ig gamma chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C:Accession: S42180
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42180
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <MOJ>
A:Cross-references: EMBL:225449; NID:9407818; PION:CA80936.1; PID:9407819
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 91.5%; Score 54; DB 2; Length 102;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
|||||:|
DB 26 GYFTSYNMH 35

RESULT 10
S17230
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17230
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17230
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 88.1%; Score 52; DB 2; Length 96;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
|||||:|
DB 19 GYFTSYTMH 28

RESULT 11
S17621
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17621
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17621
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 88.1%; Score 52; DB 2; Length 96;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
|||||:|
DB 19 GYFTSYTMH 28

RESULT 12
S17620
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17620
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17620
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 88.1%; Score 52; DB 2; Length 96;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
|||||:|
DB 19 GYFTSYTMH 28

RESULT 13
S26471
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26471
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26471
A:Status: preliminary
A:Molecule type: mRNA

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
|||||:|
DB 19 GYFTSYTMH 28

RESULT 11
S17621
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17621
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17621
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 88.1%; Score 52; DB 2; Length 96;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
|||||:|
DB 19 GYFTSYTMH 28

RESULT 12
S17620
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17620
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17620
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 88.1%; Score 52; DB 2; Length 96;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
|||||:|
DB 19 GYFTSYTMH 28

RESULT 13
S26471
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26471
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26471
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-102 <KAV>
 A:Cross-references: EMBL:X59110; NID:g51951; PIDN:CAA1836.1; PID:g51952
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 86.4%; Score 51; DB 2; Length 97;
 Best Local Similarity 80.0%; Pred. No. 0.027;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
 |||||
 DB 26 GYFTSYDMH 35

RESULT 14
 S17609
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S17609
 R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
 Nature 352, 624-628, 1991
 A:Title: Making antibody fragments using phage display libraries.
 A:Reference number: S17230; MUID:91326098; PMID:1907718
 A:Accession: S17609
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-96 <CLAV>
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:8-91/Domain: Immunoglobulin homology <IMM>

Query Match 86.4%; Score 51; DB 2; Length 96;
 Best Local Similarity 90.0%; Pred. No. 0.027;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
 |||||
 DB 19 GYFTSYDMH 28

RESULT 15
 S26890
 Ig heavy chain V region (DP-48) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S26890
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
 A:Reference number: S26885; MUID:93021117; PMID:1404388
 A:Accession: S26890
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-97 <TOM>
 A:Cross-references: EMBL:Z12348; NID:g32916; PIDN:CAA78218.1; PID:g32917
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:15-97/Domain: Immunoglobulin homology <IMM>

Query Match 86.4%; Score 51; DB 2; Length 97;
 Best Local Similarity 80.0%; Pred. No. 0.027;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
 |||||
 DB 26 GYFTSYDMH 35

Search completed: February 25, 2003, 10:33:52
 Job time: 1.26667 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:57 ; Search time 3.3 Seconds
(without alignments)
403.790 Million cell updates/sec

Title: US-09-743-482A-8
Perfect score: 59
Sequence: 1 GYPTSTYDMH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: A_Geneseq.101002.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	10	21	AA178322
2	59	100.0	123	21	AA178325
3	59	100.0	532	21	AA178328
4	35	93.2	850	22	ABG04634
5	35	91.5	122	20	AA121816
6	34	91.5	140	8	AA170627
7	34	91.5	140	10	AA194780
8	34	91.5	140	15	AA155215
9	34	91.5	140	18	AA10588
10	34	91.5	140	18	AA16343

Result No.	Score	Query Match	Length	ID	Description
11	54	91.5	140	18	AA10242
12	54	91.5	140	19	AA1070
13	54	91.5	140	19	AA17513
14	54	91.5	140	19	AA17520
15	54	91.5	140	20	AA189540
16	54	91.5	140	22	AA18092
17	54	91.5	140	22	AA18092
18	54	91.5	140	22	AA18092
19	54	91.5	140	22	AA18092
20	54	91.5	140	22	AA18092
21	54	91.5	140	22	AA18092
22	54	91.5	140	22	AA18092
23	54	91.5	140	22	AA18092
24	54	91.5	140	22	AA18092
25	54	91.5	140	22	AA18092
26	54	91.5	140	22	AA18092
27	54	91.5	140	22	AA18092
28	54	91.5	140	22	AA18092
29	54	91.5	140	22	AA18092
30	54	91.5	140	22	AA18092
31	54	91.5	140	22	AA18092
32	54	91.5	140	22	AA18092
33	54	91.5	140	22	AA18092
34	54	91.5	140	22	AA18092
35	54	91.5	140	22	AA18092
36	54	91.5	140	22	AA18092
37	54	91.5	140	22	AA18092
38	54	91.5	140	22	AA18092
39	54	91.5	140	22	AA18092
40	54	91.5	140	22	AA18092
41	54	91.5	140	22	AA18092
42	54	91.5	140	22	AA18092
43	54	91.5	140	22	AA18092
44	54	91.5	140	22	AA18092
45	54	91.5	140	22	AA18092

ALIGNMENTS

RESULT 1
AA178322
ID AA178322 standard; Protein: 10 AA.
XX
AC AA178322;
XX
DT 04-MAY-2000 (first entry)
XX
DE Anti-zeta-chain antibody 2-B-5 VH-region CDR1 protein sequence.
XX
KW Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
KW complementary determining region; CDR; autoimmune disease; cytotoxic;
KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.
XX
OS Rattus norvegicus.
XX
PN WO200003016-A1.
XX
PD 20-JAN-2000.
XX
PF 09-JUL-1999; 99WO-EP04838.
XX
PR 10-JUL-1998; 98EP-0112867.
XX
PA (CONN-) CONNEX GMBH.
XX
PI Reiter C;
XX
DR WPI: 2000-160926/14.
XX
PT N-PSDB: AA288320.
XX
New oligonucleotide, polypeptide, antibody useful for treating

PT autoimmune disease, immune deficiencies, T-cell malignancies and
PT infectious diseases -
XX Claim 10; Fig 6; 79pp; English.
XX
CC The present invention describes a nucleic acid molecule (I) encoding at
CC least one complementary determining region (CDR) of a variable region of
CC an antibody which specifically interacts with the extracellular domain of
CC the human zeta-chain. The antibody whose CDR of a variable region is
CC encoded by (I), is obtained by immunising a rat with jurkat cells and
CC subsequently with a conjugate comprising a carrier molecule and a
CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
CC anti-zeta-chain antibody is useful for the treatment and prevention of
CC autoimmune diseases, immune deficiencies, T-cell malignancies,
CC infectious diseases and the suppression of immune response preferably in
CC order to avoid graft rejection after organ transplantation, malignancies,
CC or viral infections. The antibody and fragments of it, can be useful for
CC the enhancement or suppression of NK-cell dependent immunity or for the
CC treatment of NK-cell derived malignancies. It can also be useful for the
CC determination of zeta-chain or eta-chain expression on NK-cells,
CC T-lymphocytes or their precursors. The present sequence represents the
CC CDR1 of the VH-region of the anti-zeta-chain antibody 2-B-5, produced
CC by rats from the present invention.
XX
SQ Sequence 10 AA:

Query Match 100.0%; Score 59; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
| | | | | | | | | |
Db 1 GYFTSYDMH 10

RESULT 2
AAV78325
ID AAV78325 standard; protein: 123 AA.
XX
AC AAV78325;

DT 04-MAY-2000 (first entry)
XX
DE Anti-zeta-chain antibody 2-B-5 VH-region protein sequence.
XX

KW Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
KW complementary determining region; CDR; autoimmune disease; cytostatic;
KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.
XX
OS Rattus norvegicus.
XX
PN WO200003016-A1.
XX
PD 20-JAN-2000.
XX
PF 09-JUL-1999; 99WO-EP04838.
XX
PR 10-JUL-1998; 98EP-0112867.
XX
PA (CONN-) CONNEX GMBH.
XX
PI Reiter C;
XX
DR WPI: 2000-160926/14.
DR N-PSDB: AA288323.
XX
XX

PT New oligonucleotide, polypeptide, antibody useful for treating
PT autoimmune disease, immune deficiencies, T-cell malignancies and
PT infectious diseases -
XX Claim 8; Fig 6; 79pp; English.
XX
PS

CC The present invention describes a nucleic acid molecule (I) encoding at
CC least one complementary determining region (CDR) of a variable region of
CC an antibody which specifically interacts with the extracellular domain of
CC the human zeta-chain. The antibody whose CDR of a variable region is
CC encoded by (I), is obtained by immunising a rat with jurkat cells and
CC subsequently with a conjugate comprising a carrier molecule and a
CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
CC anti-zeta-chain antibody is useful for the treatment and prevention of
CC autoimmune diseases, immune deficiencies, T-cell malignancies,
CC infectious diseases and the suppression of immune response preferably in
CC order to avoid graft rejection after organ transplantation, malignancies,
CC or viral infections. The antibody and fragments of it, can be useful for
CC the enhancement or suppression of NK-cell dependent immunity or for the
CC treatment of NK-cell derived malignancies. It can also be useful for the
CC determination of zeta-chain or eta-chain expression on NK-cells,
CC T-lymphocytes or their precursors. The present sequence represents the
CC VH-region of the anti-zeta-chain antibody 2-B-5, produced by rats from
CC the present invention.
XX
SQ Sequence 123 AA:

Query Match 100.0%; Score 59; DB 21; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
| | | | | | | | | |
Db 26 GYFTSYDMH 35

RESULT 3
AAV78328
ID AAV78328 standard; protein: 532 AA.
XX
AC AAV78328;

DT 04-MAY-2000 (first entry)
XX

DE Bispecific anti-zeta-chain/anti-EPCAM antibody protein sequence.
XX

KW Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
KW complementary determining region; CDR; autoimmune disease; cytostatic;
KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.
XX
OS Rattus norvegicus.
XX
PN WO200003016-A1.
XX
PD 20-JAN-2000.
XX
PF 09-JUL-1999; 99WO-EP04838.
XX
PR 10-JUL-1998; 98EP-0112867.
XX
PA (CONN-) CONNEX GMBH.
XX
PI Reiter C;
XX
DR WPI: 2000-160926/14.
DR N-PSDB: AA288358.
XX
XX

PT New oligonucleotide, polypeptide, antibody useful for treating
PT autoimmune disease, immune deficiencies, T-cell malignancies and
PT infectious diseases -
XX Example 9; Page 74-76; 79pp; English.
XX
PS

CC The present invention describes a nucleic acid molecule (I) encoding at
CC least one complementary determining region (CDR) of a variable region of
CC an antibody which specifically interacts with the extracellular domain of
CC the human zeta-chain. The antibody whose CDR of a variable region is

CC encoded by (I), is obtained by immunising a rat with jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,
 CC infectious diseases and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC or viral infections. The antibody, and fragments of it, can be useful for
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC treatment of NK-cell derived malignancies. It can also be useful for the
 CC determination of zeta-chain or eta-chain expression on NK-cells,
 CC T-lymphocytes or their precursors. The present sequence represents a
 CC bispecific anti-zeta-chain/anti-EpCAM antibody, from an example from
 CC the present invention.

XX Sequence 532 AA:

Query Match 100.0%; Score 59; DB 21; Length 532;
 Best Local Similarity 100.0%; Pred. No. 0.023; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

OY 1 GYFTSYDMH 10
 |||||||||
 DB 167 GYFTSYDMH 176

RESULT 4

ABG04634
 ID ABG04634 standard; Protein: 850 AA.

XX ABG04634:

XX 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #4625.

XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-Oct-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

XX N-PSDB: AMS68821.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

XX Claim 20: SEQ ID NO 34993; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 850 AA:

Query Match 93.2%; Score 55; DB 22; Length 850;
 Best Local Similarity 90.0%; Pred. No. 0.19; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0;

OY 1 GYFTSYDMH 10
 |||||||||
 DB 298 GYFTSYDMH 307

RESULT 5

AAV21816
 ID AAV21816 standard; Protein: 122 AA.

XX AAV21816:

XX 10-SEP-1999 (first entry)

XX Anti-STX1 heavy chain variable region.

XX Humanised; monoclonal antibody; Mab; Shiga toxin; immunoglobulin;

XX Ig constant region; enterohemorrhagic Escherichia coli; EHEC; uremia;

XX edema; bloody diarrhea; hemorrhagic colitis; hemolytic uremic syndrome;

XX thrombocytopenia; EHEC-mediated disease; anti-STX1.

XX Shigella dysenteriae.

XX Key Location/Qualifiers

XX MISC-difference 23 /note= "encoded by AAG"

XX Region 31..35 /note= "complementarily determining region (CDR) 1;
 specifically claimed for in claim 10"

XX Region 50..66 /note= "complementarily determining region (CDR) 2;
 specifically claimed for in claim 10"

XX Region 99..111 /note= "complementarily determining region (CDR) 3;
 specifically claimed for in claim 10"

XX WO9932645-A1.

XX 01-JUL-1999.

XX 22-DEC-1998; 98WO-US27267.

XX 18-DEC-1998; 98US-0215163.

XX 23-DEC-1997; 97US-0086635.

XX (MELT/) MELTON-CELSA A.

XX (O'BRIEN A D. (SCHMILT C K. (STINSON J L. (WONG H. (WONG H.

XX Melton-Celsa A, O'Brien AD, Schmitt CK, Stinson JL;

XX Wong H;

XX WPI: 1999-418935/35.

DR N-PSDB: AAX82028.
 XX
 PT Humanized monoclonal antibodies against Shiga toxins, useful for
 PT protection against enterohemorrhagic Escherichia coli or other Shiga
 PT toxin producing bacteria
 XX
 PS Claim 5: Fig 3: 75pp: English.
 XX
 CC The invention relates to humanised monoclonal antibodies (Mab) against
 CC Shiga toxins. The humanised Mab that binds to Shiga toxin comprises a
 CC constant and a variable region, where: (a) the constant region contains
 CC at least part of a human Immunoglobulin (Ig) constant region; and (b) the
 CC variable region contains at least part of a non-human Ig variable region.
 CC Host cells transformed with vectors encoding a humanised Mab against
 CC Shiga toxin type 2 is useful for treating a patient with an infection
 CC caused by enterohemorrhagic Escherichia coli (EHEC) or other Shiga toxin
 CC produced by bacteria. The humanised Mab can also be used to reduce illness
 CC caused by EHEC or other Shiga toxin producing bacteria. EHEC are
 CC associated with food-borne outbreaks of bloody diarrhoea (hemorrhagic
 CC colitis) and the hemolytic uremic syndrome. In particular, the humanised
 CC Mabs ameliorate edema, thrombocytopenia and uremia associated with EHEC-
 CC mediated disease. The present sequence represents an anti-STX1 heavy
 CC chain variable region.
 XX
 SQ Sequence 122 AA:
 Query Match 91.5%; Score 54; DB 20; Length 122;
 Best Local Similarity 90.0%; Pred. No. 0.04;
 Matches 9: Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GYFTSYDMH 10
 DB 26 GYFTSYDMH 35
 XX
 RESULT 6
 AAP70627 ID AAP70627 standard; protein: 140 AA.
 XX
 AC AAP70627;
 XX
 DT 03-OCT-2002 (updated)
 DT 09-APR-1991 (first entry)
 XX
 DE Sequence encoded by the 2H7 VH sequence which contains JH1
 DE sequences and DSE.2 sequence elements.
 XX
 KW Chimeric antibody: Anti-cancer antibody.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.
 XX
 FH Key
 FH Location/Qualifiers
 FT 1..19
 FT /*tag= a
 FT /label=leader peptide
 FT 20..49
 FT /*tag= b
 FT /label=FRL
 FT 50..54
 FT /*tag= c
 FT /label=CDR1
 FT 55..68
 FT /*tag= d
 FT /label=FRL
 FT 69..85
 FT /*tag= e
 FT /label=CDR2
 FT 86..117
 FT /*tag= f
 FT /label=FRL
 FT 118..130
 FT /*tag= g
 FT Region
 FT Region
 FT Region
 FT Region

FT
 FT Region
 FT 125..140
 FT /*tag= h
 FT /label=JH1
 FT 131..140
 FT /*tag= i
 FT /label=FR4
 FT
 PN W08702671-A.
 XX
 PD 07-MAY-1987.
 XX
 PD 27-OCT-1986: 86W0-US02269.
 XX
 PR 01-NOV-1985: 85US-0793980.
 XX
 PA (ITGE-) INT GENETIC ENG INC.
 PA (ROBI/) ROBINSON R. R.
 XX
 PI ROBINSON RR, Liu AY, Horwitz AH, Wall R;
 XX
 DR WPI: 1987-136004/19.
 DR N-PSDB: AAN70971.
 XX
 PT Prodn. of immunoglobulin chains and molecules - is by recombinant
 PT DNA procedures, with chimeric antibodies etc. related to cancer
 PT specific antigens.
 XX
 PS Example: Fig 21: 126pp: English.
 XX
 CC The patentors claim a chimeric antibody molecule comprising 2 light
 CC chains and 2 heavy chains, each comprising a constant human region
 CC and a variable non-human region. Coding sequences for the Ig chains
 CC are also claimed. The invention provides consensus sequences of
 CC light and heavy chain J regions useful in the design of
 CC oligonucleotides (UTGs) for use as primers or probes for cloning
 CC immunoglobulinlight or heavy chain mRNAs or genes. Depending on the
 CC nature of design of a particular URG, it may be capable of
 CC hybridizing to all Ig mRNAs or genes containing a single specific J
 CC sequence. URG denotes universal Immunoglobulin gene.
 CC (updated on 03-OCT-2002 to add missing OS field.)
 XX
 SQ Sequence 140 AA:
 Query Match 91.5%; Score 54; DB 8; Length 140;
 Best Local Similarity 90.0%; Pred. No. 0.045;
 Matches 9: Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GYFTSYDMH 10
 DB 45 GYFTSYDMH 54
 XX
 RESULT 7
 AAP94780 ID AAP94780 standard; protein: 140 AA.
 XX
 AC AAP94780;
 XX
 DT 06-JUL-1990 (first entry)
 DT 2 H7 VH gene.
 XX
 DE 2 H7 VH gene.
 XX
 KW Antibodies: passive immunisation; pH3-12a; ss.
 KW Synthetic.
 XX
 OS Synthetic.
 OS
 FH Key
 FH Location/Qualifiers
 FT 1..19
 FT /label=leader peptide.
 FT 20..49
 FT /label=FRL.
 FT 50..54
 FT Domain
 FT Domain


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PF 01-NOV-1985; 85US-0793980.
XX
PR 29-MAR-1990; 90US-0501092.
PR 01-NOV-1985; 85US-0793980.
PR 27-OCT-1986; 86WO-US02269.
PR 24-JUL-1987; 87US-0077528.
PR 11-JAN-1988; 88US-0142039.
PR 08-DEC-1992; 92US-0987555.
PR 18-AUG-1994; 94US-0299085.
XX
PA (XOMA ) XOMA CORP.
XX
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
PI Wall R, Wilcox GL;
XX
DR N-PSDB; AAT36316.
XX
PT WPI: 1997-107579/10.
XX
CC Nucleic acid encoding immunoglobulin fragment - comprising
CC di:ctronic transcription unit with pectate lyase signal sequences
XX
PS Example: Fig 21; 95pp; English.
XX
CC The present sequence is the heavy chain variable region of
CC the 2H7 antibody. The 2H7 cDNA was used in the preparation of
CC a novel polynucleotide molecule encoding an Ig fragment. The DNA
CC molecule comprises 2 DNA sequences encoding 2 pectate lyase
CC secretion signal sequences respectively linked to a DNA sequence
CC encoding an Ig Fd molecule or Ig light chain, operably linked to a
CC single prokaryotic promoter so as to form a di:ctronic
CC transcription unit, provided that the Ig fragment can bind an
CC antigen and is produced and secreted by an E. coli host cell when
CC the nucleic acid molecule is expressed in the host cell.
CC The polynucleotide molecule is used for the production of
CC recombinant antibodies, which can be used for passive immunisation
CC without negative immune reactions (e.g. serum sickness and
CC anaphylactic shock), in labelled forms as immunoassay or imaging
CC reagents, in complement mediated lysis and for therapeutic
CC purposes when coupled to a toxin or other therapeutic agent.
XX
SQ Sequence 140 AA:
Query Match 91.5%; Score 54; DB 18; Length 140;
Best Local Similarity 90.0%; Pred. No. 0.045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 GYTFTSYDMH 10
DB 45 GYTFTSYNMH 54
RESULT 10
AAW16343
ID AAW16343 standard; Protein; 140 AA.
XX
AC AAW16343;
XX
DT 04-SEP-1997 (first entry)
XX
DE 2H7 heavy chain variable sequence.
XX
KW Antibody engineering; heavy chain; light chain; chimaeric antibody;
KW passive immunisation; diagnosis; hybridoma; monoclonal antibody;
KW 2H7; B-cell antigen; Bp35.
XX
XX OS Mus sp.
XX
FH Key Location/Qualifiers
FT 1..19
FT Peptide /label= Sig-peptide
FT 20..49
FT Region /label= FRI
FT /note= "framework region 1"

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FT Region 50..54
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT Region 55..68
FT /label= FR2
FT /note= "framework region 2"
FT Region 69..85
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT Region 86..117
FT /label= FR3
FT /note= "framework region 3"
FT Region 118..130
FT /label= CDR3
FT /note= "Complementarity determining region 3"
FT Region 131..140
FT /label= FR4
FT /note= "framework region 4"
XX
XX US5618920-A.
XX
PD 08-APR-1997.
XX
XX
PF 01-NOV-1985; 85US-0793980.
XX
PR 29-MAR-1990; 90US-0501092.
PR 01-NOV-1985; 85US-0793980.
PR 27-OCT-1986; 86WO-US02269.
PR 24-JUL-1987; 87US-0077528.
PR 11-JAN-1988; 88US-0142039.
PR 17-APR-1992; 92US-0870404.
PR 29-APR-1994; 94US-0235225.
XX
XX (XOMA ) XOMA CORP.
XX
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
PI Wall R, Wilcox GL;
XX
DR WPI: 1997-225473/20.
DR N-PSDB; AAT70868.
XX
PT Secretable immunoglobulin heavy and light chain fragments - capable
PT of assembling into chimeric antibodies, useful for e.g. passive
PT immunisation, diagnosis, etc
XX
PS Example 4; Fig 21; 96pp; English.
XX
CC A polypeptide (AAW16343) comprises the heavy chain variable region of
CC mouse monoclonal antibody 2H7, which recognises human B-cell surface
CC antigen Bp35. It is encoded by a cDNA clone (AAT70868) obtd. from a
CC 2H7 cDNA library by PCR amplification. The 2H7 light chain variable
CC sequence (AAW16344) is also provided. A novel human-mouse chimaeric
CC antibody with specificity for the human B-cell antigen has been
CC constructed.
XX
SQ Sequence 140 AA:
Query Match 91.5%; Score 54; DB 18; Length 140;
Best Local Similarity 90.0%; Pred. No. 0.045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 GYTFTSYDMH 10
DB 45 GYTFTSYNMH 54
RESULT 11
AAW10242
ID AAW10242 standard; Protein; 140 AA.
XX
AC AAW10242;
XX
DT 06-AUG-1997 (first entry)

```



```

XX DE Heavy chain variable sequence of 2H7.
XX
XX KW pectate lyase; signal sequence; Gram-negative bacterium; immunoglobulin;
XX KW protein production; human; constant region; passive immunisation; toxin;
XX KW serum sickness; anaphylaxis; sweetener; thymatin; cytoplasm; periplasm;
XX KW antibody; Ig; heavy-chain; hepatitis; mouse; lung carcinoma; cancer;
XX KW myeloma cell.
XX OS Mus musculus.
XX
XX Key Location/Qualifiers
XX FH 1..19
XX FT /note= "leader peptide"
XX FT 20..49
XX FT /note= "framework region 1"
XX FT 50..54
XX FT /note= "complementarily determining region 1"
XX FT 55..68
XX FT /note= "framework region 2"
XX FT 69..85
XX FT /note= "complementarily determining region 2"
XX FT 86..117
XX FT /note= "framework region 3"
XX FT 118..130
XX FT /note= "complementarily determining region 3"
XX FT 131..140
XX FT /note= "framework region 4"
XX PN US5576195-A.
XX
XX 19-NOV-1996.
XX
XX 01-NOV-1985; 85US-0793980.
XX
XX 29-MAR-1990; 90US-0501092.
XX PR 01-NOV-1985; 85US-0793980.
XX PR 27-OCT-1986; 86WO-US02269.
XX PR 24-JUL-1987; 87US-0077528.
XX PR 11-JAN-1988; 88US-0142039.
XX PR 08-DEC-1992; 92US-0987555.
XX PR 22-FEB-1993; 93US-0020671.
XX PR 09-DEC-1994; 94US-0357234.
XX
XX (XOMA ) XOMA CORP.
XX PI Better M, Lei S, Robinson RR, Wilcox GL;
XX DR WPI: 1997-011254/01.
XX DR N-PSDB; AAT51042.
XX
XX Improved prodn. of protein in Gram -ve bacteria using signal
XX PT sequence - from pectate lyase to ensure transport of protein from
XX PT the cytoplasm, esp. for prodn. of antibodies
XX
XX Example 4; Fig 21; 86pp; English.
XX
XX This sequence represents the heavy chain variable region of the 2H7
XX mouse monoclonal antibody. The 2H7 antibody recognises the human B-cell
XX surface antigen BP35, which plays a role in B-cell activation. This
XX sequence was used in a human-mouse chimeric antibody with human B-cell
XX antigen specificity, that was produced using the method of the invention.
XX The method of the invention is for the production of a protein in a
XX Gram-negative bacterium. The method improves on current techniques, by
XX using a vector including DNA encoding the pectate lyase signal sequence
XX (see AAT51034), attached to the sequence encoding the protein for
XX production. The method is especially used to make immunoglobulins (Ig),
XX particularly those with a human constant region, suitable for passive
XX immunisation (without risk of serum sickness or anaphylaxis) or for in
XX vivo/in vitro diagnosis and imaging. The Ig may also be used
XX therapeutically, optionally coupled to toxins, etc. Alternatively the
XX protein to be produced is the sweetener thymatin. The presence of this
XX signal sequence means that the protein is exported from the cytoplasm

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CC and can be recovered from the culture medium or periplasm, in active and
CC correctly folded form. The method allows the class of any antibody to be
CC switched, e.g. most human-human Ig are of M class, easily reduced and
CC aggregated, and these can now be changed to G, A or E classes.
XX
XX Sequence 140 AA:
XX
XX Query Match 91.5%; Score 54; DB 18; Length 140;
XX Best Local Similarity 90.0%; Pred. No. 0.045;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GYFTSYDMH 10
XX DB 45 GYFTSYNMH 54
XX
XX RESULT 12
XX ID AAM41070
XX AA AAM41070 standard; Protein; 140 AA.
XX
XX AC AAM41070;
XX
XX 01-JUN-1998 (first entry)
XX
XX Mouse 2H7 antibody heavy chain variable region.
XX
XX KW Mouse; murine; heavy chain; variable region;
XX KW immunoglobulin fragment production; Ig fragment production;
XX KW monoclonal antibody 2H7; human B-cell surface antigen.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX FH 1..19
XX FT /label= sig-peptide
XX FT 20..140
XX FT /label= mat-peptide
XX
XX US5693493-A.
XX
XX 02-DEC-1997.
XX
XX 25-MAY-1995; 95US-0450731.
XX
XX 29-MAR-1990; 90US-0501092.
XX PR 01-NOV-1985; 85US-0793980.
XX PR 27-OCT-1986; 86WO-US02269.
XX PR 24-JUL-1987; 87US-0077528.
XX PR 11-JAN-1988; 88US-0142039.
XX PR 08-DEC-1992; 92US-0987555.
XX PR 18-AUG-1994; 94US-0299085.
XX PR 25-MAY-1995; 95US-0450731.
XX
XX (XOMA ) XOMA CORP.
XX PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
XX PI Wall R, Wilcox GL;
XX DR WPI: 1998-031749/03.
XX DR N-PSDB; AAV03926.
XX
XX Production of chimeric antibody fragments - by culturing E. coli
XX PT transformed with dicistronic expression cassette
XX
XX Example IV; Fig 21; 98pp; English.
XX
XX The present sequence was used in the development of a novel method
XX for the production of an immunoglobulin (Ig) fragment capable of
XX binding an antigen. The method comprises culturing an E. coli host
XX cell that has been transformed with a nucleic acid molecule encoding the
XX Ig fragment, under conditions so that the Ig fragment is produced
XX and secreted. The nucleic acid molecule comprises DNA sequences
XX encoding: (a) pectate lyase secretion signal sequence operably

```

CC linked to a DNA sequence encoding at least the variable region of
 CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
 CC operably linked to a DNA sequence encoding at least the variable
 CC region of an Ig light chain, where (a) and (b) are operably linked
 CC to a single prokaryotic promoter to form a dicistronic
 CC transcription unit. The method is used to produce chimeric Fab
 CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
 CC against human B-cell surface antigen. The invention provides a
 CC novel approach for producing genetically engineered antibodies of
 CC desired variable region specificity and constant region
 CC properties. The cloned Ig gene products can be produced by
 CC expression in genetically engineered organisms. The application of
 CC chemical gene synthesis, recombinant DNA cloning and production of
 CC specific Ig chains in various organisms provides an effective
 CC solution for the efficient large scale production of human
 CC monoclonal antibodies. The invention also provides a solution to
 CC the problem of class switching antibody molecules.

SO Sequence 140 AA:

Query Match 91.5%; Score 54; DB 19; Length 140;
 Best Local Similarity 90.0%; Pred. No. 0.045;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
 |||||:
 DB 45 GYFTSYNMH 54

RESULT 13

AAW47513
 ID AAW47513 standard; Protein; 140 AA.

AC AAW47513:

DT 05-JUN-1998 (first entry)

DE Mouse 2H7 antibody heavy chain variable region.

XX Mouse; murine; heavy chain; variable region;

KW immunoglobulin fragment production; Ig fragment production;
 KW monoclonal antibody 2H7; human B-cell surface antigen.

OS Mus sp.

XX Key Location/Qualifiers

FT Peptide 1..19 /label= sig-peptide

FT Peptide 20..140 /label= mat-peptide

XX US5698435-A.

PD 16-DEC-1997.

PE 06-JUN-1995; 95US-0467140.

XX 29-MAR-1990; 90US-0501092.

PR 01-NOV-1985; 85US-0793980.

PR 27-OCT-1986; 86WO-US02269.

PR 24-JUL-1987; 87US-0077528.

PR 11-JAN-1988; 88US-0142039.

PR 08-DEC-1992; 92US-0987555.

PR 18-AUG-1994; 94US-0299085.

PR 06-JUN-1995; 95US-0467140.

XX (XOMA) XOMA CORP.

PI Better M. Horwitz AH, Lei S, Liu AY, Robinson RR;

XX WPI; 1998-051492/05.

DR N-PSDB; AA18557.

XX DNA encoding secretable immunoglobulin fragments - comprising at
 PT least the variable regions of light or heavy chains
 XX
 PS Example IV; Fig 21; 98pp; English.

CC The present sequence was used in the development of a novel method
 CC for the production of an immunoglobulin (Ig) fragment capable of
 CC binding an antigen. The method comprises culturing an E. coli host
 CC that has been transformed with a nucleic acid molecule encoding the
 CC Ig fragment, under conditions so that the Ig fragment is produced
 CC and secreted. The nucleic acid molecule comprises DNA sequences
 CC encoding: (a) pectate lyase secretion signal sequence operably
 CC linked to a DNA sequence encoding at least the variable region of
 CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
 CC operably linked to a DNA sequence encoding at least the variable
 CC region of an Ig light chain, where (a) and (b) are operably linked
 CC to a single prokaryotic promoter to form a dicistronic
 CC transcription unit. The method is used to produce chimeric Fab
 CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
 CC against human B-cell surface antigen. The invention provides a
 CC novel approach for producing genetically engineered antibodies of
 CC desired variable region specificity and constant region
 CC properties. The cloned Ig gene products can be produced by
 CC expression in genetically engineered organisms. The application of
 CC chemical gene synthesis, recombinant DNA cloning and production of
 CC specific Ig chains in various organisms provides an effective
 CC solution for the efficient large scale production of human
 CC monoclonal antibodies. The invention also provides a solution to
 CC the problem of class switching antibody molecules.

SO Sequence 140 AA:

Query Match 91.5%; Score 54; DB 19; Length 140;
 Best Local Similarity 90.0%; Pred. No. 0.045;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
 |||||:
 DB 45 GYFTSYNMH 54

RESULT 14

AAW47520
 ID AAW47520 standard; Protein; 140 AA.

AC AAW47520:

DT 05-JUN-1998 (first entry)

DE Mouse 2H7 antibody heavy chain variable region.

XX Mouse; murine; heavy chain; variable region;

KW immunoglobulin fragment production; Ig fragment production;
 KW monoclonal antibody 2H7; human B-cell surface antigen.

OS Mus sp.

XX Key Location/Qualifiers

FT Peptide 1..19 /label= sig-peptide

FT Peptide 20..140 /label= mat-peptide

XX US5698417-A.

PD 16-DEC-1997.

PE 06-JUN-1995; 95US-0466203.

XX 29-MAR-1990; 90US-0501092.

PR 01-NOV-1985; 85US-0793980.

PR 27-OCT-1986; 86WO-US02269.

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PR 24-JUL-1987; 87US-0077528.
PR 11-JAN-1988; 88US-0142039.
PR 08-DEC-1992; 92US-0987555.
PR 18-AUG-1994; 94US-0290985.
PR 25-MAY-1995; 95US-0450731.
PR 06-JUN-1995; 95US-0466203.
PA (XOMA ) XOMA CORP.
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
PI Wall R, Wilcox GL;
XX WPI: 1998-051487/05.
DR N-PSDB: AAV18593.
XX
XX Production of recombinant immunoglobulin fragment - comprising Fd
PT molecule and light chain
XX
XX Example IV; Fig 21; 98pp; English.
XX
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
CC against human B-cell surface antigen. The invention provides a
CC novel approach for producing genetically engineered antibodies of
CC desired variable region specifically and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
XX
SQ Sequence 140 AA;
XX
Query Match 91.5%; Score 54; DB 19; Length 140;
Best Local Similarity 90.0%; Pred. No. 0.045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYFTSYDMH 10
   |||||:|
Db 45 GYFTSYNMH 54

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RESULT 15
AAW89540 standard; Protein; 140 AA.
ID AAW89540;
XX AAW89540;
AC
XX 30-MAR-1999 (first entry)
DT
XX
XX Mouse antibody 2H7 heavy chain variable region.
DE
XX
XX pelB pectate lyase; secretion signal; chimeric antibody;
KW heavy chain; B-cell antigen; antibody 2H7.
XX
XX Mus sp.
OS
XX
XX US5846818-A.
PN
XX

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PD 08-DEC-1998.
XX
XX 06-JUN-1995; 95US-0472696.
PF
XX 29-MAR-1990; 90US-0501092.
PR 01-NOV-1985; 85US-0793980.
PR 24-JUL-1987; 87US-0077528.
PR 11-JAN-1988; 88US-0142039.
PR 08-DEC-1992; 92US-0987555.
PR 22-FEB-1993; 93US-0020671.
PR 09-DEC-1994; 94US-0357234.
PR 06-JUN-1995; 95US-0472696.
PA (XOMA ) XOMA CORP.
XX
XX Better M, Horowitz AH, Lei S, Liu AY, Robinson RR;
PI Wall R, Wilcox GL;
XX
XX WPI: 1999-059072/05.
DR N-PSDB: AAV82357.
XX
XX pelB pectate lyase signal sequence - and vector for expression of
PT secreted proteins in Gram-negative bacteria
XX
XX Example 4; Fig 21; 98pp; English.
XX
CC The present sequence represents the mouse antibody 2H7 heavy chain
CC variable region. Antibody 2H7 is specific for human B-cell antigen. The
CC antibody sequence was used to construct a chimeric human-mouse antibody,
CC in the course of the invention. The chimeric antibody is expressed in a
CC secretion vector comprising a pelB pectate lyase secretion signal
CC peptide. The pelB pectate lyase secretion sequence is useful for
CC producing a protein such as a chimeric antibody in a bacterial host.
XX
SQ Sequence 140 AA;
XX
Query Match 91.5%; Score 54; DB 20; Length 140;
Best Local Similarity 90.0%; Pred. No. 0.045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYFTSYDMH 10
   |||||:|
Db 45 GYFTSYNMH 54

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Search completed: February 25, 2003, 10:32:29
Job Time : 4.3 secs

Sat Mar 1 08:17:10 2003

us-09-743-482a-8.open.rapb

Page 1

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OM protein - protein search, using sw model

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(without alignments)
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Sequence: 1 GYFTSYDMH 10

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Gapop 10.0, Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	91.5	140	9	US-09-905-928-6
2	51	86.4	92	10	US-09-864-761-38566
3	51	86.4	102	10	US-09-864-761-43848
4	51	86.4	470	10	US-09-859-053-32
5	51	86.4	470	10	US-09-859-053-36
6	50	84.7	120	12	US-10-025-687-2
7	50	84.7	152	10	US-09-881-823-20
8	50	84.7	438	9	US-09-903-327A-6
9	50	84.7	448	10	US-09-917-410-6
10	50	84.7	456	9	US-09-903-327A-2
11	50	84.7	493	9	US-09-903-327A-13
12	50	84.7	510	9	US-09-903-327A-12
13	50	84.7	597	9	US-09-903-327A-11
14	50	84.7	613	9	US-09-903-327A-14
15	49	83.1	122	1	US-08-779-784-28
16	49	83.1	140	10	US-09-748-960-4
17	49	83.1	143	1	US-08-779-784-26
18	49	83.1	180	10	US-09-748-960-6
19	48	81.4	92	10	US-09-864-761-47202

20	48	81.4	138	1	US-08-779-784-31	Sequence 31, Appl
21	48	81.4	139	12	US-10-006-773-13	Sequence 13, Appl
22	48	81.4	146	10	US-09-925-299-1050	Sequence 1050, Ap
23	48	81.4	149	9	US-09-187-693-57	Sequence 57, Appl
24	48	81.4	153	10	US-09-861-294-4	Sequence 4, Appl1
25	48	81.4	232	10	US-09-754-998-2	Sequence 2, Appl1
26	48	81.4	232	10	US-09-811-384-10	Sequence 10, Appl
27	48	81.4	241	10	US-09-940-166A-1	Sequence 1, Appl1
28	48	81.4	300	10	US-09-940-166A-7	Sequence 7, Appl
29	48	81.4	300	10	US-09-811-384-12	Sequence 12, Appl
30	47	79.7	229	10	US-09-808-037-6	Sequence 6, Appl1
31	46	78.0	98	12	US-10-025-687-17	Sequence 17, Appl
32	46	78.0	116	10	US-09-741-843-4	Sequence 4, Appl1
33	46	78.0	116	10	US-09-741-843-8	Sequence 8, Appl1
34	46	78.0	116	10	US-09-741-843-9	Sequence 9, Appl1
35	46	78.0	132	9	US-09-982-107-14	Sequence 14, Appl
36	46	78.0	230	10	US-09-995-693-2	Sequence 2, Appl1
37	46	78.0	470	10	US-09-859-053-28	Sequence 28, Appl
38	45	76.3	669	9	US-09-807-721-2	Sequence 16, Appl
39	45	76.3	97	10	US-09-158-120A-16	Sequence 7, Appl
40	45	76.3	119	9	US-09-144-886-73	Sequence 16, Appl
41	45	76.3	119	9	US-09-144-886-74	Sequence 7, Appl
42	45	76.3	127	10	US-09-998-831-7	Sequence 7, Appl1
43	45	76.3	142	10	US-09-964-329A-13	Sequence 13, Appl
44	45	76.3	142	10	US-09-855-153-13	Sequence 13, Appl
45	45	76.3	142	10	US-09-854-811-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-905-928-6
Sequence 6, Application US/09905928
Publication No. US20030021781A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lympho
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/905,928
FILING DATE: 17-JUL-2001
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/475,813
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:

PRIOR FILING DATE: 2001-01-29

;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43848
LENGTH: 102
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AB019440.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.89
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.95
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OTHER INFORMATION: EST_HUMAN HIT: AM405458.1, EVALU2 3.00e-43
OTHER INFORMATION: SWISSPROT HIT: P01766, EVALU2 2.00e-39
US-09-864-761-43848

Query Match 86.4%; Score 51; DB 10; Length 102;
Best Local Similarity 80.0%; Pred. No. 0.024;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
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DB 17 GFTSSYDMH 26

RESULT 4
US-09-859-053-32
Sequence 32, Application US/09859053
Patent No. US20020102658A1
GENERAL INFORMATION:
APPLICANT: Tsuji, Takashi
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658A1uaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-053-32

Query Match 86.4%; Score 51; DB 10; Length 470;
Best Local Similarity 80.0%; Pred. No. 0.11;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
1:|||||
DB 45 GFTSSYDMH 54

RESULT 5
US-09-859-053-36
Sequence 36, Application US/09859053
Patent No. US20020102658A1
GENERAL INFORMATION:
APPLICANT: Tsuji, Takashi
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658A1uaki

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-053-36

Query Match 86.4%; Score 51; DB 10; Length 470;
Best Local Similarity 80.0%; Pred. No. 0.11;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
1:|||||
DB 45 GFTSSYDMH 54

RESULT 6
US-10-025-687-2
Sequence 2, Application US/10025687
Patent No. US20020142255A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-025-687-2

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Best Local Similarity 90.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
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DB 26 GYFTSYDMH 35

RESULT 7
US-09-881-823-20
Sequence 20, Application US/09881823
Patent No. US20020068066A1
GENERAL INFORMATION:
APPLICANT: SHI, WENYUAN
APPLICANT: ANDERSON, MAXWELL
APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
APPLICANT: WIMS, LERITTA
APPLICANT: CHEN, LI
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
FILE REFERENCE: 22851-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20

NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 152
TYPE: PRT
ORGANISM: Murine
US-09-881-823-20

Query Match 84.7%; Score 50; DB 10; Length 152;
Best Local Similarity 80.0%; Pred. No. 0.054;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
|||||1:11
DB 45 GYFTSYDMH 54

RESULT 8
US-09-903-327A-6
Sequence 6, Application US/09903327A
Patent No. US2002016433A1
GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: GENE
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 438
TYPE: PRT
ORGANISM: Mouse
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (0)...(0)
OTHER INFORMATION: Portion of DAV-1 heavy chain used for fusion protein
OTHER INFORMATION: bifunctional antibody
US-09-903-327A-6

Query Match 84.7%; Score 50; DB 9; Length 438;
Best Local Similarity 80.0%; Pred. No. 0.16;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
|||||1:11
DB 45 GYFTSYDMH 54

RESULT 9
US-09-917-410-6
Sequence 6, Application US/09917410
Patent No. US20020098183A1
GENERAL INFORMATION:
APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
CO. Man S.
TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
PREVENTION OF ACUTE ORGAN DAMAGE AFTER
EXTRACORPOREAL BLOOD CIRCULATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII, Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/917,410
FILING DATE: 26-Jul-2001
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: <unknown>

APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, NO. US20020098183A1man D.

REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 448 amino acid residues
TYPE: amino acid
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-917-410-6

Query Match 84.7%; Score 50; DB 10; Length 448;
Best Local Similarity 90.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
|||||1:11
DB 26 GYFTSYDMH 35

RESULT 10
US-09-903-327A-2
Sequence 2, Application US/09903327A
Patent No. US2002016433A1
GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR
TITLE OF INVENTION: GENE
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 456
TYPE: PRT
ORGANISM: Mouse
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (0)...(0)
OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody
US-09-903-327A-2

Query Match 84.7%; Score 50; DB 9; Length 456;
Best Local Similarity 80.0%; Pred. No. 0.16;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
|||||1:11
DB 45 GYFTSYDMH 54

RESULT 11
US-09-903-327A-13
; Sequence 13, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erqiang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
US-09-903-327A-13

Query Match
Best Local Similarity 84.7%; Score 50; DB 9; Length 493;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYFTSYDMH 10
||||| 1:11
Db 45 GYFTDYNMH 54

RESULT 12
US-09-903-327A-12
; Sequence 12, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erqiang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
US-09-903-327A-12

Query Match
Best Local Similarity 84.7%; Score 50; DB 9; Length 510;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYFTSYDMH 10
||||| 1:11
Db 45 GYFTDYNMH 54

RESULT 13
US-09-903-327A-11

; Sequence 11, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erqiang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
US-09-903-327A-11

Query Match
Best Local Similarity 84.7%; Score 50; DB 9; Length 597;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYFTSYDMH 10
||||| 1:11
Db 45 GYFTDYNMH 54

RESULT 14
US-09-903-327A-14
; Sequence 14, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erqiang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
US-09-903-327A-14

Query Match
Best Local Similarity 84.7%; Score 50; DB 9; Length 613;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYFTSYDMH 10
||||| 1:11
Db 45 GYFTDYNMH 54

RESULT 15
US-08-779-784-28
; Sequence 28, Application US/08779784
; Patent No. US20020164325A1
; GENERAL INFORMATION:

APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-779-784-28

Query Match 83.1%; Score 49; DB 1; Length 122;
Best Local Similarity 90.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
||||| 11
Db 26 GYFTSYWMH 35

Search completed: February 25, 2003, 10:57:19
Job time: 1.81667 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 : Search time 4.30667 Seconds

(without alignments)
813.344 Million cell updates/sec

Title: US-09-743-482a-10
Perfect score: 104
Sequence: 1 WIYPGNGNTKYNOKFNG 17

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-rvirus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	90	86.5	481	11	Q91WT1	Q91WT1 mus musculu
2	76	73.1	147	11	Q925S3	Q925S3 mus musculu
3	68	65.4	473	11	Q99L25	Q99L25 mus musculu
4	67	64.4	463	11	Q99LC4	Q99LC4 mus musculu
5	66	63.5	118	11	Q921C4	Q921C4 mus musculu
6	65	62.5	111	11	Q9D9B8	Q9D9B8 mus musculu
7	63	60.6	143	11	Q924Q0	Q924Q0 mus musculu
8	61	58.7	117	11	Q9QXFO	Q9QXFO mus musculu
9	61	58.7	117	11	Q9QXFE	Q9QXFE mus musculu
10	61	58.7	613	11	Q8VCX7	Q8VCX7 mus musculu
11	61	58.7	614	11	Q96GA6	Q96GA6 homo sapien
12	60	57.7	168	11	Q8VDC9	Q8VDC9 mus musculu
13	59	56.7	426	11	Q9DCD9	Q9DCD9 mus musculu
14	58	55.8	110	11	Q9JL83	Q9JL83 mus musculu
15	58	55.8	110	11	Q9JL77	Q9JL77 mus musculu
16	58	55.8	488	11	Q91WR1	Q91WR1 mus musculu

17	57	54.8	473	11	Q9DBL4	Q9DBL4 mus musculu
18	56	53.8	489	11	Q8VCX4	Q8VCX4 mus musculu
19	56	53.8	497	4	Q8WY24	Q8WY24 homo sapien
20	55	52.9	109	11	Q9JL75	Q9JL75 mus musculu
21	55	52.9	474	11	Q8R3H6	Q8R3H6 mus musculu
22	55	52.9	481	11	Q8VCV5	Q8VCV5 mus musculu
23	53	51.0	170	11	Q925S2	Q925S2 mus musculu
24	52	50.0	125	4	Q9UL95	Q9UL95 homo sapien
25	52	50.0	140	11	Q924P8	Q924P8 mus musculu
26	52	50.0	142	11	Q924Q1	Q924Q1 mus musculu
27	52	50.0	255	16	Q8VFE3	Q8VFE3 bruceella me
28	52	50.0	500	4	Q8BRV0	Q8BRV0 homo sapien
29	51	49.0	119	4	Q9UL94	Q9UL94 homo sapien
30	51	49.0	137	11	Q924R6	Q924R6 mus musculu
31	51	49.0	139	11	Q924R5	Q924R5 mus musculu
32	51	49.0	140	11	Q924R2	Q924R2 mus musculu
33	51	49.0	141	11	Q924Q4	Q924Q4 mus musculu
34	51	49.0	143	11	Q924R7	Q924R7 mus musculu
35	51	49.0	143	11	Q924R0	Q924R0 mus musculu
36	51	49.0	143	11	Q924Q5	Q924Q5 mus musculu
37	51	49.0	143	11	Q91VA2	Q91VA2 mus musculu
38	51	49.0	144	11	Q924P5	Q924P5 mus musculu
39	51	49.0	145	11	Q924R4	Q924R4 mus musculu
40	51	49.0	145	11	Q924R3	Q924R3 mus musculu
41	51	49.0	145	11	Q924R1	Q924R1 mus musculu
42	51	49.0	145	11	Q924Q9	Q924Q9 mus musculu
43	51	49.0	145	11	Q924Q7	Q924Q7 mus musculu
44	51	49.0	145	11	Q924Q6	Q924Q6 mus musculu
45	51	49.0	145	11	Q924P7	Q924P7 mus musculu

ALIGNMENTS

RESULT 1
Q91WT1 PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 52.1 kDa protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AH13490.1; -
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein;
KW NCBI_CurID=10090;
SQ
SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
Query Match 86.5%; Score 90; DB 11; Length 481;
Best Local Similarity 82.4%; Pred. No. 7.8e-06;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Caps 0;
QY 1 WIYPGNGNTKYNOKFNG 17
Db 69 WIYPGNGNTKYNEKFG 85
RESULT 2
Q925S3 PRELIMINARY; PRT; 147 AA.
AC Q925S3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

```

DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE MRP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.,
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240165; AAK43731.1; -.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; Ig; 1.16274 MW; 800594A12B97191F CRC64;
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match
Best Local Similarity 73.1%; Score 76; DB 11; Length 147;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPGNGNTKYNOKFNG 17
Db 52 WIFEGEGSTEYNEKFG 68

RESULT 3
O99L25 PRELIMINARY; PRT; 473 AA.
AC O99L25;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003886; AAH03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE989B7986DA155 CRC64;

Query Match
Best Local Similarity 65.4%; Score 68; DB 11; Length 473;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPGNGNTKYNOKFNG 17

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Db 69 YIYRDSSTKYNEKFG 85
:||||:||||:||||

RESULT 4
O99LC4 PRELIMINARY; PRT; 463 AA.
AC O99LC4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match
Best Local Similarity 64.4%; Score 67; DB 11; Length 463;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 IYPGNGNTKYNOKFNG 17
Db 70 IYPSGNTYSEKFG 85

RESULT 5
O92IC4 PRELIMINARY; PRT; 118 AA.
AC O92IC4;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Anti-porcine VCAM mab 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller J.P., Giamoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U78801; AAD00293.1; -.
DR HSSP; P01810; 2FBU.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.

```


Matches 10: Conservative 2: Mismatches 4: Indels 0: Gaps 0:

OY 2 IYPGNGNTKYNOKFNG 17
| : : : | : : : |
DB 70 IIPGSGRTYNKEKFG 85

RESULT 13

O9DCD9 PRELIMINARY: PRT: 426 AA.

AC O9DCD9.

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Adult male kidney cDNA, RIKEN full-length enriched library,
clone:0610041A01, full insert sequence.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

SEQUENCE FROM N.A.

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa A., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schrinl L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690(2001).

DR EMBL: AK002875, BAB22422.1; -

DR HSSP: P01810; 2PBJ.

DR InterPro: IPR003599; 1g.

DR InterPro: IPR003597; 1g-cl.

DR InterPro: IPR003600; 1g-like.

DR InterPro: IPR003006; 1g_MHC.

DR Pfam: PF00047; 1g; 4.

DR SMART: SM00409; 1g; 3.

DR SMART: SM00407; 1gcl; 3.

DR SMART: SM00410; 1g-like; 1.

DR PROSITE: PS00290; 1g_MHC; UNKNOWN.1.

SQ SEQUENCE 426 AA; 45819 MW; 56E1275BA48F6F81 CRC64;

Query Match 56.7% Score 59; DB 11; Length 426;
Best Local Similarity 76.9% Pred. No. 0.47;
Matches 10: Conservative 1: Mismatches 2: Indels 0: Gaps 0;

OY 5 GNGNTKYNOKFNG 17
| : : | : : | : : |
DB 16 GNGDTYNOKFNG 28

RESULT 14

O9JL83 PRELIMINARY: PRT: 110 AA.

AC O9JL83.

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Anti-myosin immunoglobulin heavy chain variable region
(Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

SEQUENCE FROM N.A.

RA STRAIN-BALB/C;

RA MEDLINE=20448942; PubMed=10992488;

RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;

RT "T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin."

RL Infect. Immun. 68:5803-5808(2000).

DR EMBL: AF206023; AAF69321.1; -

DR HSSP: P01810; 2PBJ.

DR InterPro: IPR003006; 1g_MHC.

DR InterPro: IPR003596; 1g-v.

DR Pfam: PF00047; 1g; 1.

DR SMART: SM00406; 1g; 1.

FT NON_TER 1

FT NON_TER 110

SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 55.8% Score 58; DB 11; Length 110;
Best Local Similarity 62.5% Pred. No. 0.15;
Matches 10: Conservative 2: Mismatches 4: Indels 0: Gaps 0;

OY 2 IYPGNGNTKYNOKFNG 17
| : : : | : : : |
DB 43 IYPGSDAVYNGKFG 58

RESULT 15

O9JL77 PRELIMINARY: PRT: 110 AA.

AC O9JL77.

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Anti-myosin immunoglobulin heavy chain variable region
(Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

SEQUENCE FROM N.A.

RA STRAIN-DBA/2;

RA MEDLINE=20448942; PubMed=10992488;

RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;

RT "T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin."

RL Infect. Immun. 68:5803-5808(2000).

DR EMBL: AF206029; AAF69327.1; -

DR HSSP: P01810; 2PBJ.

DR InterPro: IPR003006; 1g_MHC.

DR InterPro: IPR003596; 1g-v.

DR Pfam: PF00047; 1g; 1.

DR SMART: SM00407; 1g; 1.

DR SMART: SM00406; 1g; 1.

FT NON_TER 1

FT NON_TER 110

SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;

Query Match 55.8% Score 58; DB 11; Length 110;
Best Local Similarity 56.2% Pred. No. 0.15;
Matches 9: Conservative 4: Mismatches 3: Indels 0: Gaps 0;

OY 2 IYPGNGNTKYNOKFNG 17
| : : | : : | : : |
DB 43 IIPGSGRTYNKEKFG 58

Sat Mar 1 08:15:47 2003

us-09-743-482a-10.open.rspt

Page 6

Search completed: February 25, 2003, 10:36:32
Job time : 5.30667 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 : Search time 1.50167 Seconds
(without alignments)
469.543 Million cell updates/sec

Title: US-09-743-482A-10

Perfect score: 104
Sequence: 1 WIRPGNGNTKYNKFKNG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	85	81.7	117 1	HY52_MOUSE P06327 mus musculu
2	69	66.3	120 1	HY03_MOUSE P01747 mus musculu
3	61	58.7	117 1	HY12_MOUSE P01756 mus musculu
4	61	58.7	117 1	HY13_MOUSE P01757 mus musculu
5	61	58.7	117 1	HY14_MOUSE P01758 mus musculu
6	61	58.7	118 1	HY51_MOUSE P06330 mus musculu
7	58	55.8	117 1	HY04_MOUSE P01749 mus musculu
8	58	55.8	117 1	HY05_MOUSE P01750 mus musculu
9	58	55.8	140 1	HY02_MOUSE P01746 mus musculu
10	55	52.9	117 1	HY06_MOUSE P01750 mus musculu
11	52	50.0	117 1	HY05_MOUSE P01749 mus musculu
12	52	50.0	120 1	HY09_MOUSE P01753 mus musculu
13	51	49.0	117 1	HY09_MOUSE P01754 mus musculu
14	51	49.0	117 1	HY10_MOUSE P06328 mus musculu
15	51	49.0	117 1	HY49_MOUSE P01745 mus musculu
16	51	49.0	121 1	HY01_MOUSE P01745 mus musculu
17	51	49.0	139 1	HY07_MOUSE P01751 mus musculu
18	50	48.1	147 1	HY1C_HUMAN P01744 homo sapien
19	49.5	47.6	226 1	KAD3_BOVIN P08760 bos taurus
20	48	46.2	117 1	HY1B_HUMAN P23083 homo sapien
21	48	46.2	117 1	HY1G_HUMAN P23083 homo sapien
22	47	45.2	692 1	YK06_YEAST P36062 saccharomyc
23	46	44.2	681 1	RP3A_MOUSE P47709 rattus norv
24	46	44.2	830 1	PAM1_YEAST P37304 saccharomyc
25	46	44.2	830 1	PAM1_YEAST P37304 saccharomyc
26	45	43.3	1658 1	ITN2_MOUSE P17627 leprospira
27	44	42.3	556 1	PHL_LEPIN P17666 haemophilus
28	44	42.3	629 1	T3MH_HAEIN Q9wcp7 mus musculu
29	43.5	41.8	219 1	KAD3_MOUSE Q9uif7 homo sapien
30	43.5	41.8	226 1	KAD3_HUMAN P29411 rattus norv
31	43.5	41.8	226 1	KAD3_HUMAN P29411 rattus norv
32	43	41.3	138 1	HY48_MOUSE P03980 mus musculu
33	43	41.3	146 1	VA28_VACCV P21086 vaccinia vl

34	43	41.3	397 1	YEDS_ECOLI P76335 escherichia
35	43	41.3	1270 1	ITN1_XENLA O42287 xenopus lae
36	43	41.3	1696 1	ITN2_HUMAN O9wuz3 homo sapien
37	42.5	40.9	223 1	KAD4_MOUSE O9wuz3 mus musculu
38	42.5	40.9	223 1	KAD4_MOUSE O9wuz3 mus musculu
39	42	40.9	223 1	KAD4_MOUSE O9wuz3 mus musculu
40	42	40.4	240 1	XYNC_STRII P26220 streptomyc
41	42	40.4	327 1	A85B_MYCIE P31951 mycobacteri
42	42	40.4	347 1	A85A_MYCAN O52956 mycobacteri
43	42	40.4	376 1	ERG6_CANAL O74198 candida alb
44	42	40.4	434 1	VADA_YERPS P10858 yersinia ps
45	42	40.4	486 1	YAIT_ECOLI P77199 escherichia
			1753 1	YEW2_YEAST P32634 saccharomyc

ALIGNMENTS

RESULT 1
ID HY52_MOUSE STANDARD: PRT: 117 AA.

AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85093940; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unarranged VH gene segments.";
RL Cell 40:271-281(1985).

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CC EMBL: M13787; AAA38499.1; -
DR PIR: A02029; HVMSA1.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003596; Ig_V.
DR InterPro: IPR003596; Ig_V.
DR PIR: P00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12971 MW: 808C138856DFC9D CRC64;

Query Match 81.7%; Score 85; DB 1; Length 117;
Best local similarity 76.5%; Pred. No. 2.2e-06;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 WIRPGNGNTKYNKFKNG 17
Db 69 WIRPGDSTKYNKFKNG 85

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RESULT 2
HV03_MOUSE STANDARD; PRT; 120 AA.
ID HV03_MOUSE
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8131846; PubMed=6186498;
RA Stekevitz M., Geffer M.L., Brodeur P., Rildet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
DR HSSP: A02028; HWSG7.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B65AF CRC64;

Query Match
Best Local Similarity 66.3%; Score 69; DB 1; Length 120;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 IYPGNGNTKYNGKENG 17
DB 49 YINPGNGYTKYNEKFG 65

RESULT 3
HV12_MOUSE STANDARD; PRT; 117 AA.
ID HV12_MOUSE
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A02039; MHMS4E.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; Glycoprotein.

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FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE47E41 CRC64;

Query Match
Best Local Similarity 58.7%; Score 61; DB 1; Length 117;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 IYPGNGNTKYNGKENG 17
DB 51 INPNNGTGYNGKFG 66

RESULT 4
HV13_MOUSE STANDARD; PRT; 117 AA.
ID HV13_MOUSE
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Cleveringer B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS. MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A26242; MHMSJ5.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE47E41 CRC64;

Query Match
Best Local Similarity 58.7%; Score 61; DB 1; Length 117;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 IYPGNGNTKYNGKENG 17
DB 51 INPNNGTGYNGKFG 66

RESULT 5
HV14_MOUSE STANDARD; PRT; 117 AA.
ID HV14_MOUSE
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 108A precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;

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"Diversity of germ-line immunoglobulin VH genes."
Nature 292:426-430(1981).

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DR EMBL: J00488; AAA8519.1; -
DR PIR: A02041; HVMS8A.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1
FT SIGNAL 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12972 MW: 428CB44DF25D1BC2 CRC64;

Query Match 58.7%; Score 61; DB 1; Length 117;
Best Local Similarity 73.3%; Pred. No. 0.011;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IYPGNGNTKYNOKF 15
DB 69 YIYPNGTGYNOKF 83

RESULT 6
HV15_MOUSE STANDARD: PRT: 118 AA.
ID HV15_MOUSE
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Silekavitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes."
RL EMO J 3:517-523(1984).
DR PIR: A02040; MHMS38.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA: 12934 MW: 94F7BEE4C762A018 CRC64;

Query Match 58.7%; Score 61; DB 1; Length 118;
Best Local Similarity 68.8%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 7
HV04_MOUSE STANDARD: PRT: 117 AA.
ID HV04_MOUSE
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Boltwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC PIR: A02030; HVMS23.
CC HSSP: P01810; 2FBJ.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00406; Ig; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12772 MW: C530F829C906F69B CRC64;

Query Match 55.8%; Score 58; DB 1; Length 117;
Best Local Similarity 71.4%; Pred. No. 0.032;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IYPGNGNTKYNOKF 15
DB 70 INFGNGTGYNOKF 83

RESULT 8
HV15_MOUSE STANDARD: PRT: 136 AA.
ID HV15_MOUSE
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blatner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
RL

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CC -----
DR EMBL: J00494; AAA38130.1; -
DR PIR: A02042; HYMSB1.
DR HSSP: P01772; 2FBA.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
KM Immunoglobulin V region; Signal.
FT SIGNAL
FT CHAIN 1
FT NON_TER 20 136 IG HEAVY CHAIN V REGION BCL1.
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match
Best Local Similarity 83.3%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 NGNTRYNGKENG 17
Db 74 NGNTRYNGKENG 85

RESULT 9
HV05_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabblits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -----
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CC -----
DR EMBL: J00493; AAA38128.1; -
DR PIR: A02028; HYMSG7.
DR HSSP: P01810; 2FBU.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
KM Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL
FT CHAIN 1
FT NON_TER 20 140 IG HEAVY CHAIN V REGION 93G7.
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

```

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Query Match
Best Local Similarity 58.8%; Pred. No. 0.038;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 WYPCNGNTRYNGKENG 17
Db 69 YINPCNGYINYEKFG 85

RESULT 10
HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC -----
DR HSSP: P01810; 2FBU.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DE Immunoglobulin V region; Signal.
FT SIGNAL
FT CHAIN 1
FT NON_TER 20 117 IG HEAVY CHAIN V REGION 102;
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFD 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65D851FCA8C CRC64;

Query Match
Best Local Similarity 52.9%; Score 55; DB 1; Length 117;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 IYPCNGNTRYNGKENG 17
Db 70 IHPSDPTNYNGKENG 85

RESULT 11
HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 3 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE-81234548; PubMed-6788376;
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00536; AAA38605.1; .
DR PIR; A02031; HVMS3.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1
FT SIGNAL 19
FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975E9C CRC64;

Query Match
Best Local Similarity 50.0%; Score 52; DB 1; Length 117;
Pred. No. 0.27;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNGTKYNOKF 15
DB 70 IYPSDSETHYNOKF 83

RESULT 12
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38.15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE-84182519; PubMed-6201362;
RA Dildrop R., Boyens J., Stekevitz M., Beyreuther K., Rajewsky K.;
RT "A v region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBL J 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.

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FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match
Best Local Similarity 50.0%; Score 52; DB 1; Length 120;
Pred. No. 0.27;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNGTKYNOKF 15
DB 51 IYNSGNTYNOKF 64

RESULT 13
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE-81234548; PubMed-6788376;
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
DR PIR; B02034; HVMS1.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1
FT SIGNAL 19
FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match
Best Local Similarity 49.0%; Score 51; DB 1; Length 117;
Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNGTKYNOKF 15
DB 70 IYNSGNTYNOKF 83

RESULT 14
ID HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Ig heavy chain V region 145 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6789376;
RA Botheil A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC -----
DR EMBL: J00533; AAA38602.1;
DR PIR: C02034; HVMS45.
DR HSSP: P01810; 2FBU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 117 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 49.0%; Score 51; DB 1; Length 117;
Best Local Similarity 64.3%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNGTKYNOKF 15
DB 70 IDPNSGCTKYNEKF 83

RESULT 15
HV49_MOUSE
ID HV49_MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JAN-1988 (rel. 06, Created)
DT 01-JAN-1988 (rel. 06, Last sequence update)
DT 15-JUL-1993 (rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8509340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RL Cell 40:271-281(1985).
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CC -----
DR EMBL: M13788; AAA38506.1;
DR PIR: A02035; MHMSB4.
DR HSSP: P01810; 2FBU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 117 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12834 MW; B8862EAC67ABD345 CRC64;

Query Match 49.0%; Score 51; DB 1; Length 117;
Best Local Similarity 64.3%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNGTKYNOKF 15
DB 70 IDPNSGCTKYNEKF 83

Search completed: February 25, 2003, 10:37:31
Job time: 2.50167 secs

```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 : Search time 2.15333 seconds
(without alignments)
758.956 Million cell updates/sec

Title: US-09-743-482a-10

Perfect score: 104

Sequence: 1 WIPGNGNTRKYNGKENG 17

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:**

1: PIR1:**

2: PIR2:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	91.3	115	2	A54378
2	90	86.5	107	2	H28833
3	90	86.5	109	2	PH0999
4	90	86.5	109	2	PH0997
5	90	86.5	111	2	PH0998
6	90	86.5	111	2	S38950
7	90	86.5	106	2	S40295
8	88	84.6	106	2	PH1002
9	88	84.6	109	2	PH1001
10	86	82.7	120	2	G28195
11	86	82.7	138	2	S21810
12	85	81.7	104	2	S26466
13	85	81.7	117	1	HYMSA1
14	79	76.0	112	2	S26473
15	79	76.0	120	2	F28195
16	79	76.0	469	2	S37483
17	77	74.0	93	2	S42182
18	77	74.0	94	2	S42177
19	77	74.0	95	2	S42178
20	77	74.0	97	2	S42181
21	77	74.0	101	2	S42179
22	77	74.0	101	2	S42184
23	77	74.0	102	2	S42180
24	76	73.1	91	2	PL0242
25	76	73.1	107	2	PL0240
26	76	73.1	107	2	PL0243
27	76	73.1	107	2	PL0241
28	76	73.1	115	2	PL0238
29	76	73.1	117	2	S18553

30	75	72.1	110	2	PL0244	Ig heavy chain V r
31	75	72.1	112	2	PL0245	Ig heavy chain V r
32	75	72.1	112	2	PH0979	Ig heavy chain V r
33	73	70.2	114	2	PH1667	Ig heavy chain V r
34	73	70.2	118	2	PH1666	Ig heavy chain V r
35	72	69.2	96	2	PH1655	Ig heavy chain V r
36	72	69.2	102	2	S42176	Ig heavy chain V r
37	72	69.2	108	2	PH0975	Ig gamma chain V r
38	72	69.2	110	2	PH1000	Ig heavy chain V r
39	71	68.3	91	2	PH1004	Ig heavy chain V r
40	71	68.3	96	2	H28195	Ig heavy chain V r
41	71	68.3	109	2	PH1003	Ig heavy chain V r
42	71	68.3	117	2	S5541	Ig heavy chain V r
43	70	67.3	88	2	F25155	Ig heavy chain V r
44	70	67.3	88	2	F25155	Ig heavy chain V r
45	70	67.3	88	2	G25155	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A54378

Ig heavy chain V region anti-triplex DNA - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

C:Accession: A54378

R:Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.

J. Biol. Chem. 269, 7019-7023, 1994

A:Title: Characterization of a new monoclonal antibody to triplex DNA and Immunoglobulin

A:Reference number: A54378; MUID:94165109; PMID:7509814

A:Accession: A54378

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-115 <AG>

A:Cross-references: GB:S68981; MID:9545744; PIDN:AAB30095.1; PID:9545745

A:Experimental source: spleen and myeloma cell line MOPC 315.43

A>Note: sequence inconsistent with nucleotide translation

A>Note: sequence extracted from NCBI backbone (NCBIN:144172, NCBI:144173)

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:15-98/Domain: immunoglobulin homology <IM>

Query Match

Best Local Similarity 91.3%; Score 95; DB 2; Length 115;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIPGNGNTRKYNGKENG 17

DB 50 WIPGNGNTRKYNEKFG 66

RESULT 2

H28833

Ig kappa chain V region (HP22.202.16) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-May-1997

C:Accession: H28833

J:Corbett, S.; Hlrm, M.; Roth, C.; Theze, J.; Fougereau, M.; Schiffr, C.

A:Title: Allelic manipulation of the GAT idiotype cascade. Immunization of C57BL

A:Reference number: A92827; MUID:88285674; PMID:3135311

A:Accession: H28833

A:Molecule type: mRNA

A:Residues: 1-67 <COR>

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

Query Match

Best Local Similarity 86.5%; Score 90; DB 2; Length 67;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIPGNGNTRKYNGKENG 17

Db 19 WIYPGSGNTRYNEKFKG 35

RESULT 3

Ig heavy chain V region (clone 74-cl) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH0999
 R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH0999
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-107 <TIL>
 A:Experimental source: B cell, strain (NZB x NZW)F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 90; DB 2; Length 107;
 Best Local Similarity 82.4%; Pred. No. 5.1e-07;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 49 WIYPGSGNTRYNEKFKG 65

RESULT 4

Ig heavy chain V region (clone 17s-c2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH0997
 R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH0997
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-109 <TIL>
 A:Experimental source: B cell, strain (NZB x NZW)F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 90; DB 2; Length 109;
 Best Local Similarity 82.4%; Pred. No. 5.2e-07;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 50 WIYPGSGNTRYNEKFKG 66

RESULT 5

Ig heavy chain V region (clone 165.3) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH0998
 R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH0998
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA

A:Residues: 1-111 <TIL>
 A:Experimental source: B cell, strain (NZB x NZW)F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 90; DB 2; Length 111;
 Best Local Similarity 82.4%; Pred. No. 5.3e-07;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 50 WIYPGSGNTRYNEKFKG 66

RESULT 6

Ig gamma chain - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
 C:Accession: S38950
 R:Kiebert, S.; Kretzlin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;
 Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
 A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against aIp
 A:Reference number: S38950; MUID:94128242; PMID:8297501
 A:Accession: S38950
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-246 <KLE>
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 90; DB 2; Length 246;
 Best Local Similarity 82.4%; Pred. No. 1.2e-06;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 50 WIYPGSGNTRYNEKFKG 66

RESULT 7

Ig gamma-2a chain (mAb735) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
 C:Accession: S40295
 R:Kiebert, S.; Kretzlin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;
 submitted to the EMBL Data Library, January 1993
 A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again
 A:Reference number: S40295
 A:Accession: S40295
 A:Molecule type: protein
 A:Residues: 1-446 <KLE>
 C:Genetics:
 A:Map position: 12
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
 F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
 F:1-117/Domain: V-D-J region <VDJ>
 F:118-446/Domain: C region <CHR>
 F:118-214/Domain: C1 region <CH1>
 F:215-230/Region: hinge
 F:231-340/Domain: C2 region <CH2>
 F:341-446/Domain: C3 region <CH3>
 F:360-427/Domain: immunoglobulin homology <IMM>
 F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
 F:122-96,144-199,261-321,367-425/disulfide bonds: #status predicted
 F:132/disulfide bonds: interchain (to light chain) #status predicted
 F:224,227,229/disulfide bonds: interchain #status predicted
 F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 86.5%; Score 90; DB 2; Length 446;
Best Local Similarity 82.4%; Pred. No. 2.4e-06;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WIYPGNGTKYNOKEFG 17
|||||:|||||:|
DB 50 WIYPGSGMTKYNEKFKG 66

RESULT 8

PH1002

Ig heavy chain V region (clone 165.45) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1002

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1002

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-106 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 84.6%; Score 88; DB 2; Length 106;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPGNGTKYNOKEFG 17
|||||:|||||:|
DB 49 WIYPGSGMTKYNEKFKG 65

RESULT 9

PH1001

Ig heavy chain V region (clone 111.68) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1001

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1001

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-109 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 84.6%; Score 88; DB 2; Length 109;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPGNGTKYNOKEFG 17
|||||:|||||:|
DB 50 WIYPGSGMTKYNEKFKG 66

RESULT 10

G28195

Ig heavy chain V region (anti-haloperidol antibody B) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 23-Jul-1999

C:Accession: G28195

R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.

J. Biol. Chem. 263, 4059-4063, 1988

A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino ac

A:Reference number: A28195; MUID:88153717; PMID:3267217

A:Accession: G28195

A:Molecule type: mRNA

A:Residues: 1-120 <SHE>

A:Cross-references: GB:M19772; NID:9195520; PIDN:AAA38340.1; PID:9195521

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 82.7%; Score 86; DB 2; Length 120;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPGNGTKYNOKEFG 17
|||||:|||||:|
DB 50 WIYPGNVNTKYNEKFKG 66

RESULT 11

S21810

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S21810

R:Ostermeyer, M.; Brack, C.H.; Trautnecker, A.; Koehler, G.

submitted to the EMBL Data Library, January 1991

A:Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy

A:Reference number: S21810

A:Accession: S21810

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-138 <OST>

A:Cross-references: EMBL:X56936; NID:954163; PIDN:CAA40257.1; PID:954164

C:Genetics:

A:Insertions: 15/3

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 82.7%; Score 86; DB 2; Length 138;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPGNGTKYNOKEFG 17
|||||:|||||:|
DB 69 WIYPGNVNTKYNEKFKG 85

RESULT 12

S26466

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26466

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26466

A:Accession: S26466

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-104 <KAV>

A:Cross-references: EMBL:X59116; NID:951933; PIDN:CAA41842.1; PID:951934

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:3-86/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 81.7%; Score 85; DB 2; Length 104;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 WIYPGNGTKYNOKEFG 17
|||||:|||||:|

Db 38 WIYPGDSGTKYNEKEFKG 54

RESULT 13

HVMSAI

Ig heavy chain precursor V region (A1/A4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 22-Jun-1999

C:Accession: A02029

R:Tanopoulos, G.D.; Alt, F.W.

Cell 40, 271-281, 1985

A:Title: Developmentally controlled and tissue-specific expression of unrearranged V-H

A:Reference number: A90860; MUID:85099340; PMID:2578321

A:Accession: A02029

A:Molecule type: DNA

A:Residues: 1-117 <I>AN>

A:Cross-references: GB:M13787; NID:g196006; PIDN:AAA38499.1; PID:g466291

A:Note: the sequence was determined from the germline gene

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotrimer; Immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (A1/A4) #status predicted <MAT>

F:34-49/Region: Framework 1

F:34-117/Domain: Immunoglobulin homology <IMM>

F:50-54/Region: complementarity-determining 1

F:55-68/Region: Framework 2

F:69-85/Region: complementarity-determining 2

F:86-117/Region: Framework 3

F:41-115/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 81.7%; Score 85; DB 1; Length 117;

Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIYPGNGTKYNOKEFKG 17

|||||:|||||:|

Db 69 WIYPGDSGTKYNEKEFKG 85

RESULT 14

S26473

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26473

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26473

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 <KAV>

C:Cross-references: EMBL:X59111; NID:g51955; PIDN:CAA41837.1; PID:g51956

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotrimer; Immunoglobulin

F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 76.0%; Score 79; DB 2; Length 112;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIYPGNGTKYNOKEFKG 17

|||||:|||||:|

Db 50 WIYPXNVNTKYNEKEFKG 66

RESULT 15

F28195

Ig heavy chain V region (anti-haloperidol antibody A) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 16-Aug-1996

C:Accession: F28195

R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.

J. Biol. Chem. 263, 4059-4063, 1988

A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino ac

A:Reference number: A28195; MUID:88153717; PMID:3267217

A:Accession: F28195

A:Molecule type: mRNA

A:Residues: 1-120 <SHE>

C:Cross-references: GB:M19772

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotrimer; Immunoglobulin

F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 76.0%; Score 79; DB 2; Length 120;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIYPGNGTKYNOKEFKG 17

|||||:|||||:|

Db 50 WIYPXNVNTKYNEKEFKG 66

Search completed: February 25, 2003, 10:33:52
Job time : 2.15333 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 1.11667 Seconds
(without alignments)
263.489 Million cell updates/sec

Title: US-09-743-482A-8
Perfect score: 59
Sequence: 1 GYFTSYDMH 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq Length: 0
Maximum DB seq Length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents:AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	91.5	140	1	US-08-476-275-6
2	54	91.5	140	4	US-08-475-815B-11
3	51	86.4	116	1	US-07-634-278-3
4	51	86.4	116	1	US-07-634-278-5
5	51	86.4	116	1	US-07-634-278-14
6	51	86.4	116	1	US-08-477-128-5
7	51	86.4	116	1	US-08-477-128-14
8	51	86.4	116	1	US-08-477-128-14
9	51	86.4	116	1	US-08-474-040-3
10	51	86.4	116	1	US-08-474-040-3
11	51	86.4	116	1	US-08-474-040-14
12	51	86.4	116	1	US-08-487-200-3
13	51	86.4	116	1	US-08-487-200-5
14	51	86.4	116	1	US-08-487-200-14
15	51	86.4	116	1	US-08-488-113B-167
16	51	86.4	116	1	US-08-488-113B-168
17	51	86.4	116	1	US-08-488-113B-169
18	51	86.4	116	1	US-08-477-484B-167
19	51	86.4	116	1	US-08-477-484B-168
20	51	86.4	116	1	US-08-477-484B-169
21	51	86.4	116	1	US-08-107-669D-53
22	51	86.4	116	1	US-08-107-669D-54
23	51	86.4	116	1	US-08-107-669D-55
24	51	86.4	116	1	US-08-472-788A-54
25	51	86.4	116	1	US-08-472-788A-85
26	51	86.4	116	1	US-08-472-788A-86
27	51	86.4	116	2	US-08-477-531B-53

Result No.	Score	Query Match	Length	ID	Description
28	51	86.4	116	2	US-08-477-531B-54
29	51	86.4	116	2	US-08-477-531B-55
30	51	86.4	116	2	US-08-646-360-167
31	51	86.4	116	2	US-08-646-360-168
32	51	86.4	116	2	US-08-646-360-169
33	51	86.4	116	2	US-08-082-842A-54
34	51	86.4	116	2	US-08-082-842A-85
35	51	86.4	116	2	US-08-082-842A-86
36	51	86.4	116	3	US-08-934-841-1
37	51	86.4	116	3	US-09-393-409-1
38	51	86.4	116	4	US-08-839-765-167
39	51	86.4	116	4	US-08-839-765-168
40	51	86.4	116	4	US-08-839-765-169
41	51	86.4	116	4	US-09-136-389-167
42	51	86.4	116	4	US-09-136-389-168
43	51	86.4	116	4	US-09-136-389-169
44	51	86.4	116	4	US-08-484-537-3
45	51	86.4	116	4	US-08-484-537-5

ALIGNMENTS

RESULT 1
US-08-476-275-6
; Sequence 6, Application US/08476275
; Patent No. 5776456
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Leonard, John E.
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
; TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-cell
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,275
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-476-275-6

Query Match
Best Local Similarity 91.5%; Score 54; DB 1; Length 140;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDMH 10
|||||:11
DB 45 GYTFTSYNMH 54

RESULT 2
US-08-475-815B-11
Sequence 11, Application US/08475815B
Patent No. 6399061

GENERAL INFORMATION:

APPLICANT: ANDERSON, DARRELL R.

APPLICANT: HANNA, NABIL

APPLICANT: LEONARD, JOHN E.

APPLICANT: NEMAN, ROLAND A.

APPLICANT: REEF, MITCHELL E.

APPLICANT: RASTETER, WILLIAM H.

TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELLED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: PILLSBURY WINTHROP
STREET: 1100 New York Avenue, N.W., Ninth FL.
CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,815B

FILING DATE: 07-JUN-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/149,099

FILING DATE: 03-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/978,891

FILING DATE: 13-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 23522-0157

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000

TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 140 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-475-815B-11

Query Match
Best Local Similarity 91.5%; Score 54; DB 4; Length 140;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDMH 10
|||||:11
DB 45 GYTFTSYNMH 54

RESULT 3
US-07-634-278-3
Sequence 3, Application US/07634278
Patent No. 5530101

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLF, Nicholas F.

APPLICANT: COELING, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourile and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/634,278

FILING DATE: 19-DEC-1990

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: Protein

LOCATION: 1..116

OTHER INFORMATION:

OTHER INFORMATION: anti-Tac antibody heavy chain."

US-07-634-278-3

Query Match
Best Local Similarity 86.4%; Score 51; DB 1; Length 116;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDMH 10
|||||:11
DB 26 GYTFTSYNMH 35

RESULT 4

US-07-634-278-5
Sequence 5, Application US/07634278

Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELING, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..116
OTHER INFORMATION: /note="Variable region of the PDL
OTHER INFORMATION: humanized anti-Tac antibody heavy chain."
US-07-634-278-5
Query Match 86.4%: Score 51: DB 1: Length 116;
Best Local Similarity 90.0%: Pred. No. 0.071:
Matches 9: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 1 GYFTSYDMH 10
| | | | | | | |
Db 26 GYFTSYDMH 35

RESULT 5
US-07-634-278-14
Sequence 14, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELING, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..116
OTHER INFORMATION: /note="Anti-Tac heavy chain amino
OTHER INFORMATION: acid sequence."
US-07-634-278-14
Query Match 86.4%: Score 51: DB 1: Length 116;
Best Local Similarity 90.0%: Pred. No. 0.071:
Matches 9: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 1 GYFTSYDMH 10
| | | | | | | |
Db 26 GYFTSYDMH 35

RESULT 6
US-08-477-728-3
Sequence 3, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..116
OTHER INFORMATION: /note= "Variable region of the mouse
OTHER INFORMATION: anti-Tac antibody heavy chain."
US-08-477-728-3
Query Match 86.4%; Score 51; DB 1; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYFTSYDMH 10
|||||
DB 26 GYFTSYRMH 35
RESULT 7
US-08-477-728-5
Sequence 5, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California

COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..116
OTHER INFORMATION: /note= "Variable region of the pDL
OTHER INFORMATION: humanized anti-Tac antibody heavy chain."
US-08-477-728-5
Query Match 86.4%; Score 51; DB 1; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYFTSYDMH 10
|||||
DB 26 GYFTSYRMH 35
RESULT 8
US-08-477-728-14
Sequence 14, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..116
OTHER INFORMATION: /note="Anti-Tac heavy chain amino
OTHER INFORMATION: acid sequence."
US-08-477-728-14
Query Match 86.4%; Score 51; DB 1; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYFTSYDMH 10
DB 26 GYFTSYRMH 35
RESULT 9
US-08-474-040-3
Sequence 3, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..116
OTHER INFORMATION: /note="Variable region of the mouse
OTHER INFORMATION: anti-Tac antibody heavy chain."
US-08-474-040-3
Query Match 86.4%; Score 51; DB 1; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYFTSYDMH 10
DB 26 GYFTSYRMH 35
RESULT 10
US-08-474-040-5
Sequence 5, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/474,040
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/634,278
;; FILING DATE: 19-DEC-1990
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 116 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; HYPOTHEetical: NO
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..116
;; OTHER INFORMATION: /note="Variable region of the PDL
;; OTHER INFORMATION: humanized anti-Tac antibody heavy chain."
US-08-474-040-5
Query Match 86.4%; Score 51; DB 1; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 GYFTSYDMH 10
||||| 11
Db 26 GYFTSYDMH 35

RESULT 11
US-08-474-040-14
; Sequence 14, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLET, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040

;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/634,278
;; FILING DATE: 19-DEC-1990
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 116 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; HYPOTHEtical: NO
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..116
;; OTHER INFORMATION: /note="Anti-Tac heavy chain amino
;; OTHER INFORMATION: acid sequence."
US-08-474-040-14
Query Match 86.4%; Score 51; DB 1; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 GYFTSYDMH 10
||||| 11
Db 26 GYFTSYDMH 35

RESULT 12
US-08-487-200-3
; Sequence 3, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLET, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..116
OTHER INFORMATION: /note="Variable region of the mouse
OTHER INFORMATION: anti-Tac antibody heavy chain."
US-08-487-200-3

Query Match 86.4%; Score 51; DB 1; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
||||| 11
DB 26 GYFTSYDMH 35

RESULT 13
US-08-487-200-5
Sequence 5, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..116
OTHER INFORMATION: /note="Variable region of the PDL
OTHER INFORMATION: humanized anti-Tac antibody heavy chain."
US-08-487-200-5

Query Match 86.4%; Score 51; DB 1; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
||||| 11
DB 26 GYFTSYDMH 35

RESULT 14
US-08-487-200-14
Sequence 14, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA: US 07/634,278

FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..116
OTHER INFORMATION: /note="Anti-Tac heavy chain amino
US-08-487-200-14
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 86.4%; Score 51; DB 1; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYFTSYDMH 10
|||||
DB 26 GYFTSYRMH 35
RESULT 15
US-08-488-113B-167
Sequence 167, Application US/08488113B
Patent No. 574580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studlika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 110220S07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-167

Query Match 86.4%; Score 51; DB 1; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYFTSYDMH 10
|||||
DB 26 GYFTSYRMH 35

Search completed: February 25, 2003, 10:38:42
Job time: 2.1167 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:36:42 ; Search time 1.38833 Seconds

(without alignments)
380.447 Million cell updates/sec

Title: US-09-743-482a-10

Perfect score: 104

Sequence: 1 WIYPGNGNTRKYNOKFNG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 156504 segs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications-AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep:*

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13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep:*

14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	81.7	138	1 US-08-779-784-31	Sequence 31, Appl
2	79	76.0	139	12 US-10-006-773-13	Sequence 13, Appl
3	77	74.0	140	9 US-09-905-928-6	Sequence 6, Appl
4	76	73.1	119	10 US-09-839-447A-1	Sequence 1, Appl
5	71	68.3	17	10 US-09-861-294-15	Sequence 15, Appl
6	71	68.3	17	10 US-09-770-002-2	Sequence 2, Appl
7	71	68.3	153	10 US-09-861-294-4	Sequence 4, Appl
8	70	67.3	249	9 US-10-237-667-18	Sequence 18, Appl
9	70	67.3	249	10 US-09-984-186-18	Sequence 18, Appl
10	68	65.4	119	10 US-09-850-165-54	Sequence 54, Appl
11	67	64.4	125	9 US-09-929-665-20	Sequence 20, Appl
12	67	64.4	125	9 US-09-929-546-20	Sequence 20, Appl
13	67	64.4	132	9 US-09-982-107-14	Sequence 14, Appl
14	67	64.4	669	9 US-09-807-721-2	Sequence 2, Appl
15	66	63.5	17	9 US-10-032-482-15	Sequence 15, Appl
16	66	63.5	12	10 US-09-864-761-38566	Sequence 38566, A
17	66	63.5	111	9 US-10-032-482-5	Sequence 5, Appl
18	65	62.5	139	10 US-09-760-723-7	Sequence 7, Appl
19	65	62.5	139	10 US-09-760-723-8	Sequence 8, Appl

20	65	62.5	139	10 US-09-355-925-7	Sequence 7, Appl
21	65	62.5	139	10 US-09-355-925-8	Sequence 8, Appl
22	64	61.5	448	10 US-09-917-410-6	Sequence 6, Appl
23	63.5	61.1	244	10 US-09-940-391-1	Sequence 1, Appl
24	63	60.6	117	9 US-08-144-886-71	Sequence 71, Appl
25	61	58.7	20	10 US-09-839-447A-9	Sequence 9, Appl
26	61	58.7	115	10 US-09-800-908-5	Sequence 5, Appl
27	61	58.7	117	9 US-09-726-258-48	Sequence 48, Appl
28	61	58.7	117	9 US-09-726-258-49	Sequence 49, Appl
29	61	58.7	135	9 US-09-726-258-37	Sequence 37, Appl
30	61	58.7	253	9 US-09-726-258-44	Sequence 44, Appl
31	61	58.7	253	9 US-09-726-258-52	Sequence 52, Appl
32	61	58.7	253	9 US-09-726-258-55	Sequence 55, Appl
33	61	58.7	256	9 US-09-726-258-70	Sequence 70, Appl
34	61	58.7	298	9 US-09-726-258-60	Sequence 60, Appl
35	61	58.7	452	9 US-09-726-258-71	Sequence 71, Appl
36	60.5	58.2	129	9 US-09-956-206A-77	Sequence 77, Appl
37	60	57.7	92	10 US-09-864-761-47202	Sequence 47202, A
38	60	57.7	149	9 US-09-187-693-57	Sequence 57, Appl
39	59	56.7	17	9 US-10-146-305-13	Sequence 13, Appl
40	59	56.7	91	10 US-09-943-906-70	Sequence 70, Appl
41	59	56.7	91	10 US-09-943-906-78	Sequence 78, Appl
42	59	56.7	92	10 US-09-943-906-79	Sequence 79, Appl
43	59	56.7	92	10 US-09-943-906-85	Sequence 85, Appl
44	59	56.7	95	10 US-09-943-906-86	Sequence 86, Appl
45	59	56.7	98	12 US-10-025-687-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-779-784-31
Sequence 31, Application US/08779784
Patent No. US20020164325A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-779-784-31

Query Match
Best Local Similarity 81.7%; Score 85; DB 1; Length 138;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 WIYPGNGNTKYNQKENG 17
|||||:|||||:|

DB 69 WIYPGNGSTKYNEKFKG 85

RESULT 2
US-10-006-773-13
Sequence 13, Application US/10006773
Patent No. US2020132983A1
GENERAL INFORMATION:
APPLICANT: Jungmans, Richard P.
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
FILE REFERENCE: 003
CURRENT APPLICATION NUMBER: US/10/006,773
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/250,089
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 139
TYPE: PRT
ORGANISM: Mus sp.
US-10-006-773-13

Query Match
Best Local Similarity 76.0%; Score 79; DB 12; Length 139;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 WIYPGNGNTKYNQKENG 17
|||||:|:|:|:|

DB 69 WIYPGNGSTKYNEKFKG 85

RESULT 3
US-09-905-928-6
Sequence 6, Application US/09905928
Publication No. US20030021781A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nobil
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lymphoma
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/905,928
FILING DATE: 17-JUL-2001
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,813
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-158
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-905-928-6

Query Match
Best Local Similarity 74.0%; Score 77; DB 9; Length 140;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 IYPGNGNTKYNQKENG 17
|||||:|||||

DB 70 IYPGNGDTSYNQKFKG 85

RESULT 4
US-09-839-447A-1
Sequence 1, Application US/09839447A
Patent No. US20020058247A1
GENERAL INFORMATION:
APPLICANT: Saliberg, Matti
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
FILE REFERENCE: TRIPEP.020CP1
CURRENT APPLICATION NUMBER: US/09/839,447A
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/556605
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-09-839-447A-1

Query Match
Best Local Similarity 73.1%; Score 76; DB 10; Length 119;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPGNGNTKYNQKENG 17
|||||:|:|:|:|

DB 49 WIYPGEGSTKYNEKFKG 65

RESULT 5
US-09-861-294-15
; Sequence 15, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-861-294-15

Query Match 68.3%; Score 71; DB 10; Length 17;
Best Local Similarity 75.0%; Pred. No. 8,8e-05;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGNGNTKYNOKFG 17
|:||||:| ||||| |
Db 2 IFPGNGDTYYNOKFG 17

RESULT 6
US-09-770-002-2
; Sequence 2, Application US/09770002
; Patent No. US2002010558A1
; GENERAL INFORMATION:
; APPLICANT: Peter Lloyd Amlot
; APPLICANT: Max H. Schreier
; APPLICANT: Karin Schreier
; TITLE OF INVENTION: Use of CD25 binding molecules in the
; TITLE OF INVENTION: treatment of rheumatoid arthritis or skin diseases.
; FILE REFERENCE: 4-30583A/30967C1
; CURRENT APPLICATION NUMBER: US/09/770,002
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/EP99/05316
; PRIOR FILING DATE: 1999-07-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: mus musculus
US-09-770-002-2

Query Match 68.3%; Score 71; DB 10; Length 17;
Best Local Similarity 75.0%; Pred. No. 8,8e-05;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNGNTKYNOKFG 17
|:||||:| ||||| |
Db 2 IYPGNSDTYYNOKFG 17

RESULT 7
US-09-861-294-4
; Sequence 4, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-861-294-4

Query Match 68.3%; Score 71; DB 10; Length 153;
Best Local Similarity 75.0%; Pred. No. 0.00079;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGNGNTKYNOKFG 17
|:||||:| ||||| |
Db 70 IFPGNGDTYYNOKFG 85

RESULT 8
US-10-237-667-18
; Sequence 18, Application US/10237667
; Publication No. US20030022308A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3c43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (Patentlin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,667
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/EP93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: S792006-US
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-237-667-18

Query Match 67.3%; Score 70; DB 9; Length 249;
Best Local Similarity 75.0%; Pred. No. 0.0018;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

2 IYPGNGTKYNGKFG 17
||||:|||||
54 IYPGDDTKYNGKFG 69

RESULT 9
US-09-984-186-18
Sequence 18, Application US/09984186
Patent No. US2002015101A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentln)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-Jan-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-Jul-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-Jan-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-Jan-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-984-186-18

Query Match 67.3%; Score 70; DB 10; Length 249;
Best Local Similarity 75.0%; Pred. No. 0.0018;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

2 IYPGNGTKYNGKFG 17
||||:|||||
54 IYPGDDTKYNGKFG 69

RESULT 10
US-09-850-165-54
Sequence 54, Application US/09850165
Patent No. US20020150580A1
GENERAL INFORMATION:
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: HANNA, NABIL
APPLICANT: RAAB, RONALD W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
FILE REFERENCE: 037003-0280614
CURRENT APPLICATION NUMBER: US/09/850,165
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: 09/082,472
PRIOR FILING DATE: 1998-05-21
PRIOR APPLICATION NUMBER: 08/476,237
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/397,072
PRIOR FILING DATE: 1995-04-17
PRIOR APPLICATION NUMBER: 07/912,292
PRIOR FILING DATE: 1992-07-10
PRIOR APPLICATION NUMBER: 07/856,281
PRIOR FILING DATE: 1992-03-23
PRIOR APPLICATION NUMBER: 07/735,064
PRIOR FILING DATE: 1991-07-25
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 54
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
OTHER INFORMATION: monkey clone
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Any amino acid; preferably Gln
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (20)
OTHER INFORMATION: Leu, Ile or Val
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (24)
OTHER INFORMATION: Gly, Thr or Ala
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (70)
OTHER INFORMATION: Any amino acid
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (72)
OTHER INFORMATION: Any amino acid; preferably Met, Val or Ile
FEATURE:

RESULT 12
US-09-929-546-20
: Sequence 20, Application US/09929546
: Publication No. US20030031673A1

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1  APPLICANT: UNIVERSITY OF CENTRAL FLORIDA
2  TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS
3  FILE REFERENCE: 1463-PCT-US-00
4  CURRENT APPLICATION NUMBER: US/09/807,721
5  CURRENT FILING DATE: 2001-12-21

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;; PRIOR APPLICATION NUMBER: PCT/US01/06274
;; PRIOR FILING DATE: 2001-02-28
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 2
;; LENGTH: 669
;; TYPE: prt
;; ORGANISM: Homo sapiens
US-09-807-721-2

Query Match 64.4%; Score 67; DB 9; Length 669;
Best Local Similarity 80.0%; Pred. No. 0.014;
Matches 12: Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WTPNGNTKYNOKF 15
: ||| ||| ||| |||
Db 51 YTPNGNTKYNOKF 65

RESULT 15

US-10-032-482-15
; Sequence 15, Application US/10032482
; Publication No. US20020197270A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/10/032,482
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US/09/445,602
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 15
; TYPE: prt
; LENGTH: 17
; ORGANISM: Mus musculus
US-10-032-482-15

Query Match 63.5%; Score 66; DB 9; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.0005;
Matches 12: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 IYPNGNTKYNOKFNG 17
: ||| ||| ||| ||| |||
Db 2 IYPNGFTTYNOKFNG 17

Search completed: February 25, 2003, 10:57:20
Job time : 2.38833 secs

Chalm 8; Fig 6; 79pp; English

least one complementary region (CDR) of a variable region of an antibody which specifically interacts with the extracellular domain

CC tissues rapidly and is quickly cleared from the body. It also has
 CC reduced immunogenicity and its design facilitates binding to other
 CC moieties in drug targeting and imaging applications. The BABS
 CC is a 26-10/9-loop hybrid - it comprises framework region from 26-10 VH
 CC and the CDRs from glp-4 VH.

SO Sequence 117 AA:

Query Match 86.5%; Score 90; DB 9; Length 117;
 Best Local Similarity 82.4%; Pred. No. 1.8e-06;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPGNGNTKYNQKENG 17
 |||||
 DB 50 WIYPGNGNTKYNENFKG 66

RESULT 6

ID AAP80149 standard; protein; 117 AA.

AC AAP80149;

DT 13-OCT-1990 (first entry)

DE Biosynthetic antibody binding site.

KW Biosynthetic antibody binding site; complementarity determining region;
 KW framework region.

OS Mus musculus/Homo sapiens.

EH Key Location/Qualifiers

FT Region 10..27 /Label=newm1 framework region

FT Region 28..38 /Label=CDR

FT Region 39..45 /Label=newm2 framework region

FT Region 46..66 /Label=CDR

FT Region 67..97 /Label=newm3 framework region

FT Region 98..104 /Label=CDR

FT Region 105..117 /Label=newm4 framework region

XX WO8809344-A.

XX 01-DEC-1988.

XX 19-MAY-1988; 88WO-US01737.

XX 21-MAY-1987; 87US-0052800.

XX (CREA-) CREATIVE BIOMOLECULES INC.

XX Huston JS, Oppermann H;

XX WPI, 1988-353928/49.

PT Recombinant multifunctional protein - having antibody binding site and
 PT sequence for biological activity, ion sequestering or binding to a solid
 PT support.

PS Disclosure; 5pp; English.

XX The biosynthetic antibody binding site forms part of a single chain
 CC multi-functional biosynthetic protein. The protein also comprises
 CC an effector molecule with biological activity (eg an enzyme, toxin,
 CC receptor binding site, growth factor, lymphokine, cytokine or
 CC antimetabolite), an amino acid sequence capable of sequestering an

CC ion (eg calmodulin or metallochione), or an amino acid sequence
 CC capable of selective binding to a solid support (eg streptavidin or
 CC a fragment of protein A). The BABS contains at least one domain
 CC homologous to part/all of the variable region of an immunoglobulin
 CC capable of binding the preselected antigenic determinant. The protein
 CC can be used for specific binding assays, affinity purification, biocatalysts,
 CC drug targeting, imaging and immunological treatment of oncogenic and
 CC infectious diseases. It offers fewer cleavage sites to circulating
 CC proteolytic enzymes, and has improved stability. It reaches target
 CC tissues rapidly and is quickly cleared from the body. It also has
 CC reduced immunogenicity and its design facilitates binding to other
 CC moieties in drug targeting and imaging applications. The BABS
 CC is a newm/g-loop hybrid - it comprises framework regions from human
 CC myeloma antibody NEMM VH and the complementarity determining regions
 CC from glp-4 VH. It illustrates a humanised binding site having a
 CC human framework but an affinity for lysozyme similar to murine glp-4.

SO Sequence - 117 AA:

Query Match 86.5%; Score 90; DB 9; Length 117;
 Best Local Similarity 82.4%; Pred. No. 1.8e-06;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPGNGNTKYNQKENG 17
 |||||
 DB 50 WIYPGNGNTKYNENFKG 66

RESULT 7

ID AAB62295 standard; protein; 117 AA.

AC AAB62295;

DT 29-JUN-2001 (first entry)

DE Sequence of a chimeric Vh comprising 26-10 FRs and glp-4 CDRs.

KW Biosynthetic; antibody binding site; binding assay; drug targeting;
 KW biocatalysis; imaging; affinity purification; oncogenic;
 KW infectious disease; murine; monoclonal glp-4; anti-lysozyme; cytostatic;
 KW antimicrobial; monoclonal 26-10; anti-digoxin; chimeric.

OS Mus sp.

XX US6207804-B1.

XX 27-MAR-2001.

XX 18-DEC-1995; 95US-0575724.

XX 21-MAY-1987; 87US-0052800.

XX 12-MAR-1992; 92US-0850228.

XX 19-OCT-1993; 93US-0139901.

XX 30-JUN-1998; 98US-0213671.

XX (CURT-) CURTIS INC.

XX Huston JS, Oppermann H;

XX WPI, 2001-280767/29.

PT Novel biosynthetic antibody binding site having chimeric polypeptide
 PT which defines selective antigen binding region and has CDR and
 PT framework amino acid sequences homologous to different immunoglobulin
 PT molecules

PS Disclosure; Fig 3; 26pp; English.

XX The invention relates to a biosynthetic antibody binding site that
 CC comprises disulfide bonded heavy, light variable region (HVR, LVR)
 CC defining single, complete antigen (Ag1) binding site. HVR, LVR have
 CC polypeptide domain having sets of complementarity determining regions

(CDR) and framework (FR) amino acid sequences homologous to first and second immunoglobulin, respectively. The biosynthetic antibody binding sites are useful in specific binding assays, affinity purification, CC biocatalysis, drug targeting, imaging immunological treatment of various CC oncogenic and infectious diseases. The present sequence represents a CC the chimeric Vh comprising murine monoclonal 26-10 (anti-digoxin) FRs and CC murine monoclonal 91P-4 (anti-lysozyme) CDRs.

SQ Sequence 117 AA;

Query Match

Best Local Similarity 86.5%; Score 90; DB 22; Length 117;
Pred. No. 1.8e-06;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPGNGNTKYNOKFNG 17
|||||:|||||:|

Db 50 WIYPGNGNTKYNENFKG 66

RESULT 8

AAB62296 ID AAB62296 standard; protein; 117 AA.

XX AAB62296;

XX 29-JUN-2001 (first entry)

XX Human myeloma antibody NEMW Vh native sequence.

XX Biosynthetic; antibody binding site; binding assay; drug targeting;

XX biocatalysis; imaging; affinity purification; immunological; oncogenic;

XX infectious disease; human; myeloma; NEMW; cytosolic; antimicrobial.

XX Homo sapiens.

XX US6207804-B1.

XX 27-MAR-2001.

XX 18-DEC-1995; 95US-0575724.

XX 21-MAR-1987; 87US-0052800.

XX 12-MAR-1992; 92US-0850228.

XX 19-OCT-1993; 93US-0139901.

XX 30-JUN-1998; 98US-0213671.

XX (CURT-) CURIS INC.

XX Huston JS, Oppermann H;

XX WPI; 2001-280767/29.

XX Novel biosynthetic antibody binding site having chimeric polypeptide

XX PT which defines selective antigen binding region and has CDR and

XX PT framework amino acid sequences homologous to different immunoglobulin

XX PT molecules

XX Disclosure: Fig 3; 26pp; English.

XX The invention relates to a biosynthetic antibody binding site that

XX CC comprises disulfide bonded heavy, light variable region (HVR, LVR)

XX CC defining single, complete antigen (Ag1) binding site. HVR, LVR have

XX CC polypeptide domain having sets of complementarity determining regions

XX CC (CDR) and framework (FR) amino acid sequences homologous to first and

XX CC second immunoglobulin, respectively. The biosynthetic antibody binding

XX CC sites are useful in specific binding assays, affinity purification,

XX CC biocatalysis, drug targeting, imaging immunological treatment of various

XX CC oncogenic and infectious diseases. The present sequence represents a

XX CC heavy chain variable region of human myeloma antibody NEMW.

XX SQ Sequence 117 AA;

XX Query Match 86.5%; Score 90; DB 22; Length 117;

Best Local Similarity 82.4%; Pred. No. 1.8e-06;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;OY 1 WIYPGNGNTKYNOKFNG 17
|||||:|||||:|

Db 50 WIYPGNGNTKYNENFKG 66

RESULT 9

AAU99848 ID AAU99848 standard; protein; 117 AA.

XX AAU99848;

XX 07-OCT-2002 (first entry)

XX Mouse AC10 antibody heavy chain variable region.

XX Gene therapy; vaccine; CD30 binding; cytostatic; cytotoxic;

XX Hodgkin's Disease; mouse; AC10 antibody; heavy chain variable region.

XX Mus musculus.

XX WO200243661-A2.

XX 06-JUN-2002.

XX 28-NOV-2001; 2001WO-US44811.

XX 28-NOV-2000; 2000US-0724406.

XX (SEAT-) SEATTLE GENETICS INC.

XX Francisco JA, Risdon G, Wahl AF, Siegall CB;

XX WPI; 2002-557522/59.

XX N-PSDB; ABK88120.

XX Novel antibody that immunospecifically binds to CD30, useful for

XX PT treating Hodgkin's disease, exerts a cytostatic or cytotoxic effect on

XX PT Hodgkin's Disease cell line, and is not monoclonal antibody AC10 or

XX PT HeFl-1

XX Claim 11; Page 97; 103pp; English.

XX The invention describes an antibody (I) that immunospecifically binds to

XX CC CD30, exerts a cytostatic or cytotoxic effect on Hodgkin's Disease cell

XX CC line, and is not monoclonal antibody AC10 or HeFl-1 and does not result

XX CC from cleavage of AC10 or HeFl-1 with pepsin. (I), a protein

XX CC (II) that competes for CD30 binding with the monoclonal antibodies AC10

XX CC or HeFl, or exerts a cytotoxic or cytostatic effect on a Hodgkins'

XX CC disease cell line and the nucleic acid encoding the protein (III) are

XX CC useful for the treatment or prevention of Hodgkin's Disease in a subject,

XX CC by administering (I) to the subject, in the absence of conjugation to a

XX CC cytostatic or cytotoxic agent, respectively and a pharmaceutically

XX CC acceptable carrier. This is the amino acid sequence of the mouse AC10

XX CC antibody heavy chain variable region, a polypeptide that competes with

XX CC AC10 for CD30 binding.

XX SQ Sequence 117 AA;

XX Query Match 86.5%; Score 90; DB 23; Length 117;

XX Best Local Similarity 82.4%; Pred. No. 1.8e-06;

XX Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

XX OY 1 WIYPGNGNTKYNOKFNG 17

XX Db 50 WIYPGNGNTKYNENFKG 66

XX RESULT 10

XX AAB62293

XX ID AAB62293 standard; protein; 118 AA.

XX AC AAB62293;
XX XX
DT 29-JUN-2001 (first entry)
XX XX
DE Murine monoclonal g1p-4 Vh native sequence.
XX XX
XX Biosynthetic: antibody binding site; binding assay; drug targeting;
KM biocatalysts; imaging; affinity purification; immunological; oncogenic;
KM infectious disease; murine; monoclonal g1p-4; anti-lysozyme; cytostatic;
KM antimicrobial.
XX XX
OS Mus sp.
XX XX
PN US6207804-B1.
XX XX
PD 27-MAR-2001.
XX XX
PF 18-DEC-1995; 95US-0575724.
XX XX
PR 21-MAY-1987; 87US-0052800.
PR 12-MAR-1992; 92US-0850228.
PR 19-OCT-1993; 93US-0139901.
PR 30-JUN-1998; 98US-0213671.
XX XX
PA (CUR1-) CURIS INC.
XX XX
PI Huston JS, Oppermann H;
XX XX
DR WPI: 2001-280767/29.
XX XX
PT Novel biosynthetic antibody binding site having chimeric polypeptide
PT which defines selective antigen binding region and has CDR and
PT framework amino acid sequences homologous to different immunoglobulin
PT molecules
XX XX
PS Disclosure: Fig 3; 26pp; English.
XX XX
CC The invention relates to a biosynthetic antibody binding site that
CC comprises disulfide bonded heavy, light variable region (HVR, LVR)
CC defining single, complete antigen (Ag1) binding site. HVR, LVR have
CC polypeptide domain having sets of complementarity determining regions
CC (CDR) and framework (FR) amino acid sequences homologous to first and
CC second immunoglobulin, respectively. The biosynthetic antibody binding
CC sites are useful in specific binding assays, affinity purification,
CC biocatalysis, drug targeting, imaging immunological treatment of various
CC oncogenic and infectious diseases. The present sequence represents a
CC heavy chain variable region of murine monoclonal g1p-4 (anti-lysozyme),
CC which aids in designing a chimeric Vh.
XX XX
SQ Sequence 118 AA;

Query Match 86.5%; Score 90; DB 22; Length 118;
Best Local Similarity 82.4%; Pred. No. 1.8e-06;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPCNGNTKYNOKFNG 17
IIIIIIIIIIIIIIIIIIII
DB 50 WIYPCNGNTKYNENFKG 66

RESULT 11
AAB80154
ID AAB80154 standard; protein; 249 AA.
XX AC AAB80154;
XX XX
DT 01-JAN-1980 (first entry)
XX XX
DE Biosynthetic antibody binding site.
XX XX
KM Biosynthetic antibody binding site; framework region; assay; imaging;
KW multifunctional protein.

XX XX
PN WO8809344-A.
XX XX
PD 01-DEC-1988.
XX XX
PF 19-MAY-1988; 88WO-US01737.
XX XX
PR 21-MAY-1987; 87US-0052800.
XX XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
XX XX
PI Huston JS, Oppermann H;
XX XX
DR WPI: 1988-353928/49.
DR N-PSDB: AAN80180.
XX XX
PT Recombinant multifunctional protein - having antibody binding site and a
PT sequence for biological activity, ion sequestering or binding to a
PT solid support.
XX XX
PS Disclosure: 15pp; English.
XX XX
CC The biosynthetic antibody binding site forms part of a recombinant
CC multifunctional protein which also comprises an effector protein, an AA
CC acid sequence capable of sequestering an ion, or a sequence capable of
CC binding to a solid support. The BABS comprises the framework region from
CC murine anti-digoxin monoclonal antibody 26-10 heavy chain variable region
CC and the complementarity determining region from G-loop-4 heavy chain
CC variable region and has lysozyme specificity. The effector protein is an
CC enzyme, toxin, receptor, binding site, growth factor, cytokine
CC or antimetabolite. The sequence capable of sequestering an ion is
CC calmodulin or metallothionein. The sequence capable of binding to solid
CC support is streptavidin or a protein A fragment. The protein may be used
CC for, eg specific binding assays, affinity purification, biocatalysts, drug
CC targeting, imaging and immunological treatment of oncogenic etc.
CC diseases. The protein offers fewer cleavage sites to circulating
CC proteolytic enzymes and have improved stability. They reach target organs
CC rapidly and are cleared quickly from the body. They also have reduced
CC immunogenicity.
XX XX
SQ Sequence 249 AA;

Query Match 86.5%; Score 90; DB 9; Length 249;
Best Local Similarity 82.4%; Pred. No. 4.2e-06;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPCNGNTKYNOKFNG 17
IIIIIIIIIIIIIIIIIIII
DB 52 WIYPCNGNTKYNENFKG 68

RESULT 12
AAR79241
ID AAR79241 standard; protein; 116 AA.
XX AC AAR79241;
XX XX
DT 21-DEC-1995 (first entry)
XX XX
DE Heavy chain variable region for monoclonal antibody 4A10.
XX XX
KW Monoclonal antibody; heavy metal; mercury; variable region;
KW heavy chain.
XX XX
OS Synthetic.
XX XX
PN WO9520607-A.
XX XX
PD 03-AUG-1995.
XX XX
PF 27-JAN-1995; 95WO-US01199.
XX XX
PR 27-JAN-1994; 94US-0187407.

XX (BION-) BIONEERASKA INC.
 PA Lopez O, Wagner FW, Wylie DE;
 PI WPI: 1995-275415/36.
 XX N-PSDB: AA097498.
 DR
 XX
 PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
 PT monoclonal antibodies, used for detecting, removing, adding or
 PT neutralising heavy metals
 XX
 PS Claim 13: Page 54; 106pp; English.
 XX
 CC Hybridoma antibodies have been produced with the spleen cells of
 CC BALB/c mouse that had received multiple injections of mercuric ions
 CC reacted with glutathione to produce a mercuric ion coordinate
 CC covalent compound which was covalently bound to keyhole limpet
 CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
 CC 5B6 and 3E8) were producing MAbs that were strongly positive
 CC against glutathione-mercuric ions but negative against glutathione
 CC without mercuric ions. RNA was isolated from hybridoma cells with
 CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
 CC by MLV reverse transcriptase. The primers used for cDNA synthesis
 CC were complementary to the 5' end of the CH1 domain of the heavy
 CC chain expressed by the hybridoma of interest, or to the 5' end of
 CC the C kappa domain. Some of the primers used for cDNA synthesis are
 CC shown in AA097511-097518. The primer used for cDNA synthesis of the
 CC variable region of a particular antibody polypeptide was also used
 CC for PCR amplification of that variable region, in conjunction with
 CC an appropriate V-region primer. In addition, the VH primer AA097518
 CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences
 CC of the PCR amplified nucleotides were determined. These are given
 CC in AA097498-097510 and the deduced AA sequences in AAR79241-R79250 &
 CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
 CC and in the claims are different from the descriptions in the
 CC sequence listings. The descriptions in the sequence listings are
 CC used here.
 XX
 SO Sequence 116 AA;
 XX
 Query Match 81.7%; Score 85; DB 16; Length 116;
 Best Local Similarity 76.5%; Pred. No. 1,1e-05;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WIYPGNGNTKYNKGKENG 17
 II::II::II::II::II
 DB 50 WIYPGDGSTRKYNEKFKG 66
 XX
 RESULT 13
 AAB19871
 ID AAB19871 standard; Protein: 555 AA.
 XX
 AC AAB19871;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Activating polypeptide A-RBD-anti-MHC-I 34.1 scFv fusion.
 XX
 KW AMphotropic: MV; surface subunit; receptor binding domain; RBD;
 KW PHOV motif; activating polypeptide; envelope glycoprotein;
 KW retrovirus; fusion defective; infection; cancer; therapy;
 KW virulide; cytostatic; single chain antibody; scFv; MHC-I;
 KW major histocompatibility complex.
 XX
 OS Chimeric - Murine leukemia virus.
 OS Chimeric - Mammalia.
 XX
 PN WO200071578-A2.
 XX
 PD 30-NOV-2000.
 XX

PF 19-MAY-2000; 2000WO-EP04534.
 XX
 PR 20-MAY-1999; 99EP-0401220.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Cosset F, Lavillette D;
 XX
 DR WPI: 2001-061346/07.
 DR N-PSDB: AAA89071.
 XX
 PT Use of an activating polypeptide comprising an amino acid sequence from
 PT a surface subunit of a viral envelope glycoprotein, useful for the
 PT rescue of fusion defective viruses or retroviral glycoproteins, and for
 PT treating cancer -
 XX
 PS Disclosure: Fig 12; 96pp; English.
 XX
 CC The present sequence is that of a fusion protein between an
 CC activating polypeptide (I) comprising the receptor binding domain
 CC (RBD) and the PHOV motif of the amphotropic murine leukemia virus
 CC surface subunit (SU), and single chain antibody (scFv) 34.1, which
 CC is directed against human major histocompatibility complex type I.
 CC This is an example of activating polypeptides (I) used in the
 CC invention for the rescue of a fusion defective envelope glycoprotein
 CC (II). (I) may recognise the same or different receptors on target
 CC cells as are recognised by (II), and (I) and/or (II) may be linked to
 CC a ligand such as 34.1 scFv, that is specific to target cell receptors
 CC (in this case human cells). (I) may be expressed by a host, such
 CC as a virus or cell, or by the target cells, transformed by a
 CC nucleotide sequences coding for (I). (II) may be expressed by a
 CC host, such as a virus incorporating (II) in its envelope, or a cell
 CC transformed by nucleotide sequences coding for (II). (I) and (II)
 CC are used for the preparation of a drug for the treatment of cancer
 CC and infectious diseases, and as combined preparations for
 CC simultaneous, separate or sequential use for the rescue of the
 CC fusion defective property of (II) or for treatment of cancer
 CC pathologies (all claimed).
 CC
 XX
 SO Sequence 555 AA;
 XX
 Query Match 77.9%; Score 81; DB 22; Length 555;
 Best Local Similarity 70.6%; Pred. No. 0.00026;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WIYPGNGNTKYNKGKENG 17
 II::II::II::II::II
 DB 96 WIYPGDGSTRKYNEKFKG 112
 XX
 RESULT 14
 AAB19873
 ID AAB19873 standard; Protein: 565 AA.
 XX
 AC AAB19873;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Activating polypeptide GALV-RBD-anti-MHC-I 34.1 scFv fusion.
 XX
 KW GALV; retrovirus; surface subunit; receptor binding domain; RBD;
 KW PHOV motif; activating polypeptide; envelope glycoprotein;
 KW fusion defective; infection; cancer; therapy; virucide; cytostatic;
 KW single chain antibody; scFv; major histocompatibility complex; MHC.
 XX
 OS Chimeric - Gibbon leukemia virus.
 OS Chimeric - Mammalia.
 XX
 PN WO200071578-A2.
 XX
 PD 30-NOV-2000.
 XX
 PF 19-MAY-2000; 2000WO-EP04534.

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 : Search time 1.23667 Seconds

(without alignments)
469.543 million cell updates/sec

Title: US-09-743-482a-12

Perfect score: 87
Sequence: 1 DMHYSSYIRPFAY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	59.8	501	VNN3_HUMAN	O9ny84 homo sapien
2	44	50.6	595	BPRX_BACNO	P42780 bacteroides
3	44	50.6	1926	LPN_RABIT	P05849 oryctolagus
4	44	50.6	1927	LPN_HUMAN	P05848 homo sapien
5	43	49.4	393	VASS_BPRF	P15966 bacterioph
6	43	49.4	557	CABL_AQUAE	O67869 aquifex neo
7	43	49.4	750	NU5C_TECT	O911c2 lecomia stan
8	42	48.3	142	LYSX_DROME	P37161 drosophila
9	41.5	47.7	434	CBPS_STRCP	P35041 streptomyce
10	40	46.0	70	YAI2_ECOLI	P77273 escherichia
11	40	46.0	160	PM12_HUMAN	O01453 homo sapien
12	40	46.0	193	VF10_METJA	O56905 methanococc
13	40	46.0	507	TRA6_PSEAE	O57541 pseudomonas
14	40	46.0	629	VEL_HPV31	P17382 human papil
15	40	46.0	649	INVA_PHAUV	P29001 phaseolus a
16	40	46.0	651	SYN_HUMAN	O24509 phaseolus v
17	40	46.0	900	AG15_BRANA	P56192 homo sapien
18	39	44.8	264	AG15_BRANA	O39295 brassica na
19	39	44.8	321	CYF_GUTTH	O78494 guillardia
20	39	44.8	329	PLC_BACCE	P14262 bacillus ce
21	39	44.8	329	PLC_BACCTO	P08954 bacillus th
22	39	44.8	554	MANB_MYCPN	P75050 mycoplasma
23	39	44.8	589	LJLI_LYCPN	O04973 lycopersico
24	39	44.8	670	INV1_MAIZE	P49171 zea mays (m
25	39	44.8	1181	YV02_METJA	O60301 methanococc
26	39	44.8	1804	YFA7_YEAST	P45883 saccharomyc
27	39	44.8	2148	VIT1_AEDAE	O16927 aedes aegypt
28	38.5	44.3	648	CH44_YEAST	P43634 saccharomyc
29	38.5	44.3	944	VGJB_HSVT2	O9wrl5 herpesvirus
30	38	43.7	192	NUMG_PROWI	O37622 prototheca
31	38	43.7	198	NUMG_PROWI	P26523 synechocyst
32	38	43.7	281	ARAC_CITR	P11765 citrobacter
33	38	43.7	281	ARAC_SALTY	P03022 salmonella

34	38	43.7	292	1	ARAC_ECOLI	P03021 escherichia
35	38	43.7	357	1	YCF1_ECOLI	P75955 escherichia
36	38	43.7	414	1	YAG3_YEAST	P42838 saccharomyc
37	38	43.7	468	1	AMYB_BACCT	P96513 bacillus fi
38	38	43.7	521	1	CYOA_HAELN	P45021 haemophilus
39	38	43.7	522	1	CYDA_ECOLI	P11026 escherichia
40	38	43.7	551	1	AMYB_THERU	P19584 thermomane
41	38	43.7	575	1	AMYB_BACCI	P06547 bacillus ci
42	38	43.7	692	1	NUMG_MARPO	P06264 marchantia
43	38	43.7	1196	1	AMYB_PAPRO	P21543 penicillium
44	38	43.7	1564	1	PDR1_YEAST	P51533 saccharomyc
45	38	43.7	3411	1	POLG_YEYV1	P03314 y genome po

ALIGNMENTS

RESULT 1

VNN3_HUMAN STANDARD: PRT: 501 AA.

AC O9ny84: 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Vascular non-inflammatory molecule 3 precursor (Vanin 3).

GN VNN3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=99432008; PubMed=10501839;

RA Granjeaud S., Naquet P., Galland F.;

"An ESTs description of the new vanin gene family conserved from fly

to human.";

RT Immunogenetics 49:964-972(1999).

RI FUNCTION: PROBABLE HYDROLASE.

- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor

(Potential).

- SIMILARITY: BELONGS TO THE CN HYDROLASE FAMILY. BTD/VNN SUBFAMILY.

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EMBL: AJ238982; CAB76824.1; -

DR Genew; HGNC:16431; VNN3.

DR MIM: 606592; -

DR InterPro: IPR003010; Ntase/CNhydase.

DR Pfam: PF00795; CN_hydrolase; 1.

KW Hydrolase; Signal; Glycoprotein; GPI-anchor.

FT SIGNAL 1 22

FT CHAIN 23 470

FT PROPEP 471 501

FT LIPID 470 470

FT CARBOHYD 39 39

FT CARBOHYD 147 147

FT CARBOHYD 270 270

FT CARBOHYD 358 358

FT SIGNAL 501 AA; 56089 MW; E0B89GHA3AE1B81 CRC64;

SEQ

Query Match 59.8%; Score 52; DB 1; Length 501;

Best Local Similarity 53.8%; Pred. No. 1.3;

Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

1 DMHYSSYIRPFA 13

|||||:|:|:|:

```

Db 320 DMHAYASSVKPFS 332

RESULT 2
BPRX_BACNO
ID BPRX_BACNO STANDARD: PRT: 595 AA.
AC P42780;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Extracellular subtilisin-like protease precursor (EC 3.4.21.-).
OS Bacteroides nodosus (Dichelobacter nodosus).
OC Bacteroides; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
OC Dichelobacter.
OX NCBI_TaxID=870;
RN 11]
RP SEQUENCE FROM N.A.
RA Good R.T., Brandon R.B., Langford C.J., Moses E.K.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
CC -----
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CC -----
CC EMBL: L08175; AAA99869.1; -.
CC DR HSSP: Q99405; 1MPT.
CC DR MEROPS: S08_022; -.
CC DR InterPro: IPR000209; Peptidase-S8.
CC DR Pfam: PF00082; Peptidase-S8; 1.
CC DR PRINTS: PR00723; SUBTILISIN.
CC DR PROSITE: PS00136; SUBTILISIN.ASP. 1.
CC DR PROSITE: PS00137; SUBTILISIN.HIS. 1.
CC DR PROSITE: PS00138; SUBTILISIN.SER. 1.
CC KM Hydrolyase; Serine protease; zymogen; signal.
CC FT SIGNAL 1 21 POTENTIAL.
CC FT PROPEP 22 130 POTENTIAL.
CC FT CHAIN 131 595 EXTRACELLULAR SUBTILISIN-LIKE PROTEASE.
CC FT ACT_SITE 171 171 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 237 237 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 409 409 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC SQ SEQUENCE 595 AA; 64136 MW; 744EF9B53187442E CRC64;

Query Match 50.6%; Score 44; DB 1; Length 595;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 WHYSSY 8
Db 142 WHYSET 148

RESULT 3
LPH_RABIT
ID LPH_RABIT STANDARD: PRT: 1926 AA.
AC P09849;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Lactase-phlorizin hydrolase precursor (lactase-glycosylceramidase)
DE [Includes: Lactase (EC 3.2.1.108); Phlorizin hydrolase (EC 3.2.1.62)].
GN LCT OR LPH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN 11]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN-New Zealand white;
RX MEDLINE=89030634; PubMed=2460343;
RA Mantel N., Villa M., Enzler T., Wacker H., Boll W., James P.,
RA Hunziker W., Semenza G.;
RT "Complete primary structure of human and rabbit lactase-phlorizin
RT hydrolase: implications for biosynthesis, membrane anchoring and
RT evolution of the enzyme.";
RL EMBO J. 7:2705-2713(1988).
RN 12]
RP ACTIVE SITES.
RX MEDLINE=92406791; PubMed=1388157;
RA Wacker H., Keller P., Falchetto R., Legler G., Semenza G.;
RT "Location of the two catalytic sites in intestinal lactase-phlorizin
RT hydrolase. Comparison with sucrose-isomaltase and with other
RT glycosidases, the membrane anchor of lactase-phlorizin hydrolase.";
RL J. Biol. Chem. 267:18744-18752(1992).
CC -1- FUNCTION: LPH SPLITS LACTOSE IN THE SMALL INTESTINE.
CC -1- CATALYTIC ACTIVITY: Lactose + H(2)O = D-glucose + D-galactose.
CC -1- CATALYTIC ACTIVITY: Glycosyl-N-acylsphingosine + H(2)O = a sugar +
CC N-acylsphingosine.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. BRUSH BORDER.
CC -1- TISSUE SPECIFICITY: INTESTINE.
CC -1- DOMAIN: THE SEQUENCE EXHIBITS 4 REGIONS (I-IV) OF INTERNAL
CC HOMOLOGY; THEREFORE LPH MIGHT HAVE EVOLVED BY TWO CYCLES OF
CC PARTIAL GENE DUPLICATION.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
CC EMBL: X07995; CAA30802.1; -.
CC DR PIR: S01169; S01169.
CC DR HSSP: P26205; 1CBG.
CC DR InterPro: IPR001360; GH_1.
CC DR Pfam: PF00232; Glyco_hydro_1; 5.
CC DR PRINTS: PR00131; GLYHIDRASE1.
CC DR ProDom: PD000650; GH_1; 4.
CC DR PROSITE: PS00572; GLYCOSYL_HYDROL_F1_1; 2.
CC DR PROSITE: PS00573; GLYCOSYL_HYDROL_F1_2; 3.
CC KM Hydrolyase; Glycosidase; zymogen; signal; Transmembrane; Repeat.
CC FT SIGNAL 1 19
CC FT PROPEP 20 866 BETA-GLUCOSIDASE.
CC FT CHAIN 867 1926 LACTASE-PHLORITIN HYDROLASE.
CC FT DOMAIN 20 1882 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 1883 1901 POTENTIAL.
CC FT DOMAIN 1902 1926 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 79 1800 4 X APPROXIMATE REPEATS.
CC FT REPEAT 79 172 1.
CC FT REPEAT 360 845 2.
CC FT REPEAT 881 1367 3.
CC FT REPEAT 1375 1800 4.
CC FT ACT_SITE 1063 1063 PROTON DONOR (POTENTIAL).
CC FT ACT_SITE 1271 1271 NUCLEOPHILE.
CC FT ACT_SITE 1536 1536 PROTON DONOR (POTENTIAL).
CC FT ACT_SITE 1747 1747 NUCLEOPHILE.
CC SQ SEQUENCE 1926 AA; 217847 MW; 2A21A7370D0CFC7A CRC64;

Query Match 50.6%; Score 44; DB 1; Length 1926;
Best Local Similarity 60.0%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 2 WHYSSYRP 11
Db 580 WHHYNSHHRP 589

RESULT 4
LPH_HUMAN

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ID LPH_HUMAN STANDARD: PRT; 1927 AA.
AC P09848:
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lactase-phlorizin hydrolase precursor (Lactase-glycosylceramidase)
DE [includes: Lactase (EC 3.2.1.108); Phlorizin hydrolase (EC 3.2.1.62)].
GN LCT OR LPH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE=89030634; PubMed=2460343;
RA Mantei N., Villa M., Enzler T., Wacker H., Boll W., James P.,
RA Hunziker W., Semenza G.;
RT "Complete primary structure of human and rabbit lactase-phlorizin
RT hydrolase: implications for biosynthesis, membrane anchoring and
RT evolution of the enzyme.";
RL EMBO J. 7:2705-2713(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91206402; PubMed=1902057;
RA Boll W., Wagner P., Mantei N.;
RT "Structure of the chromosomal gene and cDNAs coding for lactase-
RT phlorizin hydrolase in humans with adult-type hypolactasia or
RT persistence of lactase.";
RL Am. J. Hum. Genet. 48:889-902(1991).
CC -1- FUNCTION: LPH SPLIT LACTOSE IN THE SMALL INTESTINE.
CC -1- CATALYTIC ACTIVITY: Lactose + H(2)O = D-glucose + D-galactose.
CC -1- CATALYTIC ACTIVITY: Glycosyl-N-acylsphingosine + H(2)O = a sugar +
CC N-acylsphingosine.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. BRUSH BORDER.
CC -1- TISSUE SPECIFICITY: INTESTINE.
CC -1- DOMAIN: THE SEQUENCE EXHIBITS 4 REGIONS (I-IV) OF INTERNAL
CC HOMOLOGU; THEREFORE LPH MIGHT HAVE EVOLVED BY TWO CYCLES OF
CC PARTIAL GENE DUPLICATION.
CC -1- DISEASE: DEFECTS IN LCT ARE THE CAUSE OF DISACCHARIDE INTOLERANCE
CC TYPE II (OR CONGENITAL LACTASE DEFICIENCY) OR III (OR ADULT
CC LACTASE DEFICIENCY). IN MANY HUMAN POPULATIONS THE ACTIVITY OF LCT
CC DECLINES IN ADULTS, LEADING TO ADULT-TYPE HYPOLACTASIA, WHEREAS IN
CC OTHER POPULATIONS THE HIGH ACTIVITY PERSISTS.
CC -1- SIMILARITY: BELONGS TO FAMILY I OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL; X07994; CAA30801.1; -;
DR EMBL; M61850; AAA59504.1; -;
DR EMBL; M61834; AAA59504.1; JOINED.
DR EMBL; M61835; AAA59504.1; JOINED.
DR EMBL; M61836; AAA59504.1; JOINED.
DR EMBL; M61837; AAA59504.1; JOINED.
DR EMBL; M61838; AAA59504.1; JOINED.
DR EMBL; M61839; AAA59504.1; JOINED.
DR EMBL; M61840; AAA59504.1; JOINED.
DR EMBL; M61841; AAA59504.1; JOINED.
DR EMBL; M61842; AAA59504.1; JOINED.
DR EMBL; M61843; AAA59504.1; JOINED.
DR EMBL; M61844; AAA59504.1; JOINED.
DR EMBL; M61845; AAA59504.1; JOINED.
DR EMBL; M61846; AAA59504.1; JOINED.
DR EMBL; M61847; AAA59504.1; JOINED.
DR EMBL; M61848; AAA59504.1; JOINED.
DR EMBL; M61849; AAA59504.1; JOINED.
DR PIR; S01168; S01168.
DR HSP; P26205; ICBG.

DR Genew: HGNC:6530; LCT.
DR MIM: 603202; -;
DR MIM: 223000; -;
DR MIM: 223100; -;
DR InterPro: IPR001360; GH_1.
DR Pfam: PF00232; Glyco_hydro_1; 4.
DR PRINTS: PR00131; GLHYDRLASE1.
DR Prodom: PD000650; GH_1; 4.
DR PROSITE: PS00572; GLYCOSYL_HYDROL_FL_1; 2.
DR PROSITE: PS00653; GLYCOSYL_HYDROL_FL_2; 3.
KW Hydrolase; Glycosidase; Zymogen; Signal; Transmembrane; Repeat.
FT SIGNAL 1
FT PROPEP 20 866
FT CHAIN 867 1927
FT DOMAIN 867 1927
FT TRANSMEM 1883 1901
FT DOMAIN 1902 1927
FT DOMAIN 87 1841
FT REPEAT 87 172
FT REPEAT 363 848
FT REPEAT 884 1365
FT REPEAT 1370 1841
FT ACT_SITE 1065 1065
FT ACT_SITE 1273 1273
FT ACT_SITE 1538 1538
FT ACT_SITE 1749 1749
FT CONFLICT 219 219
FT CONFLICT 1639 1639
SQ SEQUENCE 1927 AA; 218601 MW; FA748640B9A35A6F CRC64;
Query Match 50.6%; Score 44; DB 1; Length 1927;
Best Local Similarity 60.0%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 WHYSSYIRP 11
DB 582 WHYNSHHRP 591
RESULT 5
ID VASS_BPFR STANDARD: PRT; 393 AA.
AC P15966;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Assembly protein (Maturation protein) (A protein).
GN A.
OS Bacteriophage fr.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Leviviruses.
OX NCBI_TaxID=12017;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87316939; PubMed=3628010;
RA Adhin M.R., Avots A.J., Berezin V.M., Overbeek G.P., van Duin J.;
RA Berezin V.M., Avots A.J., Jansone I.V., Gutnere L., Tsimanis A.J.;
RT "Sequence of the genes coding for the A-protein and coat protein of
RT bacteriophage fr.";
RL Nucleic Acids Res. 15:6741-6741(1987).
CC -1- FUNCTION: THE MATURATION PROTEIN IS REQUIRED FOR THE TYPICAL
CC ATTACHMENT OF THE PHAGE TO THE SIDE OF THE BACTERIAL PLT.
CC IT ACCOMPANY THE VIRAL DNA INTO THE CELL.
CC -----
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 CC -----
 DR EMBL: X15031; CAAG3135.1; -;
 DR EMBL: M31635; AAA32188.1; -;
 DR PIR: S08017; S08017.
 KW Phage recognition.
 FT CONFLICT 232 R -> S (IN REF. 2).
 FT CONFLICT 334 T -> I (IN REF. 2).
 SO SEQUENCE 393 AA; 43956 MW; 9CD23BE75FE1459F CRC64;
 Query Match 49.4%; Score 43; DB 1; Length 393;
 Best Local Similarity 70.0%; Pred. No. 22;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DMHYSSYIR 10
 DB 53 EMHYSSYSR 62
 RESULT 6
 CABL_AQUAE STANDARD; PRT; 557 AA.
 AC 067869;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Carbamoyl-phosphate synthase large chain, N-terminal section (EC
 DE 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
 GN CABL OR AQ_2101.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
 OC Aquifex.
 ON NCBI_TaxID=63363;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VFS;
 RX MEDLINE=9819666; PubMed=9537320;
 RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus.";
 RL Nucleic Acids Res. 27:353-358(1998).
 CC -1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +
 CC phosphate + L-glutamate + carbamoyl phosphate.
 CC -1- COFACTOR: Binds three manganese ions (By similarity).
 CC -1- PATHWAY: Arginine biosynthesis.
 CC -1- PATHWAY: Pyrimidine biosynthesis; first step.
 CC -1- SUBUNIT: Composed of two chains; the small (or glutamine) chain
 CC promotes the hydrolysis of glutamine to ammonia, which is used by
 CC the large (or ammonia) chain to synthesize carbamoyl phosphate (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE CARB FAMILY. N-TERMINAL SECTION.
 CC -1- CAUTION: Sequence of carb is split into two genes in A.aeolicus
 CC (AQ_1172 and AQ_2101).
 CC -----
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 CC -----
 DR EMBL: AEO00772; AAC07826.1; -;
 DR HSSP: P00968; IJDB.
 DR InterPro: IPR005483; CPase_L.
 DR InterPro: IPR005479; CPase_L_D2.
 DR InterPro: IPR005480; CPase_L_D3.
 DR InterPro: IPR005481; CPase_L_N.
 DR Pfam: PF00289; CPase_L_chain; 1.

DR Pfam: PF02786; CPase_L_D2; 1.
 DR Pfam: PF02787; CPase_L_D3; 1.
 DR PRINTS: PR00098; CPASE.
 DR PROSITE: PS00866; CPASE_1; 1.
 DR PROSITE: PS00867; CPASE_2; 1.
 KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; ATP-binding;
 KW Manganese; Complete proteome.
 FT DOMAIN 1 402 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
 FT DOMAIN 403 543 OLIGOMERIZATION DOMAIN.
 FT NE_BIND 153 210 ATP (POTENTIAL).
 FT NE_BIND 303 353 ATP (POTENTIAL).
 FT METAL 285 285 MANGANESE 1 (BY SIMILARITY).
 FT METAL 299 299 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 301 301 MANGANESE 2 (BY SIMILARITY).
 SO SEQUENCE 557 AA; 62404 MW; 89C259FDC0170A37 CRC64;
 Query Match 49.4%; Score 43; DB 1; Length 557;
 Best Local Similarity 70.0%; Pred. No. 31;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 HYSSYIRRP 12
 DB 536 YYYSSYRPP 545
 RESULT 7
 NUSC_TRECST STANDARD; PRT; 750 AA.
 ID NUSC_TRECST
 AC Q9TLC2;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE NADH-plastoquinone oxidoreductase chain 5, chloroplast (EC 1.6.5.3).
 GN NDHF.
 OS Tecoma stans (Yellow bells).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Bignoniaceae; Tecoma.
 ON NCBI_TaxID=69904;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Kim K.-J., Jansen R.K., Olmstead R.C.;
 RT "Multiple origins of sympetaly and associated floral characters.";
 RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: NADH + plastoquinone = NAD(+) + plastoquinol.
 CC -----
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 CC -----
 DR EMBL: AF130145; AAF08107.1; -;
 DR InterPro: IPR001750; Oxidored_g1.
 DR InterPro: IPR002128; Oxidored_g1_C.
 DR InterPro: IPR001516; Oxidored_g1_N.
 DR Pfam: PF00361; Oxidored_g1; 1.
 DR Pfam: PF00662; Oxidored_g1_N; 1.
 DR Pfam: PF01010; Oxidored_g1_C; 1.
 KW Oxidoreductase; NAD; Plastoquinone; Chloroplast.
 SO SEQUENCE 750 AA; 85200 MW; DB3CBB6C73FBB648 CRC64;
 Query Match 49.4%; Score 43; DB 1; Length 750;
 Best Local Similarity 58.3%; Pred. No. 41;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DMHYSSYIRRP 12
 DB 659 DMSYRATYIDPP 670

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RESULT 8
LVSX_DROME
ID LVSX_DROME STANDARD: PRT: 142 AA.
AC P37161: 09WOK1.
DT 01-OCT-1994 (Rel. 30, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lvszyme X precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase X).
LVSX OR CG9120.
OS Drosophila melanogaster (fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227.
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Arif J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertzer S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegan C.,
RA Jallat M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kerchum K.A.,
RA Kimmel B.E., Kodali C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Stiden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Slier E., Stradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN 121
RP SEQUENCE OF 62-142 FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=94211204; PubMed=8159165;
RA Daffre S., Kystlen P., Samakovlis C., Hultmark D.;
RT "The lyszyme locus in Drosophila melanogaster: an expanded gene
RT family adapted for expression in the digestive tract."
RL Mol. Gen. Genet. 242:152-162(1994).
CC -1- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE
CC DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE
CC GUT BEFORE METAMORPHOSIS.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
CC acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
CC heteropolymers of the prokaryotes cell walls.
CC -1- TISSUE SPECIFICITY: FOUND IN THE MIDGUT.

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CC -1- DEVELOPMENTAL STAGE: RISES DRAMATICALLY IN THE LATE THIRD INSTAR,
CC THEN DECREASES GRADUALLY DURING THE PUPAL STAGES. LOW EXPRESSION
CC IS FOUND IN ADULTS.
CC -1- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
CC EMBL: AE003470; AAF7445.1; -
CC EMBL: Z22224; CA80226.1; -
CC PIR: S32650; S32650.
CC HSP: P00698; 1A75.
CC Flybase: FBgn0004431; LvsX.
CC InterPro: IPR001916; GH_22.
CC Pfam: PF00062; Lys_1.
CC PRINTS: PR00135; LY2LACT.
CC SMART: SMO0263; LY2L_1.
CC PROSITE: PS00128; LACTALBUMIN_LYSOZYME; 1.
CC Hydrolyase; glycosidase; Bacteriolytic enzyme; Signal;
CC Multigene family.
CC SIGNAL 1 19 POTENTIAL.
CC CHAIN 20 142 LYSOZYME X.
CC DISULFID 25 140 BY SIMILARITY.
CC DISULFID 46 130 BY SIMILARITY.
CC DISULFID 81 97 BY SIMILARITY.
CC DISULFID 93 111 BY SIMILARITY.
CC ACT_SITE 51 51 BY SIMILARITY.
CC ACT_SITE 69 69 BY SIMILARITY.
CC CONFLECT 78 78 M -> L (IN REF. 2).
CC SEQUENCE 142 AA; 15591 MW; 2A48035364B95BC CRC64.
CC -----
Query Match 48.3%; Score 42; DB 1; Length 142;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 2 WHYISSTRP 11
DB 127 WHYCSGYLPP 136
RESULT 9
CBPS_STRCP STANDARD: PRT: 434 AA.
ID CBPS_STRCP
AC P39041.
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Zinc-carboxypeptidase precursor (EC 3.4.17.-).
OS Streptomyces capreolus.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Pseudonocardineae; Actinosynnemataceae;
OC Saccharothrix.
OX NCBI_Taxid=66854.
RN 111
RP SEQUENCE FROM N.A.
RA Thlara A.S., Cundliffe E.;
RL Submitted (AUG-1993) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: COMBINES THE SPECIFICITIES OF MAMMALIAN CPASE A
CC AND B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Peptidyl-L-amino acid + H(2)O = peptide + L-
CC amino acid.
CC -1- CATALYTIC ACTIVITY: Peptidyl-L-lysine(or L-arginine) + H(2)O =
CC peptide + L-lysine(or L-arginine).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M14.
CC -----
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RN [7]
RP REVIEW ON CMT-1A AND DSS VARIANTS.
RX MEDLINE=99103460; PubMed=9888385;
RA Nelis E., Hates N., van Broeckhoven C.;
RT "Mutations in the peripheral myelin genes and associated genes in
RL inherited peripheral neuropathies.";
RN Hum. Mutat. 13:11-28(1999).
RP VARIANT CMT-1A PRO-16, AND SEQUENCE FROM N.A.
RX MEDLINE=93265161; PubMed=1303281;
RA Valentijn L.J., Baas F., Wolterman R.A., Hoogendijk J.E.,
RA van den Bosch N.H.A., Zorn I., Gabreels-Festen A.A.W.M., de Visser M.,
RA Bolhuis P.A.;
RT "Identical point mutations of PMP-22 in Trembler-J mouse and Charcot-
RL Marie-Tooth disease type 1A.";
RN Nat. Genet. 2:288-291(1992).
RN [9]
RP VARIANTS DSS LYS-69, LEU-72; CMT-1A CYS-79, AND VARIANT MET-118.
RX MEDLINE=94073197; PubMed=8252046;
RA Roa B.B., Garcia C.A., Pentao L., Killian J.M., Trask B.J.,
RA Suter U., Snipes G.J., Ortiz-Lopez R., Shooter E.M., Patel P.I.,
RA Lupski J.R.;
RT "Evidence for a recessive PMP22 point mutation in Charcot-Marie-Tooth
RL disease type 1A.";
RN Nat. Genet. 5:189-194(1993).
RN [10]
RP VARIANTS DSS LYS-69 AND LEU-72.
RX MEDLINE=94100982; PubMed=8275092;
RA Roa B.B., Dyck P.J., Marks H.G., Chance P.F., Lupski J.R.;
RT "Dejerine-Sottas syndrome associated with point mutation in the
RL peripheral myelin protein 22 (PMP22) gene.";
RN Nat. Genet. 5:269-273(1993).
RN [11]
RP VARIANT CMT-1A CYS-79.
RX MEDLINE=93286088; PubMed=8510709;
RA Roa B.B., Garcia C.A., Suter U., Kulpa D.A., Wise C.A., Mueller J.,
RA Weicher A.A., Snipes G.J., Shooter E.M., Patel P.I., Lupski J.R.;
RT "Charcot-Marie-Tooth disease type 1A. Association with a spontaneous
RL point mutation in the PMP22 gene.";
RN New Engl. J. Med. 329:96-101(1993).
RN [12]
RP VARIANT CMT1 ARG-105.
RX MEDLINE=96191764; PubMed=8615087;
RA Gabreels-Festen A.A.W.M., Bolhuis P.A., Hoogendijk J.E.,
RA Valentijn L.J., Eshuis E.J., Gabreels F.J.M.;
RT "Charcot-Marie-Tooth disease type 1A: morphological phenotype of the
RL 17p duplication versus PMP22 point mutations.";
RN Acta Neuropathol. 90:645-649(1995).
RN [13]
RP VARIANT DSS GLN-12.
RX MEDLINE=95245343; PubMed=7728152;
RA Valentijn L.J., Ouvrier R.A., van den Bosch N.H.A., Bolhuis P.A.,
RA Baas F., Nicholson G.A.;
RT "Dejerine-Sottas neuropathy is associated with a de novo PMP22
RL mutation.";
RN Hum. Mutat. 5:76-80(1995).
RN [14]
RP VARIANT DSS LEU-72.
RX MEDLINE=95405644; PubMed=7675244;
RA Ionasescu V.V., Ionasescu R., Searby C.C., Neahring R.;
RT "Dejerine-Sottas disease with de novo dominant point mutation of the
RL PMP22 gene.";
RN Neurology 45:1766-1767(1995).
RN [15]
RP VARIANT CMT-1A ARG-93.
RX MEDLINE=96241146; PubMed=8777804;
RA Ohnishi A., Yoshimura T., Kanehisa Y., Fukushima Y.;
RT "A case of hereditary motor and sensory neuropathy type I with a new
RL type of peripheral myelin protein (PMP)-22 mutation.";
RN Rinsho Shinkagaku 35:788-792(1995).
RX MEDLINE=96209919; PubMed=8655153;
RA Navon R., Seifried B., Gal-On N.S., Sadeh M.;
RT "A new point mutation affecting the fourth transmembrane domain of
RL PMP22 results in severe de novo Charcot-Marie-Tooth disease.";
RN Hum. Genet. 97:685-687(1996).
RN [17]
RP VARIANTS DSS TRP-72, ILE-76 AND PRO-80.
RX MEDLINE=97208855; PubMed=9055797;
RA Tyson J., Ellis D., Fairbrother U., King R.H., Muntoni F., Jacobs J.,
RA Malcom S., Harding A.E., Thomas P.K.;
RT "Hereditary demyelinating neuropathy of infancy. A genetically complex
RL syndrome.";
RN Brain 120:47-63(1997).
RN [18]
RP VARIANT DSS ARG-100.
RX MEDLINE=97331335; PubMed=9187667;
RA Bort S., Nelis E., Timmerman V., Sevilla T., Cruz-Martinez A.,
RA Martinez F., Millan J.M., Arpa J., Vilchez J.J., Prieto F.,
RA van Broeckhoven C., Palau F.;
RT "Mutational analysis of the PMP22 and Cx32 genes in patients of
RL Spanish ancestry with Charcot-Marie-Tooth disease and hereditary
RN neuropathy with liability to pressure palsies.";
RN Hum. Genet. 99:746-754(1997).
RN [19]
RP VARIANT DSS ASP-150.
RX MEDLINE=97151053; PubMed=8995589;
RA Ionasescu V.V., Searby C.C., Ionasescu R., Chakraborty S., Patel N.,
RA Koenigsberger R.;
RT "Dejerine-Sottas neuropathy in mother and son with same point mutation
RL of PMP22 gene.";
RN Muscle Nerve 20:97-99(1997).
RN [20]
RP VARIANT MET-118.
RX MEDLINE=97141911; PubMed=8988161;
RA Nelis E., Holmberg B., Adolfsson R., Holmgren G., van Broeckhoven C.;
RT "PMP22 Thr(118)Met: recessive CMT1 mutation or polymorphism?";
RN Nat. Genet. 15:13-14(1997).
RN [21]
RP VARIANT CMT-1A VAL-107.
RX MEDLINE=97193152; PubMed=9040744;
RA Marrosu M.G., Vaccargiu S., Marrosu G., Vannelli A., Cianchetti C.,
RA Muntoni F.;
RT "A novel point mutation in the peripheral myelin protein 22 (PMP22)
RL gene associated with Charcot-Marie-Tooth disease type 1A.";
RN Neurology 48:489-493(1997).
RN [22]
RP VARIANT DSS GLU-100.
RX MEDLINE=98244766; PubMed=9585367;
RA Marques W., Jr., Thomas P.K., Sweeney M.G., Carr L., Wood N.M.;
RT "Dejerine-Sottas neuropathy and PMP22 point mutations: a new base pair
RL substitution and a possible 'hot spot' on Ser72.";
RN Ann. Neurol. 43:680-683(1998).
RN [23]
RP VARIANT DSS CYS-150.
RX MEDLINE=98204401; PubMed=9544841;
RA Ikegami T., Ikeda H., Aoyama M., Matsuki T., Imota T., Fukuchi Y.,
RA Amano T., Toyoshima I., Ishihara Y., Endoh H., Haysaka K.;
RT "Novel mutations of the peripheral myelin protein 22 gene in two
RL pedigrees with Dejerine-Sottas disease.";
RN Hum. Genet. 102:294-298(1998).
RN [24]
RP VARIANT DSS PRO-79.
RX MEDLINE=98112432; PubMed=9452053;
RA Bort S., Sevilla T., Garcia-Planells J., Blesa D., Paricio N.,
RA Vilchez J.J., Prieto F., Palau F.;
RT "Dejerine-Sottas neuropathy associated with de novo S79P mutation of
RL the peripheral myelin protein 22 (PMP22) gene.";
RN Hum. Mutat. Suppl. 1:S95-S98(1998).
RN [25]
RP VARIANT MET-118.
RX MEDLINE=98112478; PubMed=9452099;
RA Sorour E., Upadhyaya M.;
RT "Mutation analysis in Charcot-Marie-Tooth disease type I (CMT1).";


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Query Match          46.0%: Score 40; DB 1; Length 160;
Best Local Similarity 50.0%: Pred. No. 26;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DMHYSSYRPPAY 14
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 123 EWHLNSDYSYGFAV 136

RESULT 12
VF10_METVA          ,
VF10_METVA          STANDARD; PRT; 193 AA.
AC Q58905;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ1510.
CN MJ1510.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
CX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sulten G.G., Blake O., Olsen G.J., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerelevage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reisch C.J.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Ullrich T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Colton M.P., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: BELONGS TO THE UPF0130 FAMILY.
CC -----
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CC -----
CC CC EMBL: U67592; AAB9529.1; -.
CC DR TIGR: MJ1510; -.
CC DR InterPro: IPR003827; DUF207.
CC DR Pfam: PF02676; DUF207; 1.
CC KM Hypothetical protein; Complete proteome.
CC SQ SEQUENCE 193 AA; 22401 MW; D8E149EC784A51C9 CRC64;

Query Match          46.0%: Score 40; DB 1; Length 193;
Best Local Similarity 71.4%: Pred. No. 31;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WHYYSY 8
    1 1 1 1 1 1 1 1
Db 71 WHYHASY 77

RESULT 13
TRAF_PSEAE
ID TRAF_PSEAE          STANDARD; PRT; 507 AA.
AC Q57541;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Transposase for insertion sequences IS1326/IS1353.
CN ISTA.
OS Pseudomonas aeruginosa, and

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OS Shigella flexneri.
OC Plasmid pVSL.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
CX NCBI_TaxID=287, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON-Tn21;
RC MEDLINE=96345606; PubMed=8755869;
RX Brown H.J., Stokes H.W., Hall R.M.;
RA "The integrons In0, In2, and In5 are defective transposon
RT derivatives."
RL J. Bacteriol. 178:4429-4437(1996).
CC -1- FUNCTION: REQUIRED FOR THE TRANSDUCTION OF THE INSERTION ELEMENT
CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE IS21/IS408/IS162 FAMILY OF
CC TRANSPOSASES.
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CC -----
CC DR EMBL: U49101; AAC44320.1; -.
CC DR EMBL: U38187; AAA9725.1; -.
CC DR EMBL: U42226; AAC53729.1; -.
CC DR InterPro: IPR001584; RVE.
CC DR Pfam: PF00665; rve; 1.
CC KM Transposable element; Transposition; DNA-binding; DNA recombination;
CC plasmid.
CC SQ SEQUENCE 507 AA; 57965 MW; C90AA7512A5CCALP CRC64;

Query Match          46.0%: Score 40; DB 1; Length 507;
Best Local Similarity 34.8%: Pred. No. 78;
Matches 8; Conservative 3; Mismatches 2; Indels 10; Gaps 1;

Qy 1 DMHYSSYR-----PRA 13
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 384 DMHNYLVLQKKRPGALRNGCPFA 406

RESULT 14
VE1_HPV31
ID VE1_HPV31          STANDARD; PRT; 629 AA.
AC P17382;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Replication protein E1.
CN E1.
OS Human papillomavirus type 31.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
CX NCBI_TaxID=10585;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89299478; PubMed=2545036;
RX Goldsborough M.D., Dislvestre D., Temple G.F., Lorincz A.T.;
RA "Nucleotide sequence of human papillomavirus type 31: a cervical
RT neoplasia-associated virus."
RL Virology 171:306-311(1989).
CC -1- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -----
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CC -----
 DR EMBL: J04353; AAA46952.1; -
 DR PIR: C32444; W1WLJ1.
 DR InterPro: IPR001177; Papillon_E1.
 DR Pfam: PF00519; E1.1.
 DR Pfam: PF00524; E1_N.1.
 DR Early protein: DNA replication; Helicase; ATP-binding; DNA-binding;
 KW Nuclear protein.
 FT NP_BIND 457 464 ATP (POTENTIAL).
 FT SEQUENCE 629 AA; 71227 MW; 701D063AE8F6300D CRC64;

Query Match 46.0%; Score 40; DB 1; Length 629;
 Best Local Similarity 55.6%; Pred. No. 96;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 WHYSSYR 10
 Db 509 WHYDNTLR 517

RESULT 15
 ID INVA_PHAU STANDARD; PRT; 649 AA.
 AC P29001;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Acid beta-fructofuranosidase precursor (EC 3.2.1.26) (Acid sucrose-6-
 DE phosphate hydrolase) (Acid invertase) (AI) (Vacuolar invertase).
 GN INVA.
 OS Phaseolus aureus (Mung bean) (Vigna radiata).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
 OX NCBI_TaxID=3916;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 329-360.
 RC TISSUE=Hypocotyl;
 RA Arai M., Mori H., Imaseki H.;
 RT "Cloning and sequence of cDNAs for an intracellular acid invertase
 RT from etiolated hypocotyls of mung bean and expression of the gene
 RT during growth of seedlings.";
 RL Plant Cell Physiol. 33:245-252(1992).
 CC -1- FUNCTION: POSSIBLE ROLE IN THE CONTINUED MOBILIZATION OF SUCROSE
 CC TO SINK ORGANS.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing beta-D-
 CC fructofuranoside residues in beta-D-fructofuranosides.
 CC -1- PATHWAY: FIRST ENZYME INVOLVED IN THE METABOLISM OF INCOMING
 CC SUCROSE.
 CC -1- SUBUNIT: PRESENT IN TWO FORMS, A 70 kDa MONOMER AND A HETERODIMER
 CC OF THE 30 kDa AND 38 kDa SUBUNITS. THE RATIO OF THE LEVELS OF THE
 CC TWO FORMS WITHIN CELLS APPEARS TO BE REGULATED DEVELOPMENTALLY.
 CC -1- SUBCELLULAR LOCATION: Vacuolar (Probable).
 CC -1- DEVELOPMENTAL STAGE: APPEARS AFTER GERMINATION AND MAINTAINED AT
 CC HIGH LEVELS IN RAPIDLY GROWING TISSUES.
 CC -1- INDUCTION: REGULATION OF SYNTHESIS APPEARS TO BE RELATED TO THE
 CC GROWTH OF SEEDLINGS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
 CC -----
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CC -----
 DR EMBL: D10265; BAA0107.1; -
 DR InterPro: IPR001362; GH_32.

DR Pfam: PF00251; Glyco_hydro_32; 1.
 DR PROSITE: PS00609; GLYCOSYL_HYDROL_F32; 1.
 KW Hydrolase; Glycosidase; Glycoprotein; Zymogen; Signal.
 FT SIGNAL 1 36
 FT PROPEP 37 101
 FT CHAIN 102 328
 FT CHAIN 329 649
 FT ACT_SITE 130 130
 FT CARBOHYD 210 210
 FT CARBOHYD 275 275
 FT CARBOHYD 618 618
 FT SEQUENCE 649 AA; 72167 MW; 0E0375B8C60017B9 CRC64;

Query Match 46.0%; Score 40; DB 1; Length 649;
 Best Local Similarity 46.2%; Pred. No. 99;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 WHYSSYRPFAY 14
 Db 631 WQMSAFIRPPF 643

Search completed: February 25, 2003, 10:37:32
 Job time : 2.23667 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 1.77333 Seconds
(without alignments)
758.956 Million cell updates/sec

Title: US-09-743-482A-12

Perfect score: 87
Sequence: 1 DMHYSSYIRPFAY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	55.2	663	2 T30621	hypothetical prote
2	47	54.0	392	2 A33445	spore-cortex-lytic
3	46	52.9	372	2 A61896	hypothetical prote
4	46	52.9	993	2 T09129	probable erythrocy
5	45	51.7	611	2 A75573	probable oligendo
6	45	51.7	1701	2 T09127	probable erythrocy
7	44	50.6	614	2 AC0310	NADH2 dehydrogenas
8	44	50.6	1918	2 S43719	lactase (EC 3.2.1.
9	44	50.6	1920	2 S43721	lactase (EC 3.2.1.
10	44	50.6	1926	2 S01169	beta-glycosidase c
11	44	50.6	1927	2 S01168	beta-glycosidase c
12	43	49.4	105	2 B70578	hypothetical prote
13	43	49.4	363	2 T30964	hypothetical prote
14	43	49.4	393	2 S08017	maturation protein
15	43	49.4	557	2 A70480	carbamoyl phosphat
16	43	49.4	698	2 T12590	NADH2 dehydrogenas
17	43	49.4	760	2 T13724	chloride channel -
18	42	48.3	81	2 S41580	lysozyme (EC 3.2.1
19	42	48.3	162	2 D97539	hypothetical prote
20	42	48.3	328	2 A70127	phosphate ABC tran
21	42	48.3	403	2 C75405	streptomycin biosy
22	41.5	47.7	435	2 T08038	probable mitochond
23	41	47.1	179	2 AB1352	hypothetical prote
24	41	47.1	179	2 AB1322	hypothetical prote
25	41	47.1	206	2 G81071	conserved hypothet
26	41	47.1	474	2 T31104	hemolysin accessor
27	41	47.1	512	2 T18218	hypothetical prote
28	41	47.1	1036	2 S76027	hypothetical prote
29	41	47.1	3165	2 S15010	hypothetical prote

30	40	46.0	71	2 AB0549	probable membrane
31	40	46.0	114	2 D64766	membrane protein y
32	40	46.0	114	2 P90682	hypothetical prote
33	40	46.0	114	2 B85533	hypothetical prote
34	40	46.0	160	2 JN0503	periplasmic myelin
35	40	46.0	163	1 E69231	conserved hypothet
36	40	46.0	193	2 E64488	hypothetical prote
37	40	46.0	232	2 B97147	enzyme of sideroph
38	40	46.0	274	2 T50986	hypothetical prote
39	40	46.0	338	2 T39635	short-chain dehydr
40	40	46.0	342	2 T43038	hypothetical prote
41	40	46.0	365	2 T24416	hypothetical prote
42	40	46.0	435	2 S77156	processing protein
43	40	46.0	580	2 F84828	probable lactase (
44	40	46.0	629	1 W1WL31	El protein - human
45	40	46.0	651	2 T12083	beta-fructofuranos

ALIGNMENTS

RESULT 1

T30621
hypothetical protein 19L - Molluscum contagiosum virus 1
N:Alternate names: MC019L
C:Species: Molluscum contagiosum virus 1
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
C:Accession: T30621
R:Senkevich, T.G.; Bugert, J.J.; Sleser, J.R.; Koonin, E.V.; Darat, G.; Moss, B.
Science 273, 813-816, 1996
A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific hos
A:Reference number: 220876; MUID:96325459; PMID:8670425
A:Accession: T30621
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-663 <SEN>
A:Cross-References: EMBL:U60315; PIDN:AAC5147.1
C:Genetics:
A>Note: MC019L

Query Match 55.2% Score 48: DB 2: Length 663:
Best Local Similarity 57.1% Pred. No. 8:
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 DMHYSSYIRPFAY 14
Db 619 DMHYSSYIRPFAY 632

RESULT 2

AF3445
spore-cortex-lytic enzyme prepeptide precursor [Imported] - Brucella melitensis (str
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AF3445
R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanc
-; Mazur, M.; Goldsman, E.; Selkov, E.; Elser, P.H.; Hagius, S.; O'Callaghan, D.; Le
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AD3252; PMID:11756688
A:Accession: AF3445
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-392 <KUR>
A:Cross-References: GB:AE008917; PIDN:AAL52729.1; PID:q17983559; GSPDB:GN00190
A:Experimental source: strain 10M
C:Genetics:
A:Gene: BMEI1548
A:Map position: 1

Query Match 54.0% Score 47: DB 2: Length 392:
Best Local Similarity 60.0% Pred. No. 6.8:
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 HYYSSYIRPF 12
|||:|:|:|
Db 358 HYYATVRPF 367

RESULT 3

AC1896
hypothetical protein al10721 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: AG1896

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuriatz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AG1896

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-372 <KUR>

A:Cross-references: GB:BA000019; PIDN:BAW72678.1; PID:g17130066; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: al10721

Query Match
Best Local Similarity 52.9%; Score 46; DB 2; Length 372;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 YSSYIRPFAY 14
||| | | | |
Db 184 YSSYIRPFAY 194

RESULT 4

T09129

probable erythrocyte-binding protein MAEBL - Plasmodium berghei (fragment)

C:Species: Plasmodium berghei

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: T09129

R:Kapke, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.

Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1235, 1998

A:Title: A family of chimeric erythrocyte binding proteins of malaria parasites.

A:Reference number: Z16577; MUID:98115903; PMID:9448314

A:Accession: T09129

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-993 <KAP>

A:Cross-references: EMBL:AF031887; NID:g2947229; PIDN:AAC05367.1; PID:g2947230

A:Experimental source: strain ANKA

C:Genetics:

A:Gene: maeb1

A:Introns: 62/1

C:Keywords: alternative splicing; cell binding; erythrocyte invasion; malaria

Query Match
Best Local Similarity 52.9%; Score 46; DB 2; Length 993;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DMHYYSSYIRP 11
||| | | | |
Db 308 DMHYYSSYIRP 318

RESULT 5

A75573

probable oligonucleotide phosphatase F - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 11-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: A75573

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, C.;

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: A75573

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-611 <WHI>

A:Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12423.1; PID:g646

A:Experimental source: strain R1

C:Genetics:

A:Gene: DRA0206

A:Map position: 2

Query Match
Best Local Similarity 51.7%; Score 45; DB 2; Length 611;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 WHYYHIFQYFFY 14
||| | | | |
Db 529 WHYYHIFQYFFY 541

RESULT 6

T09127

probable erythrocyte-binding protein MAEBL - Plasmodium yoelii

C:Species: Plasmodium yoelii

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C:Accession: T09127

R:Kapke, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.

Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1235, 1998

A:Title: A family of chimeric erythrocyte binding proteins of malaria parasites.

A:Reference number: Z16577; MUID:98115903; PMID:9448314

A:Accession: T09127

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1701 <KAP>

A:Cross-references: EMBL:AF031886; NID:g2947227; PID:g2947228

A:Experimental source: subspecies yoelii; strain YM

C:Genetics:

A:Gene: maeb1

A:Introns: 62/1; 1648/1; 1674/2; 1697/1

C:Keywords: alternative splicing; cell binding; erythrocyte invasion

Query Match
Best Local Similarity 51.7%; Score 45; DB 2; Length 1701;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DMHYYSSYIRP 11
||| | | | |
Db 308 DMHYYSSYIRP 318

RESULT 7

AG0310

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain L [imported] - Yersinia pestis (s

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 03-Jun-2002

C:Accession: AG0310

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AG0310

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-614 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC91347.1; PID:g15980536; GSPDB:GN00175

C:Genetics:

A:Gene: nuol

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: oxidoreductase

Query Match 50.6%; Score 44; DB 2; Length 614;
Best Local Similarity 35.7%; Pred. No. 32;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 1 DMHYSSYIRPAY 14
||:|:|:|:|:
Db 544 DMLYHNLFPVRYLM 557

RESULT 8

lactase (EC 3.2.1.108) / glycosylceramidase (EC 3.2.1.62) (clone BL70) - rabbit (fragment)
N:Alternate names: lactase / phlorizin hydrolase
C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C>Date: 13-Jan-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C:Accession: S43719
R:Villa, M.; Brunschweiler, D.; Gaechter, T.; Boll, W.; Semenza, G.; Mantel, N.
FEBS Lett. 336, 70-74, 1993
A:Title: Region-specific expression of multiple lactase-phlorizin hydrolase genes in int
A:Reference number: S43719; MUID:94085594; PMID:8262219
A:Accession: S43719
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-1918 <VIL>
A:Cross-references: EMBL:227166
C:Keywords: carbohydrate digestion; glycosidase; hydrolase; intestine

Query Match 50.6%; Score 44; DB 2; Length 1918;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 WHYSSYIRP 11
||:|:|:|:|:
Db 573 WHYNSHHRP 582

RESULT 9

lactase (EC 3.2.1.108) / glycosylceramidase (EC 3.2.1.62) (clone BL70) - rabbit (fragment)
N:Alternate names: lactase / phlorizin hydrolase
C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C>Date: 13-Jan-1995 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: S43720; S43721
R:Villa, M.; Brunschweiler, D.; Gaechter, T.; Boll, W.; Semenza, G.; Mantel, N.
FEBS Lett. 336, 70-74, 1993
A:Title: Region-specific expression of multiple lactase-phlorizin hydrolase genes in int
A:Reference number: S43719; MUID:94085594; PMID:8262219
A:Accession: S43720
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-1920 <VIL>
A:Cross-references: EMBL:227167; NID:9415864; PIDN:CAA81691.1; PID:9415865
A:Accession: S43721
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 'MELFWS', '1-11', 'Q', '13-207' <VIZ>
A:Cross-references: EMBL:227168; NID:9415866; PIDN:CAA81692.1; PID:9415867
C:Keywords: carbohydrate digestion; glycosidase; hydrolase; intestine

Query Match 50.6%; Score 44; DB 2; Length 1920;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 WHYSSYIRP 11
||:|:|:|:|:
Db 574 WHYNSHHRP 583

RESULT 10

S01169

beta-glycosidase complex precursor - rabbit

N:Contains: glycosylceramidase (EC 3.2.1.62); lactase (EC 3.2.1.108)
C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 05-Nov-1999
C:Accession: S01169
R:Mantel, N.; Villa, M.; Enzler, T.; Wacker, H.; Boll, W.; James, P.; Hunziker, W.;
EMBO J. 7, 2705-2713, 1988
A:Title: Complete primary structure of human and rabbit lactase-phlorizin hydrolase:
A:Reference number: S01169; MUID:89030634; PMID:2460343
A:Accession: S01169
A:Molecule type: mRNA
A:Residues: 1-1926 <MAN>
A:Cross-references: EMBL:X07995; NID:91616; PIDN:CAA30802.1; PID:91617
A>Note: The authors translated the codon GCC for residue 1551 as Gly and CCA for res
C:Keywords: carbohydrate digestion; glycosidase; hydrolase; intestine; transmembrane
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-866/Domain: signal sequence #status predicted <PRO>
F:867-1926/Product: beta-glycosidase complex #status experimental <MAT>
F:1893-1901/Domain: transmembrane #status predicted <TM>

Query Match 50.6%; Score 44; DB 2; Length 1926;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 WHYSSYIRP 11
||:|:|:|:|:
Db 580 WHYNSHHRP 589

RESULT 11

beta-glycosidase complex precursor - human
N:Contains: glycosylceramidase (EC 3.2.1.62); lactase (EC 3.2.1.108)
C:Species: *Homo sapiens* (man)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Jul-2000
C:Accession: S01168
R:Mantel, N.; Villa, M.; Enzler, T.; Wacker, H.; Boll, W.; James, P.; Hunziker, W.;
EMBO J. 7, 2705-2713, 1988
A:Title: Complete primary structure of human and rabbit lactase-phlorizin hydrolase:
A:Reference number: S01168; MUID:89030634; PMID:2460343
A:Accession: S01168
A:Molecule type: mRNA
A:Residues: 1-1927 <MAN>
A:Cross-references: EMBL:X07994; NID:934399; PIDN:CAA30801.1; PID:934400
C:Keywords: carbohydrate digestion; glycosidase; hydrolase; intestine; transmembrane
F:1-19/Domain: signal sequence #status predicted <PRO>
F:20-866/Domain: signal sequence #status predicted <SIG>
F:867-1927/Product: beta-glycosidase complex #status predicted <MAT>
F:1893-1901/Domain: transmembrane #status predicted <TM>

Query Match 50.6%; Score 44; DB 2; Length 1927;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 WHYSSYIRP 11
||:|:|:|:|:
Db 582 WHYNSHHRP 591

RESULT 12

hypothetical protein RV2142c - Mycobacterium tuberculosis (strain H37RV)
C:Species: *Mycobacterium tuberculosis*
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: B70578
R:Cole, S.T.; Brosch, P.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: B70578
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-105 <CON>
 A:Cross-references: GB:295388; GB:AL123456; NID:g3261759; PIDN:CAB08651.1; PID:g2104336
 A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: RV2142c
 C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV2142c

Query Match 49.4%; Score 43; DB 2; Length 105;
 Best Local Similarity 58.3%; Pred. No. 7.5;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 HYYSSYIRPF 14
 ||| ||| |||
 Db 58 HHHHLLRPFR 69

RESULT 13
 T30964
 hypothetical protein R04B3.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T30964
 R:Galtung, S.; Pauley, A.
 submitted to the EMBL Data Library, August 1999
 A:Description: The sequence of C. elegans cosmid R04B3.
 A:Reference number: 220947
 A:Accession: T30964
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-363 <CAT>
 A:Cross-references: EMBL:U50198; PIDN:AAA91259.1
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Map position: X
 A:Introns: 60/3; 139/1; 181/2; 237/1; 297/2; 327/3
 A:Note: R04B3.1

Query Match 49.4%; Score 43; DB 2; Length 363;
 Best Local Similarity 58.3%; Pred. No. 27;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 WHYSSYIRPFA 13
 ||| ||| |||
 Db 300 WNYENSIRPFA 311

RESULT 14
 S08017
 maturation protein - phage fr
 C:Species: phage fr
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
 C:Accession: S08017; S13075
 R:Adlin, M.R.; Avots, A.; Berzin, V.; Overbeek, G.P.; van Duin, J.
 submitted to the EMBL Data Library, April 1989
 A:Description: Complete nucleotide sequence of RNA bacteriophage fr.
 A:Reference number: S08017
 A:Accession: S08017
 A:Molecule type: genomic RNA
 A:Residues: 1-393 <ADH>
 A:Cross-references: EMBL:X15031; NID:g15071; PIDN:CAA33135.1; PID:g579112
 R:Adlin, M.R.; Avots, A.; Berzin, V.; Overbeek, G.P.; van Duin, J.
 Biochim. Biophys. Acta 1050, 104-109, 1990
 A:Title: Complete nucleotide sequence of the group I RNA bacteriophage fr.
 A:Reference number: S13075; MUID:91002624; PMID:2207135
 A:Accession: S13075
 A:Molecule type: genomic RNA
 A:Residues: 2-393 <ADM>
 A:Cross-references: GB:X15031; NID:g15071; PIDN:CAA33135.1; PID:g579112
 C:Genetics:
 A:Start codon: GTC

C:Superfamily: phage maturation protein
 C:Keywords: phage maturation

Query Match 49.4%; Score 43; DB 2; Length 393;
 Best Local Similarity 70.0%; Pred. No. 29;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DMHYSSYIR 10
 ||| ||| |||
 Db 53 EMHYSSYSR 62

RESULT 15
 A70480
 carbamoyl-phosphate synthase large subunit - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 22-Jun-1999
 C:Accession: A70480
 R:Deckerl, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666; PMID:9537320
 A:Accession: A70480
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-557 <AOE>
 A:Cross-references: GB:AE000772; NID:g2984299; PIDN:AAC07826.1; PID:g2984303; GB:AE00
 A:Experimental source: strain VFS
 C:Genetics:
 A:Gene: carB2
 C:Superfamily: carbamoyl-phosphate synthase large chain; biotin carboxylase homology
 F:9-468/Domain: biotin carboxylase homology <BCH>

Query Match 49.4%; Score 43; DB 2; Length 557;
 Best Local Similarity 70.0%; Pred. No. 42;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 HYYSSYIRPF 12
 ||| ||| |||
 Db 536 YYYSSYRPF 545

Search completed: February 25, 2003, 10:33:55
 Job time : 4.77333 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 : Search time 1.89833 Seconds
(without alignments)
263.489 Million cell updates/sec

Title: US-09-743-482a-10

Perfect score: 104

Sequence: 1 WIYGGNGMTKYNCKENG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents,AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfilest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	81.7	116	2	US-08-888-366-2
2	80	76.9	138	3	US-08-603-024-2
3	80	76.9	139	1	US-08-253-877C-8
4	80	76.9	139	1	US-08-253-877C-19
5	80	76.9	139	2	US-08-452-164A-8
6	80	76.9	139	2	US-08-452-164A-19
7	80	76.9	139	3	US-08-603-024-18
8	77	74.0	140	1	US-08-475-815B-11
9	77	74.0	140	4	US-08-475-815B-11
10	76	73.1	119	2	US-08-561-521-10
11	76	73.1	119	2	US-08-561-521-12
12	76	73.1	119	2	US-08-561-521-13
13	76	73.1	119	4	US-09-556-605-1
14	76	73.1	119	4	US-09-438-954-41
15	76	73.1	119	5	PCT-US95-01219-10
16	76	73.1	119	5	PCT-US95-01219-12
17	76	73.1	119	5	PCT-US95-01219-13
18	72	69.2	98	3	US-08-881-037-64
19	72	69.2	98	4	US-08-881-037-64
20	71	68.3	106	2	US-08-793-490-9
21	71	68.3	117	4	US-08-479-089A-8
22	71	68.3	117	4	US-08-479-089A-2
23	71	68.3	117	4	US-08-479-089A-3
24	71	68.3	117	4	US-09-096-244-4
25	70.5	67.8	236	4	US-09-049-672A-13
26	70	67.8	273	2	US-08-403-853-18
27	69	66.3	122	3	US-08-797-689-18

28	68	65.4	119	1	US-08-478-039-65	Sequence 65, Appl
29	68	65.4	119	1	US-08-476-349A-65	Sequence 65, Appl
30	68	65.4	119	1	US-08-458-516-10	Sequence 10, Appl
31	68	65.4	119	1	US-08-458-516-11	Sequence 11, Appl
32	68	65.4	119	1	US-08-458-516-7	Sequence 7, Appl
33	68	65.4	222	1	US-08-458-516-22	Sequence 22, Appl
34	68	65.4	235	1	US-08-458-516-23	Sequence 23, Appl
35	68	65.4	449	1	US-08-458-516-13	Sequence 13, Appl
36	67	64.4	121	1	US-08-207-0047-23	Sequence 23, Appl
37	67	64.4	121	3	US-08-964-690-23	Sequence 20, Appl
38	67	64.4	125	4	US-09-357-710A-20	Sequence 21, Appl
39	67	64.4	128	1	US-08-202-047-21	Sequence 21, Appl
40	67	64.4	128	3	US-08-964-690-21	Sequence 14, Appl
41	67	64.4	132	3	US-08-434-000A-14	Sequence 14, Appl
42	67	64.4	132	4	US-09-312-157-14	Sequence 14, Appl
43	66	63.5	117	2	US-08-822-028-2	Sequence 2, Appl
44	66	63.5	117	3	US-08-545-809A-91	Sequence 91, Appl
45	66	63.5	117	4	US-08-479-285-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-888-366-2
Sequence 2, Application US/08888366
Patent No. 5972656
GENERAL INFORMATION:
APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwane E.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Thereof
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 NO. 5972656west Ctr.
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648,39USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acids
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-688-366-2

Query Match 81.7%; Score 85; DB 2; Length 116;
Best Local Similarity 76.5%; Pred. No. 2,4e-05;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIYPGNGTKYKNGKNG 17
|||||:|||||:|||||
DB 50 WIPGDSGNTKYNEKFKG 66

RESULT 2

US-08-603-024-2
Sequence 2, Application US/08603024
Patent No. 6015562

GENERAL INFORMATION:

APPLICANT: Himman, Lois M.
APPLICANT: Menendez, Ana T.
APPLICANT: Hamann, Philip R.

TITLE OF INVENTION: TARGETED FORMS OF METHYLTRITHIO
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany

STATE: NJ

COUNTRY: USA

ZIP: 07054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/603,024
FILING DATE: 16-FEB-1996
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,932-03

TELECOMMUNICATION INFORMATION:

TELEPHONE: 973-683-2158
TELEFAX: 973-683-4117

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-603-024-2

Query Match 76.9%; Score 80; DB 3; Length 138;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPGNGTKYKNGKNG 17
|||||:|||||:|||||
DB 69 WIPGDSGNTKYNEKFKG 85

RESULT 3

US-08-253-877C-8
Sequence 8, Application US/08253877C
Patent No. 5773001

GENERAL INFORMATION:

APPLICANT: Hamann, Philip R.
APPLICANT: Himman, Lois
APPLICANT: Hollander, Irwin

APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William

APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/253,877C
FILING DATE: 03-JUN-1994
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-831-3246
TELEFAX: 201-831-3305

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-253-877C-8

Query Match 76.9%; Score 80; DB 1; Length 139;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIYPGNGTKYKNGKNG 17
|||||:|||||:|||||
DB 69 WIPGDSGNTKYNEKFKG 85

RESULT 4

US-08-253-877C-19

Sequence 19, Application US/08253877C
Patent No. 5773001

GENERAL INFORMATION:

APPLICANT: Hamann, Philip R.
APPLICANT: Himman, Lois
APPLICANT: Hollander, Irwin

APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William

APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.

TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/253,877C
FILING DATE: 03-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-3246
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-253-877C-19

Query Match 76.9% Score 80; DB 1; Length 139;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIYPGNGNTKYKNGKENG 17
|||:|||||:|
Db 69 WIDPGSGNTKYNEKFKG 85

RESULT 5
US-08-452-164A-8
Sequence 8, Application US/08452164A
Patent No. 5877296
GENERAL INFORMATION:
APPLICANT: Hamann, Phillip R.
APPLICANT: Himman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William
APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrilthio Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,164A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-164A-8

Query Match 76.9% Score 80; DB 2; Length 139;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIYPGNGNTKYKNGKENG 17
|||:|||||:|
Db 69 WIDPGSGNTKYNEKFKG 85

RESULT 6
US-08-452-164A-19
Sequence 19, Application US/08452164A
Patent No. 5877296
GENERAL INFORMATION:
APPLICANT: Hamann, Phillip R.
APPLICANT: Himman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William
APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrilthio Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,164A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-164A-19

Query Match 76.9% Score 80; DB 2; Length 139;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIYPGNGNTKYKNGKENG 17
|||:|||||:|
Db 69 WIDPGSGNTKYNEKFKG 85

RESULT 7
US-08-603-024-18
Sequence 18, Application US/08603024
Patent No. 6015562
GENERAL INFORMATION:
APPLICANT: Himman, Lois M.
APPLICANT: Menendez, Ana T.

APPLICANT: Hamann, Philip R.
TITLE OF INVENTION: TARGETED FORMS OF METHYLTRYPTHIO
TITLE OF INVENTION: ANTITUMOR AGENTS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: NJ
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/603,024
FILING DATE: 16-FEB-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,932-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-683-2158
TELEFAX: 973-683-4117
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-603-024-18
Query Match 76.9%; Score 80; DB 3; Length 139;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 WYPGNGNTKYNOKFG 17
Db 69 WIDPGSGNTKYNEKFG 85
RESULT 8
US-08-476-275-6
Sequence 6, Application US/08476275
Patent No. 5776456
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabli
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-275-6

Query Match 74.0%; Score 77; DB 1; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.0004;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGNGNTKYNOKFG 17
Db 70 IYPGNGDTSYNOKFG 85

RESULT 9
US-08-475-815B-11
Sequence 11, Application US/08475815B
Patent No. 6399061
GENERAL INFORMATION:
APPLICANT: ANDERSON, DARRELL R.
APPLICANT: HANNA, NABLI
APPLICANT: LEONARD, JOHN E.
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: REFF, MITCHELL E.
APPLICANT: RASTETTER, WILLIAM H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELLED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY WINTROP
STREET: 1100 New York Avenue, N.W., Ninth FL.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815B
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 23522-0157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-8158-11

Query Match 74.0%; Score 77; DB 4; Length 140;
Best Local Similarity 81.2%; Pred. No. 0.0004;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 IYPGNGNTKYNOKEG 17
DB 70 IYPGNGDTYNOKEG 85

RESULT 10
US-08-561-521-10
Sequence 10 Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saidanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-10

Query Match 73.1%; Score 76; DB 2; Length 119;
Best Local Similarity 76.5%; Pred. No. 0.00048;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 WIYPGNGNTKYNOKEG 17
DB 50 WINAGNGNTKYSQKFOG 66

RESULT 11
US-08-561-521-12
Sequence 12 Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saidanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-12

Query Match 73.1%; Score 76; DB 2; Length 119;
Best Local Similarity 76.5%; Pred. No. 0.00048;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 WIYPGNGNTKYNOKEG 17
DB 50 WINAGNGNTKYSQKFOG 66

RESULT 12
US-08-561-521-13
Sequence 13 Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saidanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-13

Query Match 73.1%; Score 76; DB 2; Length 119;
Best Local Similarity 76.5%; Pred. No. 0.00048;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-13

Query Match 73.1%; Score 76; DB 2; Length 119;
Best Local Similarity 76.5%; Pred. No. 0.00048;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIYPGNGNTKYNOKFNG 17
|| |||||:|||||
DB 50 WINAGNGNTKYSOKFOG 66

RESULT 13
US-09-556-605-1
Sequence 1, Application US/09556605
Patent No. 6417324
GENERAL INFORMATION:
APPLICANT: Saliberg, Matli
APPLICANT: Lazdina, Una
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
FILE REFERENCE: HEPATITIS B VIRUS CORE AND E ANTIGENS
CURRENT APPLICATION NUMBER: US/09/556,605
CURRENT FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Oligonucleotide
US-09-556-605-1

Query Match 73.1%; Score 76; DB 4; Length 119;
Best Local Similarity 64.7%; Pred. No. 0.00048;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIYPGNGNTKYNOKFNG 17
|| |||||:|||||

DB 49 WIFPGEGSTEYNEKFKG 65

RESULT 14
US-09-438-954-41
Sequence 41, Application US/09438954
Patent No. 6458934
GENERAL INFORMATION:
APPLICANT: HONG, HYO JEONG
APPLICANT: PARK, SUNG SUP
APPLICANT: KANG, YOUNG JUN
APPLICANT: KANG, CHANG-YUL
APPLICANT: YOON, SUNG KWAN
TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
FILE REFERENCE: 1305-124P
CURRENT APPLICATION NUMBER: US/09/438,954
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 41
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Variable
US-09-438-954-41

Query Match 73.1%; Score 76; DB 4; Length 119;
Best Local Similarity 76.5%; Pred. No. 0.00048;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIYPGNGNTKYNOKFNG 17
|| |||||:|||||
DB 50 WINAGNGNTKYSOKFOG 66

RESULT 15
PCT-US95-01219-10
Sequence 10, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-10

Query Match 73.1%; Score 76; DB 5; Length 119;
Best Local Similarity 76.5%; Pred. No. 0.00048;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 WYPGNGNTKYNOKFNG 17
11 |||||||:||||
DB 50 WINAGNGNTKYSOKFOG 66

Search completed: February 25, 2003, 10:38:43
Job time : 2.89833 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 : Search time 3.54667 Seconds
(Without alignments)
813.344 Million cell updates/sec

Title: US-09-743-482a-12
Perfect score: 87
Sequence: 1 DMHYSSYIRPFAY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	53	60.9	279	17	Q96X76	Q96X76 sulfolobus
2	49.5	56.9	422	2	Q9RMP4	Q9RMP4 xenorhabdus
3	48	55.2	241	12	O11309	O11309 molluscum c
4	48	55.2	489	5	Q8T7Y1	Q8T7Y1 plasmodium
5	48	55.2	663	12	Q98188	Q98188 molluscum c
6	48	55.2	1722	4	O60449	O60449 homo sapien
7	48	55.2	1722	4	O75913	O75913 homo sapien
8	48	55.2	2055	5	Q8T5C7	Q8T5C7 plasmodium
9	47	54.0	392	16	Q8TFH4	Q8TFH4 bruceella me
10	46	52.9	274	12	O71104	O71104 bovine aden
11	46	52.9	372	16	Q8YX1	Q8YX1 anabaena sp
12	46	52.9	993	5	O61015	O61015 plasmodium
13	45	51.7	436	6	O951L5	O951L5 macaca fasc
14	45	51.7	611	16	Q9RYV0	Q9RYV0 delinococcus
15	45	51.7	993	2	Q9APG4	Q9APG4 streptococ
16	45	51.7	995	16	Q9Y9Y2	Q9Y9Y2 streptococ

17	45	51.7	1671	5	Q8T5C9	Q8T5C9 plasmodium
18	45	51.7	1701	5	O61164	O61164 plasmodium
19	45	51.7	1866	5	Q8T5C8	Q8T5C8 plasmodium
20	44	50.6	586	10	Q8S279	Q8S279 oryza sativ
21	44	50.6	595	2	Q46541	Q46541 bacteroides
22	44	50.6	614	16	Q82DL7	Q82DL7 yerstia pe
23	44	50.6	1439	3	Q9UW03	Q9UW03 botrytis ci
24	44	50.6	1459	3	Q8TFM7	Q8TFM7 monilia f
25	44	50.6	1919	6	Q29518	Q29518 oryctolagus
26	44	50.6	1920	6	Q29519	Q29519 oryctolagus
27	43.5	50.0	418	3	O14418	O14418 metarhizium
28	43	49.4	69	4	Q8WMK7	Q8WMK7 homo sapien
29	43	49.4	105	16	O06233	O06233 mycobacteri
30	43	49.4	363	5	Q21696	Q21696 caenorhabdi
31	43	49.4	516	3	Q8TGM0	Q8TGM0 candida dub
32	43	49.4	557	16	O67869	O67869 aquifex aeo
33	43	49.4	606	10	Q9SC54	Q9SC54 plumbago au
34	43	49.4	644	8	Q9TL02	Q9TL02 antiphona
35	43	49.4	698	8	Q98655	Q98655 tecoma stan
36	43	49.4	1426	3	Q96W59	Q96W59 mycosphaere
37	43	49.4	2290	5	Q9VT00	Q9VT00 drosophila
38	42.5	48.9	600	2	O66396	O66396 acinetobact
39	42	48.3	162	16	Q8UB51	Q8UB51 agrobacteri
40	42	48.3	256	2	O06063	O06063 marincoccu
41	42	48.3	328	16	O51235	O51235 borelia bu
42	42	48.3	386	16	Q98121	Q98121 rhizobium l
43	42	48.3	403	16	Q9RUM2	Q9RUM2 rhizobium l
44	42	48.3	526	11	Q9DAC3	Q9DAC3 mus musculu
45	42	48.3	705	8	Q9HVG2	Q9HVG2 bytneria a

ALIGNMENTS

RESULT 1
Q96X76 PRELIMINARY: PRT: 279 AA.
ID Q96X76;
AC Q96X76;
DF 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DI 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Hypothetical protein ST2633.
GN ST2633.
OS Sulfolobus tokodali.
OC Archaea: Crenarchaeota: Thermoprotei: Sulfolobales; Sulfolobaceae;
CC Sulfolobus.
OX NCBI_TaxID=11955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JCM 10545 / 7;
RX PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankel A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodali strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL: AP000990; BAB67752.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 279 AA: 32218 MW: 51F62803F46BC2F CRC64:

Query Match 60.9%; Score 53; DB 17; Length 279;
Best local similarity 61.5%; Pred. No. 1.3;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 WHYSSYIRPFAY 14
|||||:::|
DB 26 WHYSPVPKPKAV 38

```

RESULT 2
Q9RMP4      PRELIMINARY;      PRT;      422 AA.
ID 09RMP4;
AC 09RMP4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE B10A.
GN B10A.
OS Xenorhabdus nematophilus.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Xenorhabdus.
OX NCBI_TaxID=628;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC19061/1;
RX MEDLINE-20208870; PubMed-10742251;
RA Volgyi A., Fodor A., Forst S.;
RT "Inactivation of a novel gene produces a phenotypic variant cell and
affects the symbiotic behavior of Xenorhabdus nematophilus.";
RL Appl. Environ. Microbiol. 66:1622-1628(2000).
DR EMBL: AF191556; AAF04396.1; -.
DR HSSP: P04181; 20aT.
DR InterPro: IPR000954; Aminoctran_3.
DR Pfam: PF00202; aminoctran_3; 1.
DR TIGRFAMs: TIGR00508; b10a; 1.
DR PROSITE: PS00600; AA_TRANSFER_CLASS_3; 1.
SO SEQUENCE 422 AA; 47080 MW; 247BCF8424823AEF CRC64;

Query Match      56.9%; Score 49.5; DB 2; Length 422;
Best Local Similarity 71.4%; Pred. No. 7.3;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY      2  WHYYSSYIRPF-AY 14
Db      14  WHYYTSMIRFPAY 27

|||:|||||
|:|:|:|:|

RESULT 3
ID 011309      PRELIMINARY;      PRT;      241 AA.
ID 011309;
AC 011309;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DE B-M,N,L.9 protein (Fragment).
GN B-M,N,L.9.
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97093414; PubMed-8938976;
RA Martin-Gallardo A., Moratilla M., Funes J.M., Agromayor M., Nunez A.,
Vargas A.J., Collado M., Valencia A., Lopez-Esteban J.L.,
Esteban M.;
RT "Sequence analysis of a Molluscum contagiosum virus DNA region which
includes the gene encoding protein kinase 2 and other genes with
unique organization.";
RL Virus Genes 13:19-29(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Vargas A.J.,
Lopez-Esteban J.L., Esteban M., Martin-Gallardo A.;
RT "A Random DNA Sequencing, Computer-Based Approach for the Generation
of a Gene Map of Molluscum Contagiosum Virus.";
RL Virus Genes 0:0-0(1997);
DR EMBL: U86894; AAB57939.1; -.
DR InterPro: IPR005005; Pox_F12L.
DR Pfam: PF03337; Pox_F12L; 1.
FT NON_TER
SO SEQUENCE 241 AA; 26366 MW; C131432C0825471D CRC64;

```

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Query Match      55.2%; Score 48; DB 12; Length 241;
Best Local Similarity 57.1%; Pred. No. 7;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1  DMHYYSSYIRPFAY 14
Db      197  DMHYYSSHYRAHSY 210

|||||:|:|
|:|:|:|:|

RESULT 4
ID 08T7Y1      PRELIMINARY;      PRT;      489 AA.
ID 08T7Y1;
AC 08T7Y1;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE Putative erythrocyte binding protein MAEBL (Fragment).
GN MAEBL.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Ghai M., Dutta S., Ockenhouse C.F.;
RT "Cloning, expression and characterisation of the RBC binding domain of
MAEBL from Plasmodium falciparum (3b7).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF247552; AAM1477.1; -.
FT NON_TER
FT NON_TER
SO SEQUENCE 489 AA; 57147 MW; 154F7067EA04344B CRC64;

Query Match      55.2%; Score 48; DB 5; Length 489;
Best Local Similarity 72.7%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  DMHYYSSYIRP 11
Db      301  DMYYSSSIRP 311

|||:|:|:|
|:|:|:|:|

RESULT 5
ID 098188      PRELIMINARY;      PRT;      663 AA.
ID 098188;
AC 098188;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DE MCO19L.
GN MCO19L.
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96325459; PubMed-8670425;
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
Mos B.;
RT "Genome sequence of a human tumorigenic poxvirus: Prediction of
specific host response-evasion genes.";
RL Science 273:813-816(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
Mos B.;
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL: U60315; AAC55147.1; -.
DR InterPro: IPR005005; Pox_F12L.
DR Pfam: PF03337; Pox_F12L; 1.
SO SEQUENCE 663 AA; 73099 MW; 7EA19E8A5FFEF19 CRC64;

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Query Match 55.2%; Score 48; DB 12; Length 663;

Best Local Similarity 57.1%; Pred. No. 20;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 DMHYSSYIRPFA 14

Db 619 DMHYSSHYRAHSY 632

RESULT 6

O60449 PRELIMINARY; PRT; 1722 AA.

AC O60449; (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)

DE DEC-205.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RT MEDLINE=9822117; PubMed=9553150;

RT "CDNA cloning of human DEC-205, a putative antigen-uptake receptor on dendritic cells";

RT Immunogenetics 47:442-450(1998).

DR EMBL; AF011333; AAC17656.1; -.

DR HSSP; P02751; 2FN2.

DR Interpro: IPR000562; FN_Type_II.

DR Interpro: IPR001304; Lectin_C.

DR Interpro: IPR000772; Ricin_B_Lectin.

DR Pfam: PF00040; fn2; 1.

DR ProDom: PD000995; FN_Type_II; 1.

DR SMART; SM00034; CLECT; 10.

DR SMART; SM00059; FN2; 1.

DR SMART; SM00458; Ricin; 1.

DR PROSITE; PS00615; C_Type_Lectin_1; UNKNOWN_1.

DR PROSITE; PS00041; C_Type_Lectin_2; 10.

DR PROSITE; PS00023; FIBROnectin_2; UNKNOWN_1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

RT receptor modulates B cell phenotype and is a novel member of the human

RT macrophage mannose receptor family.";

RL Eur. J. Immunol. 28:4071-4083(1998).

DR EMBL; AF064827; AAC62622.1; -.

DR HSSP; P02751; 2FN2.

DR Interpro: IPR000562; FN_Type_II.

DR Interpro: IPR001304; Lectin_C.

DR Interpro: IPR000772; Ricin_B_Lectin.

DR Pfam; PF00040; fn2; 1.

DR ProDom; PD000995; FN_Type_II; 1.

DR SMART; SM00034; CLECT; 10.

DR SMART; SM00059; FN2; 1.

DR SMART; SM00458; Ricin; 1.

DR PROSITE; PS00615; C_Type_Lectin_1; UNKNOWN_1.

DR PROSITE; PS00041; C_Type_Lectin_2; 10.

DR PROSITE; PS00023; FIBROnectin_2; UNKNOWN_1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

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DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

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DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

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DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

RT receptor modulates B cell phenotype and is a novel member of the human

RT macrophage mannose receptor family.";

RL Eur. J. Immunol. 28:4071-4083(1998).

DR EMBL; AF064827; AAC62622.1; -.

DR HSSP; P02751; 2FN2.

DR Interpro: IPR000562; FN_Type_II.

DR Interpro: IPR001304; Lectin_C.

DR Interpro: IPR000772; Ricin_B_Lectin.

DR Pfam; PF00040; fn2; 1.

DR ProDom; PD000995; FN_Type_II; 1.

DR SMART; SM00034; CLECT; 10.

DR SMART; SM00059; FN2; 1.

DR SMART; SM00458; Ricin; 1.

DR PROSITE; PS00615; C_Type_Lectin_1; UNKNOWN_1.

DR PROSITE; PS00041; C_Type_Lectin_2; 10.

DR PROSITE; PS00023; FIBROnectin_2; UNKNOWN_1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

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DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

DR PROSITE; PS50231; Ricin_B_Lectin; 1.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA Delvecchio V.G., Kapral V., Redkar R.J., Patra G., Mujar C., Los T.,
 Ivanova N., Anderson I., Bhattacharya A., Lykakis A., Rezak G.,
 Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
 Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 Haselkorn R., Kyrides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 Brucella melitensis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL: AE009590; AAL52729.1; -.
 KW Complete proteome.
 SQ SEQUENCE 392 AA; 43099 MW; B8BDAB0AFA3C8C64 CRC64;

Query Match 54.0%; Score 47; DB 16; Length 392;
 Best Local Similarity 60.0%; Pred. No. 17;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 HYSSYIRPF 12
 ||::||::||
 DB 358 HYHATYVRF 367

RESULT 10

ID 071104 PRELIMINARY; PRT; 274 AA.

AC 071104;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE 33 kDa protein.

OS Bovine adenovirus type 3 (Mastadenovirus bos3).
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=10510;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=WB-1;
 RX MEDLINE=98105785; PubMed=9445040;
 RA Reddy P.S., Idamakanti N., Zakhartchouk A.N., Baxi M.K., Lee J.B.,
 RA Pyne C., Babluk L.A., Tikoo S.K.;
 RT "Nucleotide sequence, genome organization, and transcription map of
 bovine adenovirus type 3.";
 RL J. Virol. 72:1394-1402(1998).

RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=WB-1;
 RX MEDLINE=98318755; PubMed=9654686;
 RA Baxi M.K., Reddy P.S., Zakhartchouk A.N., Idamakanti N., Pyne C.,
 RA Babluk L.A., Tikoo S.K.;
 RT "Characterization of bovine adenovirus type 3 early region 2B.";
 RL Virus Genes 16:313-316(1998).

RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN=WB-1;
 RX MEDLINE=98451815; PubMed=9778793;
 RA Lee J.B., Baxi M.K., Idamakanti N., Reddy P.S., Zakhartchouk A.N.,
 RA Pyne C., Babluk L.A., Tikoo S.K.;
 RT "Genetic organization and DNA sequence of early region 4 of bovine
 adenovirus type 3.";
 RL Virus Genes 17:99-100(1998).

RN [4]
 RP SEQUENCE FROM N.A.

RC STRAIN=WB-1;
 RX MEDLINE=99119503; PubMed=9918888;
 RA Reddy P.S., Chen Y., Idamakanti N., Pyne C., Babluk L.A., Tikoo S.K.;
 RT "Characterization of early region 1 and pIX of bovine adenovirus-3.";
 RL Virology 253:299-308(1999).

RP SEQUENCE FROM N.A.
 RC STRAIN=WB-1;
 RA Reddy P.S., Idamakanti N., Zakhartchouk A.N., Baxi M.K., Lee J.B.,
 RA Pyne C., Babluk L.A., Tikoo S.K.;
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF030154; AAD09732.1; -.
 SQ SEQUENCE 274 AA; 29643 MW; 43BC76827ABA48E5 CRC64;

Query Match 52.9%; Score 46; DB 12; Length 274;
 Best Local Similarity 72.7%; Pred. No. 16;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 HYSSYIRPFA 13
 ||::||::||
 DB 185 HYNSYCRPFA 195

RESULT 11

ID 08YXX1 PRELIMINARY; PRT; 372 AA.

AC 08YXX1;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein A110721.
 GN A110721.

OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.

RC MEDLINE=21595285; PubMed=11759840;
 RA Kaneke T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Triguichi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsuno M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 DR EMBL: AP003583; BAB72678.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 372 AA; 41909 MW; 90CBEL13B2E5FF08F CRC64;

Query Match 52.9%; Score 46; DB 16; Length 372;
 Best Local Similarity 72.7%; Pred. No. 23;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 YSSYIRPFAY 14
 ||| || ||::||
 DB 184 YSSYIRPFYS 194

RESULT 12

ID 061015 PRELIMINARY; PRT; 993 AA.

AC 061015;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Erythrocyte binding protein (Fragment).
 GN MABBL.

OS Plasmodium berghei (strain Anka).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5823;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=ANKA;
 RX MEDLINE=98115903; PubMed=9448314;
 RA Kappe S.H.I., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.;
 RT "A family of chimeric erythrocyte binding proteins of malaria
 parasites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:1230-1235(1998).

DR EMBL: AF031887; AAC05367.1; -
 RT NON_TER 993
 SQ SEQUENCE 993 AA; 115857 MW; B459D15381F9CA77 CRC64;

Query Match
 Best Local Similarity 52.9%; Score 46; DB 5; Length 993;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DMHYSSYIRP 11
 ||| : ||| : |||
 Db 308 DMHYSSYIRP 318

RESULT 13

O95LL5 PRELIMINARY; PRT; 436 AA.

ID O95LL5
 AC O95LL5
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical 49.6 kDa protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
 RA Terao K., Sugano S.;
 RT "Isolation of novel full-length cDNA clones from macaque testis cDNA
 RT libraries";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB072273; BAB69742.1; -
 DR InterPro: IPR002035; VME_A.
 DR Pfam: PF00092; Vwa; 1.
 DR PROSITE: PS50234; VMEFA; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 436 AA; 49618 MW; 4072CCFCE20DA3C0 CRC64;

Query Match 51.7%; Score 45; DB 6; Length 436;
 Best Local Similarity 35.7%; Pred. No. 38;
 Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 OY 1 DMHYSSYIRP 14
 ||| : ||| : |||
 Db 304 DMHYSSYIRP 317

RESULT 14

O9RYVO PRELIMINARY; PRT; 611 AA.

AC O9RYVO
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Oligonucleotide phosphatase F, putative.
 GN DRA0206.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R1;
 RA MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.S., Lam P., McDonald L., Utterback T., Zaleski C.,
 RA Makarewicz K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,

RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1";
 RL Science 286:1571-1577(1999).
 DR EMBL: AE001863; AAF12423.1; -
 DR TIGR: DRA0206; -
 DR InterPro: IPR001567; Peptidase_M3.
 DR InterPro: IPR000130; Zn_MTPeptide.
 DR Pfam: PF01432; Peptidase_M3; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KM Complete proteome.
 SQ SEQUENCE 611 AA; 69389 MW; 618D7102A8231DE7 CRC64;

Query Match 51.7%; Score 45; DB 16; Length 611;
 Best Local Similarity 53.8%; Pred. No. 55;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 WHYSSYIRP 14
 ||| : ||| : |||
 Db 529 WHYSSYIRP 541

RESULT 15

O9APG4 PRELIMINARY; PRT; 995 AA.

ID O9APG4
 AC O9APG4
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Secreted endoglycosidase Endos.
 GN NDO5.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=40/58;
 RA COLLIN M., OLSEN A.;
 RT "Endos", a novel secreted protein from Streptococcus pyogenes with
 RT endoglycosidase activity on human IgG.";
 RL EMBL: J. 20:3046-3055(2001).
 DR EMBL: AF296340; AAK00850.1; -
 DR InterPro: IPR001579; Chitinase_18/2.
 DR PROSITE: PS01095; CHITINASE_18; UNKNOWN_1.
 KM Glycosidase.
 SQ SEQUENCE 995 AA; 111864 MW; 22AE64AC21F9C87E CRC64;

Query Match 51.7%; Score 45; DB 2; Length 995;
 Best Local Similarity 61.5%; Pred. No. 92;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 WHYSSYIRP 14
 ||| : ||| : |||
 Db 329 WOGYSSYIRP 341

Search completed: February 25, 2003, 10:36:34
 Job time : 5.54667 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:57 : Search time 4.62 Seconds
(without alignments)
403.790 Million cell updates/sec

Title: US-09-743-482a-12

Perfect score: 87
Sequence: 1 DMHYSSYIRPAY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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3:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	14	AA178324	Anti-zeta-chain an
2	87	100.0	21	AA178325	Anti-zeta-chain an
3	87	100.0	532	AA178328	Bispecific anti-ze
4	52	59.8	243	AA193540	Human polypeptide
5	52	59.8	501	AA194010	Human polypeptide
6	48	55.2	454	AA194131	Plasmodium falcipa
7	48	55.2	1722	AA198429	Human dendritic ce
8	48	55.2	1740	ABG22846	Novel human diagno
9	48	55.2	1743	AA190644	Human DEC-205. Ho
10	46	52.9	934	AA192129	Plasmodium berghei

11	45	51.7	995	23	ABP29990
12	45	51.7	1013	23	ABP29531
13	45	51.7	1507	21	AA1924128
14	44	50.6	89	22	ABP96096
15	44	50.6	89	22	AA1935405
16	44	50.6	89	22	AA1944005
17	44	50.6	595	14	AA1944003
18	44	50.6	1297	22	AA1962491
19	43.5	50.0	147	21	AA1938660
20	43	49.4	2290	22	ABP60066
21	42	48.3	33	15	AA1958498
22	42	48.3	142	22	ABP71187
23	42	48.3	319	22	AA193146
24	41	47.1	179	24	ABP49435
25	41	47.1	3165	14	AA1938889
26	40	46.0	12	21	AA198111
27	40	46.0	53	22	AA194607
28	40	46.0	146	22	AA1932530
29	40	46.0	160	13	AA1930056
30	40	46.0	160	13	AA1930059
31	40	46.0	160	22	AA190762
32	40	46.0	264	23	AA1977110
33	40	46.0	326	22	ABP17110
34	40	46.0	374	22	ABP70213
35	40	46.0	621	22	ABP64487
36	40	46.0	629	22	AA1957585
37	40	46.0	629	22	AA1958431
38	40	46.0	875	22	AA193179
39	40	46.0	878	22	AA193180
40	40	46.0	879	22	AA193181
41	40	46.0	900	22	AA193178
42	40	46.0	920	21	AA193178
43	40	46.0	1015	19	AA193675
44	40	46.0	1015	22	AA193618
45	40	46.0	1256	22	ABP18316

ALIGNMENTS

RESULT 1	AA178324	AA178324 standard; Protein: 14 AA.
XX	AA178324;	
AC	AA178324;	
XX		
DT	04-MAY-2000 (First entry)	
XX		
XX	Anti-zeta-chain antibody 2-B-5 VH-region CDR3 protein sequence.	
DE		
XX		
KW	Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; Immunisation;	
KW	complementary determining region; CDR; autoimmune disease; cytotoxic;	
KW	immune deficiency; T-cell malignancy; infectious disease; antiviral;	
KW	immunosuppressive; antimicrobial; immune response modulator; NK-cell.	
OS	Rattus norvegicus.	
XX		
PN	WO200003016-A1.	
XX		
PD	20-JAN-2000.	
XX		
PF	09-JUL-1999; 99WO-EP04838.	
XX		
PK	10-JUL-1998; 98EP-0112867.	
XX		
PA	(CONN-) CONNEX GMBH.	
XX		
PI	Reiter C;	
XX		
DR	WPT: 2000-160926/14.	
XX	N-PSDB: AA288322.	
PT	New oligonucleotide, polypeptide, antibody useful for treating	

Streptococcus poly
Streptococcus poly
Plasmodium yoelli
Human testicular a
Human reproductive
Acidic protease B5
Acidic protease V5
P. chrysogenum ABC
Heavy chain frame
Drosophila melanog
Binding domain of
Drosophila melanog
C glutamicum prote
Listeria monocycto
Sequence encoded b
Fluorescein bindin
Human amiloacyl-TR
Human immune secre
Novel human diagno
Human PMP-22. Hom
Bovine PMP. Bos t
Human shear stress
Human amiloacyl-TR
Novel human diagno
Drosophila melanog
Drosophila melanog
Human papillomavir
Human papillomavir
Human polypeptide
Human polypeptide
Human polypeptide
Human polypeptide
Human cancer assoc
Polypeptide having
Human Kicho prote
Novel human diagno

PT autoimmune disease, immune deficiencies, T-cell malignancies and
XX infectious diseases -
PS
xx Claim 10: Fig 6; 79pp: English.

The present invention describes a nucleic acid molecule (I) encoding at least one complementary determining region (CDR) of a variable region of an antibody which specifically interacts with the extracellular domain of the human zeta-chain. The antibody whose CDR of a variable region is encoded by (I), is obtained by immunising a rat with Jurkat cells and subsequently with a conjugate comprising a carrier molecule and a peptide having an N-terminal amino acids of a rat zeta-chain. The anti-zeta-chain antibody is useful for the treatment and prevention of autoimmune diseases, immune deficiencies, T-cell malignancies, infectious diseases and the suppression of immune response preferably in order to avoid graft rejection after organ transplantation, malignancies, or viral infections. The antibody, and fragments of it, can be useful for the enhancement or suppression of NK-cell dependent immunity or for the treatment of NK-cell derived malignancies. It can also be useful for the determination of zeta-chain or eta-chain expression on NK-cells, T-1-lymphocytes or their precursors. The present sequence represents the CDR3 of the VH-region of the anti-zeta-chain antibody 2-B-5, produced by rats from the present invention.

Sequence 14 AA;

Query Match	100.0%	Score 87;	DB 21;	Length 14;
Best Local Similarity	100.0%	Pred. No. 1.5e-07;		
Matches 14; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	DWHTYSSYIRPFAY	14
Db	1	DWHTYSSYIRPFAY	14

RESULT 2
AAV78325
ID AAV78325 standard; Protein; 123 AA

AC	AAV76325;
XX	
DT	04-MAY-2000 (first entry)

DE Antl-zeta-chain antibody 2-B-5 VH-region protein sequence

KM Anti-zeta-chain antibody 2-B-5, rat; human zeta chain; immunisation;
KM complementary determining region; CDR; autoimmune disease; cytostatic
KM Immune deficiency; T-cell malignancy; infectious disease; antiviral;
KM immunosuppressive; antimicrobial; immune response modulator; NK-cell.

OS Rattus norvegicus

PN WO200003016-A1

PD 20-JAN-2000

PF 09-JUL-1999; 99WO-EP04838

PR 10-JUL-1998; 98EP-0112867

PA (CONN-) CONNEX GMBH

PI Reiter C

DR WPI; 2000-160926/14

23

PT New oligonucleotide, polypeptide, antibody useful for treating
PT autoimmune disease, immune deficiencies, T-cell malignancies and
PT infectious diseases -
XX
XS Claim 8; Fig 6; 79pp; English.

The present invention describes a nucleic acid molecule (I) encoding at least one complementary determining region (CDR) of a variable region of an antibody which specifically interacts with the extracellular domain of the human zeta-chain. The antibody whose CDR of a variable region is encoded by (I), is obtained by immunising a rat with Jurkat cells and subsequently with a conjugate comprising a carrier molecule and a peptide having 11 N-terminal amino acids of a rat zeta-chain. The anti-zeta-chain antibody is useful for the treatment and prevention of autoimmune diseases, immune deficiencies, T-cell malignancies, infectious diseases and the suppression of immune response preferably in order to avoid graft rejection after organ transplantation, malignancies, or viral infections. The antibody, and fragments of it, can be useful for the enhancement or suppression of NK-cell dependent immunity or for the treatment of NK-cell derived malignancies. It can also be useful for the determination of zeta-chain or eta-chain expression on NK-cells, T-lymphocytes or their precursors. The present sequence represents the VH-region of the anti-zeta-chain antibody 2-B-5, produced by rats from the present invention.

Sequence 123 AA;

Query Match	100.0%;	Score 87;	DB 21;	Length 123;
Best Local Similarity	100.0%;	Pred. No. 1.6e-06;		
Matches 14; Conservative	0;	Mismatches	0;	Indels 0;

```

QY      1 DMHYSSYIRPEAY 14
          |||+|||||
Db      99 DMHYSSYIRPEAY 112

```

RESULT 3
AAV78328
ID AAV78328 standard; Protein; 532 AA

AC AAY78328

DT 04-MAY-2000 (first entry)

Bispecific anti-zeta-chain/anti-EpCAM antibody protein sequence

KM Anti-zeta-chain antibody 2-3-5 rat; human zeta chain; immunostation;
KM complementary determining region; CDR; autoimmune disease; cytostatic;
KM immune deficiency; T-cell malignancy; infectious disease; antiviral;
KM immunosuppressive; antimicrobial; immune response modulator; NK-cell.

05 Rattus norvegicus

XX
W0300003016-21XX
XX
30-TAN-3000

XX 09-III-1999. 99WQ-FB04838
DE

XX 10-TIT-1008. 98FD-0112867
DB

XX
PA (CONN-) CONNEY CMPI

XX
PT Potter C.

XX
WPB: 2000-160926/1A

DR N-PSDB; AAZ88358
YY

PT New oligonucleotide, polypeptide, antibody useful for treating
PT autoimmune disease, immune deficiencies, T-cell malignancies and
XX infectious diseases -
PT

CC The present invention describes a nucleic acid molecule (I) encoding at
CC least one complementary determining region (CDR) of a variable region of
CC an antibody which specifically interacts with the extracellular domain of
CC the human zeta-chain. The antibody whose CDR of a variable region is

CC encoded by (1), is obtained by immunising a rat with jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,
 CC infectious diseases and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC or viral infections. The antibody, and fragments of it, can be useful for
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC treatment of NK-cell derived malignancies. It can also be useful for the
 CC determination of zeta-chain or eta-chain expression on NK-cells,
 CC T-lymphocytes or their precursors. The present sequence represents a
 CC bispecific anti-zeta-chain/anti-BpCAM antibody, from an example from
 CC the present invention.

XX
 XX
 SQ Sequence 532 AA;

Query Match 100.0%; Score 87; DB 21; Length 532;

Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DMHYSSYIRPFAY 14
 |||||

DB 240 DMHYSSYIRPFAY 253

RESULT 4

AAM93540
 ID AAM93540 standard; Protein: 243 AA.

XX
 XX AAM93540;

DT 06-NOV-2001 (first entry)

DE Human polypeptide, SEQ ID NO: 3289.

KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX Homo sapiens.

OS
 XX EPI130094-A2.

PN
 XX 05-SEP-2001.

PD
 XX 07-JUL-2000; 2000EP-0114089.

PF
 XX 08-JUL-1999; 99JP-0194486.

PR
 XX 11-JAN-2000; 2000JP-0118774.

PR
 XX 02-MAY-2000; 2000JP-0183765.

XX
 XX (HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX
 DR WPI: 2001-524255/58.

DR
 XX N-PSDB: AAK94470.

PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -

XX
 PS Claim 8; SEQ ID NO 3289; 1380bp + sequence listing; English.

CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been

CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
 CC molecules have been determined. Primers for synthesizing the full length

CC cDNA are useful for clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full

CC length enriched cDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily

CC without any special methods. The present sequence is a polypeptide
 CC encoded by a full length human cDNA of the invention.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.

XX
 XX
 SQ Sequence 243 AA;

Query Match 59.8%; Score 52; DB 22; Length 243;

Best Local Similarity 53.8%; Pred. No. 1.5;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 DMHYSSYIRPFA 13
 |||

DB 62 DMHAYSSVKPFS 74

RESULT 5

AAM40410
 ID AAM40410 standard; Protein: 501 AA.

XX
 XX AAM40410;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 3555.

KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW Leukaemia.

XX
 XX Homo sapiens.

OS
 XX WO200153312-A1.

PN
 XX 26-JUL-2001.

PD
 XX 26-DEC-2000; 2000WO-US34263.

PF
 XX 21-JAN-2000; 2000US-0488725.

PR
 XX 25-APR-2000; 2000US-0552317.

PR
 XX 09-JUL-2000; 2000US-0598042.

PR
 XX 19-JUL-2000; 2000US-0620312.

PR
 XX 03-AUG-2000; 2000US-0653450.

PR
 XX 14-SEP-2000; 2000US-0662191.

PR
 XX 19-OCT-2000; 2000US-0693036.

PR
 XX 29-NOV-2000; 2000US-0727344.

XX
 XX (HSE-) HSEQ INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

XX
 DR Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX
 DR WPI: 2001-442253/47.

DR
 XX N-PSDB: AAI59566.

PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -

XX
 PS Example 8; SEQ ID NO 3555; 10078bp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 501 AA;

Query Match 59.8%; Score 52; DB 22; Length 501;
 Best Local Similarity 53.8%; Pred. No. 3.2;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 DMHYSSYIRPFA 13
 ||| | : : : |||
 DB 320 DMHAYSSVKPFS 332

RESULT 6

AAW38429 ID AAW38429 standard; Protein; 1722 AA.

XX AAW38429;

XX 21-MAY-1998 (first entry)

DE Plasmodium falciparum MAEBL protein sequence SEQ ID NO:8.

KM Plasmodium malariae parasite; adhesion molecule; MAEBL; vaccine;
 KM erythrocyte binding protein; protozoicide; infection.

OS Plasmodium falciparum.

PN US6120770-A.

PD 19-SEP-2000.

PF 12-SEP-1997; 97US-0929329.

PR 12-SEP-1997; 97US-0929329.

PA (UNOT) UNIV NOTRE DAME DU LAC.

PI Adams JH, Dalton JP, Kappe S;

DR WPI; 2000-593710/56.

DR N-PSDB; AAA99268.

PT New erythrocyte binding protein (MAEBL) useful as a vaccine against
 PT malaria, for enhancing cell's resistance to infection or for
 PT alleviating symptoms associated with the disease -

PS Claim 1: Column 39-42; 31pp; English.

XX The present invention describes an isolated polypeptide (I) comprising
 CC a Plasmodium parasite (malaria parasite) erythrocyte binding protein
 CC (MAEBL). Also described is an immunogenic composition comprising an
 CC isolated polypeptide and a carrier, where the polypeptide comprises an
 CC amino acid sequence, which includes a MAEBL protein cysteine domain.
 CC MAEBL polypeptides and compositions containing them are useful as
 CC vaccines against malaria, to enhance a cell's resistance to infection
 CC by Plasmodium parasites or to alleviate the symptoms associated with
 CC the disease. The present sequence represents a MAEBL protein, which is
 CC used in the exemplification of the present invention.

XX Sequence 454 AA;

Query Match 55.2%; Score 48; DB 21; Length 454;
 Best Local Similarity 72.7%; Pred. No. 13;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DMHYSSYIRP 11
 ||| | : : : |||
 DB 278 DMHYSSYIRP 288

RESULT 7
 ID AAW38429
 AAW38429; Protein; 1722 AA.

XX AAW38429;

XX 21-MAY-1998 (first entry)

DE Human dendritic cell receptor DEC-205.

KW Dendritic cell receptor; DEC-205; human; ligand; cell targeting;
 KW antigen; toxin; immunosuppressive; therapy; prophylaxis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..26

FT Domain 27..1666

FT Domain 27..158

FT Peptide 71..106

FT Domain 158..212

FT Domain 216..342

FT Domain 361..488

FT Domain 501..625

FT Domain 643..792

FT Domain 811..932

FT Domain 951..1091

FT Domain 1097..1222

FT Peptide 1208..1323

FT Domain 1239..1382

FT Domain 1394..1513

FT Domain 1539..1661

FT Domain 1667..1691

FT Domain 1692..1722

FT Modified-site 135

FT Modified-site 345

FT Modified-site 377

FT Modified-site 529

FT Modified-site 843

FT Modified-site 865

FT Modified-site 904

FT Modified-site 1076

FT Modified-site 1103

FT Modified-site 1225

FT Modified-site /note= "N-glycosylated"
 FT 1320 /note= "N-glycosylated"
 FT Modified-site 1392 /note= "N-glycosylated"
 FT Modified-site 1392 /note= "N-glycosylated"
 FT Modified-site 1593 /note= "N-glycosylated"
 FT Modified-site 1626 /note= "N-glycosylated"
 FT Modified-site 1703 /note= "N-glycosylated"
 FT Modified-site 1719 /note= "O-phosphorylated"
 FT Modified-site /note= "O-phosphorylated"
 PN W09745449-A1.
 PD 04-DEC-1997.
 XX 29-MAY-1997; 97WO-N200068.
 XX 29-MAY-1996; 96NZ-0286692.
 PR 29-MAY-1996; 96NZ-0286692.
 PA (HART/) HART D N J.
 PI Hart DNU;
 XX WPI: 1998-032580/03.
 DR N-PSDB: AAV04024.
 XX Human dendritic cell receptor, DEC-205 - useful to develop ligands
 PT for isolation and targeted cell delivery of antigen or toxin
 PS Claim 2; Fig 11; 53pp; English.
 CC This protein comprises the human homologue of mouse dendritic cell
 CC receptor DEC-205. Its amino acid sequence was deduced from DEC-205
 CC cDNA (see AAV04024) obtained from Hodgkin's disease-derived L428
 CC cells. It shows 77% overall identity with the mouse protein. The
 CC predicted mol.wt. is 198-205 kDa. The invention provides isolated
 CC human DEC-205, its extracellular domain and equivalent fragments,
 CC and polynucleotides encoding these polypeptides as well as vectors
 CC which include such polynucleotides, and a method of producing
 CC recombinant DEC-205 polypeptides in host cells transformed or
 CC transfected with such vectors. Further provided are ligands
 CC (preferably an antibody or antibody binding fragment) that bind to
 CC human DEC-205, as well as constructs for use in prophylaxis and
 CC therapy that comprise such a ligand, human DEC-205 or an
 CC extracellular domain coupled to an antigen capable of inducing a
 CC protective immune response in a patient, or to a toxin (e.g. ricin
 CC A chain to specifically destroy dendritic cells as part of an
 CC immunosuppressive process).
 XX
 SQ Sequence 1722 AA;
 Query Match 55.2%; Score 48; DB 19; Length 1722;
 Best Local Similarity 50.0%; Pred. No. 53;
 Matches 8; Conservative 2; Mismatches 2; Indels 4; Gaps 1;
 OY 2 WHYSS---YTRPFA 13
 II: I I: I I I I I
 DB 766 WHFYDDREFYLRPFA 781

RESULT 8
 ABG22846
 ID ABG22846 standard; Protein; 1740 AA.
 AC ABG22846;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #22837.
 XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 PN W0200175067-A2.
 PD 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 PF 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB: AAS87033.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 PS Claim 20; SEQ ID NO 53205; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1740 AA;
 Query Match 55.2%; Score 48; DB 22; Length 1740;
 Best Local Similarity 50.0%; Pred. No. 53;
 Matches 8; Conservative 2; Mismatches 2; Indels 4; Gaps 1;
 OY 2 WHYSS---YTRPFA 13
 II: I I: I I I I I
 DB 784 WHFYDDREFYLRPFA 799

RESULT 9
 AAW00644
 ID AAW00644 standard; Protein; 1743 AA.
 AC AAW00644;
 XX
 DT 19-NOV-1996 (first entry)
 XX
 DE Human DEC-205.
 XX
 KW Dendritic and epithelial cell 205 kDa; DEC-205; receptor;
 KW C-type lectin; antigen presentation; immune stimulation; vaccine;

KW Immune suppression.
 XX
 OS Homo sapiens.
 XX
 PN W09623882-A1.
 XX
 PD 08-AUG-1996.
 XX
 PF 31-JAN-1996: 96MO-US01383.
 XX
 PR 31-JAN-1995: 95US-0381528.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Jiang W, Nussenzweig MC, Steelman RM, Swiggard WJ;
 XX
 DR WPI: 1996-371431/37.
 DR N-PSDB: AATJ3514.
 XX
 PT Ligands for integral membrane protein DEC - useful in compns. to
 PT target molecules to partic. areas of the body, e.g. for immune
 PT modulation, and to induce immune suppression
 XX
 PS Claim 9; Page 111-116; 152pp; English.
 XX
 CC The amino acid sequence (AAW0644) of human DEC-205 (dendritic and
 CC epithelial, 205 kDa) was deduced from a cDNA clone (AATJ3514) obtd.
 CC from a B lymphoma cDNA library. DEC-205 is an integral membrane
 CC protein found primarily on dendritic cells, but also in thymic,
 CC lung and small intestine epithelial cells and brain capillaries.
 CC The 205 kDa protein has 10 lectin domains, a transmembrane domain
 CC and a cytoplasmic tail contg. a coated pit localisation consensus
 CC sequence. It can be produced in recombinant host cells, esp. CHO,
 CC COS, MDCK and NIH3T3 cells. It is useful for identifying DEC
 CC ligands. These can be used to target antigens to dendritic cells,
 CC to provide tolerance when dendritic cells are quiescent, or for
 CC immune stimulation (i.e. vaccination) when the dendritic cells are
 CC activated e.g. by stimulation with a cytokine.
 XX
 SQ Sequence 1743 AA;
 XX
 QY Query Match 55.2%; Score 48; DB 17; Length 1743;
 Best Local Similarity 50.0%; Pred. No. 53;
 Matches 8; Conservative 2; Mismatches 2; Indels 4; Gaps 1;
 XX
 Db 2 WHYYS---YIRPFA 13
 787 WHFYDDREFLYLRPFA 802
 XX
 RESULT 10
 AAB24129
 ID AAB24129 standard; Protein: 934 AA.
 XX
 AC AAB24129;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Plasmodium berghei ANKA 5' MAEBL AMA-1-like protein SEQ ID NO:6.
 XX
 KW Plasmodium; malaria; parasite; adhesion molecule; MAEBL; vaccine;
 KW erythrocyte binding protein; protozoacide; infection.
 XX
 OS Plasmodium berghei.
 XX
 PN US6120770-A.
 XX
 PD 19-SEP-2000.
 XX
 PF 12-SEP-1997: 97US-0929329.
 XX
 PR 12-SEP-1997: 97US-0929329.
 XX

PA (UNOT) UNIV NOTRE DAME DU LAC.
 XX
 PI Adams JH, Dalton JP, Kappe S;
 XX
 DR WPI: 2000-593710/56.
 DR N-PSDB: AAB99266.
 XX
 PT New erythrocyte binding protein (MAEBL) useful as a vaccine against
 PT malaria, for enhancing cell's resistance to infection or for
 PT alleviating symptoms associated with the disease
 XX
 PS Example 4; Column 33-38; 31pp; English.
 XX
 CC The present invention describes an isolated polypeptide (I) comprising
 CC a Plasmodium parasite (malaria parasite) erythrocyte binding protein
 CC (MAEBL). Also described is an immunogenic composition comprising an
 CC isolated polypeptide and a carrier, where the polypeptide comprises an
 CC amino acid sequence, which includes a MAEBL protein cysteine domain.
 CC MAEBL polypeptides and compositions containing them are useful as
 CC vaccines against malaria, to enhance a cell's resistance to infection
 CC by Plasmodium parasites or to alleviate the symptoms associated with
 CC the disease. The present sequence represents a MAEBL protein, which is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 934 AA;
 XX
 QY Query Match 52.9%; Score 46; DB 21; Length 934;
 Best Local Similarity 63.6%; Pred. No. 57;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 XX
 Db 1 DMHYSSYIRP 11
 308 DWTYSSFLRP 318
 XX
 RESULT 11
 AAB29990
 ID AAB29990 standard; Protein: 995 AA.
 XX
 AC AAB29990;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Streptococcus polypeptide SEQ ID NO 9156.
 XX
 KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus pyogenes.
 XX
 PN W0200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 DT 29-OCT-2001; 2001WO-GB04789.
 XX
 DE 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tectelin H;
 XX
 DR WPI: 2002-352536/38.
 DR N-PSDB: ABN70621.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -

XX Claim 1; Page 4038; 4525pp; English.

CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and anti-inflammatory
CC activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (1) are used to detect Streptococcus in a
CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.

XX Sequence 995 AA:

Query Match 51.7%; Score 45; DB 23; Length 995;
Best Local Similarity 61.5%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 WHYSSYIRPAY 14
| | | | | | |
Db 329 WOGYSKYIRPEQY 341

RESULT 12
ID ABP29531 standard; Protein; 1013 AA.

XX ABP29531;

XX 02-JUL-2002 (first entry)

XX Streptococcus polypeptide SEQ ID NO 8238.

DE Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;
KM group A streptococcus; Streptococcus pyogenes; antibacterial;
KW anti-inflammatory; infection; vaccine; meningitis; gene therapy.

XX Streptococcus pyogenes.

OS

XX WO200234771-A2.

PN

XX 02-MAY-2002.

PD

XX 29-OCT-2001; 2001WO-GB04789.

PF

XX 27-OCT-2000; 2000GB-0026333.

PR

XX 24-NOV-2000; 2000GB-0028727.

PR

XX 07-MAR-2001; 2001GB-0005640.

XX

PA (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

XX Telford J, Masignani V, Margarit Ros VI, Grandi G, Fraser C;
PI Tettein H;

XX WPI: 2002-352536/38.

DR N-PSDB; ABN70162.

XX New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -

XX Claim 1; Page 3942; 4525pp; English.

CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and anti-inflammatory
CC activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (1) are used to detect Streptococcus in a
CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.

XX Sequence 1013 AA:

Query Match 51.7%; Score 45; DB 23; Length 1013;
Best Local Similarity 61.5%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 WHYSSYIRPAY 14
| | | | | | |
Db 347 WOGYSKYIRPEQY 359

RESULT 13
ID AAB24128 standard; Protein; 1507 AA.

XX AAB24128;

XX 29-JAN-2001 (first entry)

XX Plasmodium yoelii YM MAEBL protein sequence SEQ ID NO:5.

DE Plasmodium; malaria; parasite; adhesion molecule; MAEBL; vaccine;
KW erythrocyte binding protein; protozoacide; infection.

XX Plasmodium yoelii.

OS

XX US6120770-A.

PN

XX 19-SEP-2000.

PD

XX 12-SEP-1997; 97US-0929329.

PF

XX 12-SEP-1997; 97US-0929329.

PR

XX 12-SEP-1997; 97US-0929329.

PR

XX (UNOT) UNIT NOTRE DAME DU LAC.

PA Adams JH, Dalton JP, Kappe S;

PI

XX WPI: 2000-593710/56.

DR N-PSDB; AAA9265.

XX New erythrocyte binding protein (MAEBL) useful as a vaccine against
PT malaria, for enhancing cell's resistance to infection or for
PT alleviating symptoms associated with the disease -

XX Example 4; Column 25-34; 31pp; English.

XX The present invention describes an isolated polypeptide (1) comprising
CC a Plasmodium parasite (malaria parasite) erythrocyte binding protein
CC (MAEBL). Also described is an immunogenic composition comprising an
CC isolated polypeptide and a carrier, where the polypeptide comprises an
CC amino acid sequence, which includes a MAEBL protein cysteine domain.
CC MAEBL polypeptides and compositions containing them are useful as
CC vaccines against malaria, to enhance a cell's resistance to infection
CC by Plasmodium parasites or to alleviate the symptoms associated with

CC the disease. The present sequence represents a MAEBL protein, which is
CC used in the exemplification of the present invention.

SO Sequence 1507 AA;

Query Match 51.7%; Score 45; DB 21; Length 1507;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DMHYSSYIRP 11

DB 308 DWTYASSFLRP 318

RESULT 14

ABB96096

ID ABB96096 standard; Protein; 89 AA.

XX ABB96096;

DT 21-JUN-2002 (first entry)

DE Human testicular antigen SEQ ID NO: 1480.

XX Human; testicular antigen; testes; cancer; metastasis; immune disorder;

KM reproductive system disorder; urinary system disorder; gene therapy;

KW cardiovascular disorder; respiratory disorder; neurological disorder;

XX gastrointestinal disease; infection; cytostatic.

OS Homo sapiens.

PN WO200155317-A2.

PD 02-AUG-2001.

XX 17-JAN-2001; 2001MO-US01329.

PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 15-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUL-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 14-AUG-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225271.

PR 14-AUG-2000; 2000US-0225272.

PR 14-AUG-2000; 2000US-0225273.

PR 14-AUG-2000; 2000US-0225274.

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PR 14-AUG-2000; 2000US-0225400.

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PR 14-AUG-2000; 2000US-0225410.

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PR 14-AUG-2000; 2000US-0225415.

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PR 14-AUG-2000; 2000US-0225421.

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PR 14-AUG-2000; 2000US-0225424.

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PR 14-AUG-2000; 2000US-0225433.

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PR 14-AUG-2000; 2000US-0225436.

PR 14-AUG-2000; 2000US-0225437.

PR 14-AUG-2000; 2000US-0225438.

PR 14-AUG-2000; 2000US-0225439.

PR 14-AUG-2000; 2000US-0225440.

PR 14-AUG-2000; 2000US-0225441.

PR 14-AUG-2000; 2000US-0225442.

PR 14-AUG-2000; 2000US-0225443.

PR 14-AUG-2000; 2000US-0225444.

PR 14-AUG-2000; 2000US-0225445.

PR 14-AUG-2000; 2000US-0225446.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225448.

PR 14-AUG-2000; 2000US-0225449.

PR 14-AUG-2000; 2000US-022545


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XX  WPI: 2001-465570/50.
DR  N-PSDB; AAL01375.
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PT  Isolated nucleic acid molecule encoding a reproductive system antigen
XX  is used in preventing, treating or ameliorating a medical condition -
XX
PS  Claim 11: SEQ ID NO 4063; 1297bp + Sequence Listing; English.
CC  The present invention provides the protein and coding sequences of a
CC  number of human reproductive system related antigens. These can be used
CC  in the prevention and treatment of reproductive system disorders,
CC  including cancer. The present sequence is a protein of the invention.
XX
SQ  Sequence      89 AA;
      ;
Query Match          50.6%; Score 44; DB 22; Length 89;
Best Local Similarity 38.5%; Pred. No. 9.6;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0.
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DB  42 WFLYASVTPYSY 54

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Job time : 6.62 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

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(without alignments)
380.447 Million cell updates/sec

Title: US-09-743-482a-12

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Searched: 156504 seqs, 31069816 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	42	48.3	319	9	US-09-738-626-6900
2	41	47.1	58	9	US-09-989-920-253
3	40	46.0	920	10	US-09-925-301-1396
4	38	43.7	342	10	US-09-886-055-207
5	38	43.7	523	10	US-09-912-020-354
6	38	43.7	1364	10	US-09-801-368-244
7	37.5	43.1	477	9	US-09-992-598-285
8	37.5	43.1	477	9	US-09-989-293A-285
9	37.5	43.1	477	9	US-09-989-735-285
10	37.5	43.1	477	9	US-09-990-444-285
11	37.5	43.1	477	9	US-09-989-730-285
12	37.5	43.1	477	9	US-09-990-436-285
13	37.5	43.1	477	9	US-09-991-181-285
14	37.5	43.1	477	9	US-09-993-687-285
15	37.5	43.1	477	9	US-09-989-734-285
16	37.5	43.1	477	9	US-10-028-072-452
17	37.5	43.1	477	9	US-09-997-653-285
18	37.5	43.1	477	9	US-09-993-667-285
19	37.5	43.1	477	9	US-10-121-049-452

20	37.5	43.1	477	9	US-10-123-904-452	Sequence 452, App
21	37.5	43.1	477	9	US-10-140-470-452	Sequence 452, App
22	37.5	43.1	477	9	US-09-990-438-285	Sequence 285, App
23	37.5	43.1	477	9	US-09-990-562-285	Sequence 285, App
24	37.5	43.1	477	9	US-09-997-428-285	Sequence 285, App
25	37.5	43.1	477	9	US-09-997-666-285	Sequence 285, App
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27	37.5	43.1	477	9	US-10-176-918-452	Sequence 452, App
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30	37.5	43.1	477	9	US-10-137-865-452	Sequence 452, App
31	37.5	43.1	477	9	US-10-140-474-452	Sequence 452, App
32	37.5	43.1	477	10	US-09-989-722-285	Sequence 285, App
33	37.5	43.1	477	10	US-09-989-723-285	Sequence 285, App
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35	37.5	43.1	477	10	US-09-989-727-285	Sequence 285, App
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39	37.5	43.1	477	10	US-09-990-442-285	Sequence 285, App
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42	37.5	43.1	477	10	US-09-990-456-285	Sequence 285, App
43	37.5	43.1	477	10	US-09-989-721-285	Sequence 285, App
44	37.5	43.1	302	10	US-09-731-872-349	Sequence 345, App
45	37	42.5	321	10	US-09-764-877-1725	Sequence 1725, App

ALIGNMENTS

RESULT 1
US-09-738-626-6900
Sequence 6900, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738, 626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6900
LENGTH: 319
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-6900

Query Match 48.3% Score 42: DB 9: Length 319:
Best Local Similarity 53.8% Pred. No. 26:
Matches 7: Conservative 3: Mismatches 3: Indels 0: Gaps 0:

Qy 1 DMHYSSYIRPEA 13
Db 254 DMHYSSYIRPEA 266

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RESULT 2
US-09-989-920-253
; Sequence 253, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Chen, Sel-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 253
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-989-920-253

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Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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DB 15 WHERHYLTKP 24

RESULT 3
US-09-925-301-1396
; Sequence 1396, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antbodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1396
; LENGTH: 920
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1396

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Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 WHYYSSYIRP 11
DB 625 WREYLYLXIRP 634

RESULT 4
US-09-886-055-207
; Sequence 207, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS

FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 207
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-055-207

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Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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DB 4 WHGFSSHLNP 13

RESULT 5
US-09-912-020-354
; Sequence 354, Application US/09912020
; Patent No. US20020045592A1
; GENERAL INFORMATION:
; APPLICANT: Zyskind, Judith
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Trawick, John
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Froelich, Jamie M.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
; TITLE OF INVENTION: ESCHERICHIA COLI
; FILE REFERENCE: ELITRA-001DV1
; CURRENT APPLICATION NUMBER: US/09/912,020
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/492,709
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/117,405
; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 485
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 354
; LENGTH: 523
; TYPE: PRT
; ORGANISM: E. COLI
US-09-912-020-354

Query Match
Best Local Similarity 43.7%; Score 38; DB 10; Length 523;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DMHYYSSYI 9
DB 81 NWSYSHYIV 89

RESULT 6
US-09-801-368-244
; Sequence 244, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
```


APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amit
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 244
LENGTH: 1564
TYPE: PRF
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-244

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Best Local Similarity 46.2%; Pred. No. 4.5e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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DB 713 WSKWISYINPLSY 725

RESULT 7
US-09-992-598-285
Sequence 285, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kjaevig, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonl, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Acids Encoding and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 43.1%; Score 37.5; DB 9; Length 477;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 WH-YSSYRP 11
DB 305 WHKYNRIQP 315

RESULT 8
US-09-989-293A-285
Sequence 285, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C66
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 43.1%; Score 37.5; DB 9; Length 477;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 WHY-ISSYIRP 11
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DB 305 WHYKXSRIOF 315

RESULT 9
US-09-989-735-285
;; Sequence 285; Application US/09989735
;; Publication No. US20020193299A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
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;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
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;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P27301C61
;; CURRENT APPLICATION NUMBER: US/09/989,735
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PRIOR FILING DATE: 1998-07-09

Query Match 43.1%; Score 37.5; DB 9; Length 477;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
Oy 2 WHY-YSSYIRP 11
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Db 305 WHYKXNSRQIP 315
RESULT 10
US-09-990-444-285
; Sequence 285, Application US/09990444
; Publication No. US20020193300A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerder, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US/09/990,444
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match      43.1%; Score 37.5%; DB 9; Length 477;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
Oy 2 WHY-YSSYIRP 11
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Db 305 WHKYNRSR10P 315

RESULT 11
US-09-989-730-285
Sequence 285, Application US/09989730
Publication No. US20020197674A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botsstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC69
CURRENT APPLICATION NUMBER: US/09/989,730
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 43.1%; Score 37.5; DB 9; Length 477;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 WH-YSSYIRP 11
DB 305 WHYKNSRIOP 315

RESULT.12
US-09-990-436-285
; Sequence 285, Application US/09990436
; Publication No. US20020198148A1

;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gertlisen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Napier, Mary A.
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;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC14
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR APPLICATION NUMBER: 60/091360
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 43.1%; Score 37.5; DB 9; Length 477;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 WHY-YSSYIRP 11
||| | | | | |

Db 305 WHYKXNSRIQP 315

RESULT 13
US-09-991-181-285
; Sequence 285, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerbert, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
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PRIOR APPLICATION NUMBER: 60/090445

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 43.1%; Score 37.5; DB 9; Length 477;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 WHY-YSSYIRP 11
DB 305 WHYKNSRIOP 315

RESULT 14
US-09-993-687-285
; Sequence 285, Application US/09993687
; Publication No. US2002019819A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC11
; CURRENT APPLICATION NUMBER: US/09/993,687
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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: PRIOR FILING DATE: 1998-06-24
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: PRIOR FILING DATE: 1998-06-24
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: PRIOR APPLICATION NUMBER: 60/090542
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: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090862
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: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091626
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: PRIOR APPLICATION NUMBER: 60/091633
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091978
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/091982
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/092182
: PRIOR FILING DATE: 1998-07-09

Query Match 43.1% Score 37.5; DB 9; Length 477;
Best Local Similarity 63.6% Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 WHY-YSSYIRP 11
Db 305 WHYKXNSRQP 315

RESULT 15
US-09-989-734-285
: Sequence 285, Application US/09989734
: Publication No. US20030003531A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerlitsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gunney, Austin L.
: APPLICANT: Kiljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel

```

APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C64
CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678

1	PRIOR FILING DATE: 1998-06-25
2	PRIOR APPLICATION NUMBER: 60/090690
3	PRIOR FILING DATE: 1998-06-25
4	PRIOR FILING DATE: 1998-06-25
5	PRIOR APPLICATION NUMBER: 60/090654
6	PRIOR FILING DATE: 1998-06-25
7	PRIOR APPLICATION NUMBER: 60/090655
8	PRIOR FILING DATE: 1998-06-25
9	PRIOR APPLICATION NUMBER: 60/090696
10	PRIOR FILING DATE: 1998-06-25
11	PRIOR APPLICATION NUMBER: 60/090862
12	PRIOR FILING DATE: 1998-06-26
13	PRIOR APPLICATION NUMBER: 60/090863
14	PRIOR FILING DATE: 1998-06-26
15	PRIOR APPLICATION NUMBER: 60/091360
16	PRIOR FILING DATE: 1998-07-01
17	PRIOR APPLICATION NUMBER: 60/091478
18	PRIOR FILING DATE: 1998-07-02
19	PRIOR APPLICATION NUMBER: 60/091544
20	PRIOR FILING DATE: 1998-07-01
21	PRIOR APPLICATION NUMBER: 60/091519
22	PRIOR FILING DATE: 1998-07-02
23	PRIOR APPLICATION NUMBER: 60/091626
24	PRIOR FILING DATE: 1998-07-02
25	PRIOR APPLICATION NUMBER: 60/091633
26	PRIOR FILING DATE: 1998-07-02
27	PRIOR APPLICATION NUMBER: 60/091978
28	PRIOR FILING DATE: 1998-07-07
29	PRIOR APPLICATION NUMBER: 60/091982
30	PRIOR FILING DATE: 1998-07-07
31	PRIOR APPLICATION NUMBER: 60/092182
32	PRIOR FILING DATE: 1998-07-09

Query Match	43.1%	Score 37.5;	DB 9;	Length 477;
Best Local Similarity	63.6%	Pred. No. 1.8e+02;		
Matches	7;	Conservative	2;	Mismatches 1;
				Indels 1;
				Gaps 1;

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QY      2 WHY-YSSYIRP 11
          ||| |:| |:|
Db      305 WHYKYNRIQP 315
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Search completed: February 25, 2003, 10:57:20
Job time : 1.14333 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 1.56333 Seconds
(without alignments)
263.489 Million cell updates/sec

Title: US-09-743-482A-12

Perfect score: 87

Sequence: 1 DMHYSSIRPEAY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	55.2	454	3	US-08-929-329-8
2	48	55.2	1722	4	US-09-194-612A-1
3	46	53.9	934	3	US-08-929-329-6
4	45	51.7	1507	3	US-08-929-329-5
5	42	48.3	33	1	US-08-176-500-125
6	42	48.3	33	1	US-08-471-052A-125
7	42	48.3	33	1	US-08-189-331-125
8	42	48.3	33	1	US-08-471-939-125
9	42	48.3	33	2	US-08-471-800-125
10	42	48.3	33	2	US-08-471-068-125
11	41	47.1	3165	2	US-08-459-146-3
12	41	47.1	3165	2	US-08-459-065-3
13	40	46.0	160	3	US-08-600-430-5
14	40	46.0	246	4	US-08-822-774-45
15	40	46.0	246	4	US-09-632-711-45
16	40	46.0	246	4	US-09-632-703B-45
17	40	46.0	246	4	US-09-632-702-45
18	40	46.0	629	4	US-09-300-909-19
19	39	44.8	264	4	US-08-904-284-3
20	39	44.8	464	3	US-09-056-783-2
21	39	44.8	1023	2	US-08-475-891A-2
22	39	44.8	1023	2	US-08-567-375-2
23	39	44.8	1023	2	US-08-587-680A-2
24	37.5	43.1	355	2	US-09-014-969-19
25	37	42.5	160	3	US-08-600-430-6
26	37	42.5	161	1	US-08-557-917A-3
27	37	42.5	161	4	US-09-084-153-3

28	37	42.5	161	4	US-09-084-079-3	Sequence 3, Appl1
29	37	42.5	170	2	US-08-708-678B-2	Sequence 2, Appl1
30	37	42.5	239	2	US-08-114-555A-12	Sequence 12, Appl1
31	37	42.5	239	3	US-08-559-387A-17	Sequence 17, Appl1
32	37	42.5	313	4	US-08-904-284-7	Sequence 7, Appl1
33	37	42.5	313	4	US-09-105-390-46	Sequence 46, Appl1
34	37	42.5	340	4	US-09-105-390-62	Sequence 62, Appl1
35	37	42.5	724	4	US-09-562-737-23	Sequence 23, Appl1
36	37	42.5	1449	3	US-08-840-062-6	Sequence 6, Appl1
37	37	42.5	1723	4	US-09-194-612A-31	Sequence 31, Appl1
38	36	41.4	163	1	US-08-463-262A-10	Sequence 10, Appl1
39	36	41.4	163	1	US-08-463-989-10	Sequence 10, Appl1
40	36	41.4	163	4	US-09-003-574-10	Sequence 10, Appl1
41	36	41.4	163	4	US-09-003-570-10	Sequence 10, Appl1
42	36	41.4	374	4	US-09-134-001C-5555	Sequence 5555, Ap
43	36	41.4	394	2	US-08-555-568B-17	Sequence 17, Appl
44	36	41.4	394	4	US-09-519-223-17	Sequence 17, Appl
45	36	41.4	475	2	US-08-484-200-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-929-329-8
; Sequence 8, Application US/08929329
; Patent No. 6120770

GENERAL INFORMATION:

APPLICANT: Adams, John H

APPLICANT: Dalton, John P

TITLE OF INVENTION: Plasmodium Proteins Useful for Preparing

TITLE OF INVENTION: Vaccine Compositions

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Barnes & Thornburg

STREET: 11 S Meridian

CITY: Indianapolis

STATE: Indiana

COUNTRY: USA

ZIP: 46204

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/929,329

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Breen, John P

REGISTRATION NUMBER: 38,833

REFERENCE/DOCKET NUMBER: 835910-28685

TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 231-7745

TELEFAX: (317) 231-7433

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 454 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYDROTHERICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

ORGANISM: Plasmodium falciparum

US-08-929-329-8

Query Match 55.2%; Score 48; DB 3; Length 454;

Best Local Similarity 72.7%; Pred. No. 5.7;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 DMHYSSYIRP 11
|||
Db 278 DMHYSSYIRP 288

RESULT 2
US-09-194-612A-1
; Sequence 1, Application US/09194612A
; Patent No. 6432666
; GENERAL INFORMATION:
; APPLICANT: HART, DEREK N.
; TITLE OF INVENTION: DENDRITIC CELL RECEPTOR
; FILE REFERENCE: 659-36
; CURRENT APPLICATION NUMBER: US/09/194,612A
; CURRENT FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: PCT/NZ97/00068
; PRIOR FILING DATE: 1997-05-29
; PRIOR APPLICATION NUMBER: NZ 286692
; PRIOR FILING DATE: 1996-05-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1722
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-612A-1

Query Match 55.2%; Score 48; DB 4; Length 1722;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

QY 2 WHYSS---YIRPFA 13
|||
Db 766 WHYDDREFYLRPFA 761

RESULT 3
US-08-929-329-6
; Sequence 6, Application US/08929329
; Patent No. 6120770
; GENERAL INFORMATION:
; APPLICANT: Adams, John H
; APPLICANT: Dalton, John P
; TITLE OF INVENTION: Plasmodium Proteins Useful for Preparing
; TITLE OF INVENTION: Vaccine Compositions
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 S Meridian
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,329
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Breen, John P
; REGISTRATION NUMBER: 38,833
; REFERENCE/DOCKET NUMBER: 835910-28685
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 231-7745
; TELEFAX: (317) 231-7433
; INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
; LENGTH: 934 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium berghei
US-08-929-329-6

Query Match 52.9%; Score 46; DB 3; Length 934;
Best Local Similarity 63.6%; Pred. No. 24;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 DMHYSSYIRP 11
|||
Db 308 DMHYSSYIRP 318

RESULT 4
US-08-929-329-5
; Sequence 5, Application US/08929329
; Patent No. 6120770
; GENERAL INFORMATION:
; APPLICANT: Adams, John H
; APPLICANT: Dalton, John P
; APPLICANT: Kappe, Stefan
; TITLE OF INVENTION: Plasmodium Proteins Useful for Preparing
; TITLE OF INVENTION: Vaccine Compositions
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 S Meridian
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,329
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Breen, John P
; REGISTRATION NUMBER: 38,833
; REFERENCE/DOCKET NUMBER: 835910-28685
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 231-7745
; TELEFAX: (317) 231-7433
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1507 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium yoellii
US-08-929-329-5

Query Match 51.7%; Score 45; DB 3; Length 1507;
Best Local Similarity 63.6%; Pred. No. 55;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 DMHYSSYIRP 11
11111111
Db 308 DMHYSSFLRP 318

RESULT 5

US-08-176-500-125
Sequence 125, Application US/08176500
Patent No. 5498538
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,500
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/013,416
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-143
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-176-500-125

Query Match 48.3%; Score 42; DB 1; Length 33;
Best Local Similarity 54.5%; Pred. No. 3.4;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 DMHYSSYIRP 11
11111111
Db 9 DMHYSSYLLP 19

RESULT 6

US-08-471-052A-125
Sequence 125, Application US/08471052A
Patent No. 5625033
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-052A-125

Query Match 48.3%; Score 42; DB 1; Length 33;
Best Local Similarity 54.5%; Pred. No. 3.4;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 DMHYSSYIRP 11
11111111
Db 9 DMHYSSYLLP 19

RESULT 7

US-08-189-331-125
Sequence 125, Application US/08189331
Patent No. 5747334
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,331
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-189-331-125

Query Match 48.3%; Score 42; DB 1; Length 33;
Best Local Similarity 54.5%; Pred. No. 3.4;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DMHYSSYIRP 11
DB 9 EWHRYSTILP 19

RESULT 8
US-08-471-939-125
Sequence 125, Application US/08471939
Patent No. 5844076

GENERAL INFORMATION:

APPLICANT: Kay, B. K.

TITLE OF INVENTION: Totally Synthetic Affinity Reagents

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,939

FILING DATE: 06-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/013,416

FILING DATE: 01-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-143

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 125:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-471-939-125

Query Match 48.3%; Score 42; DB 2; Length 33;
Best Local Similarity 54.5%; Pred. No. 3.4;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DMHYSSYIRP 11
DB 9 EWHRYSTILP 19

RESULT 9
US-08-471-800-125

Sequence 125, Application US/08471800
Patent No. 5852167

GENERAL INFORMATION:
APPLICANT: Kay, B. K.
TITLED OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,800

FILING DATE: 06-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/013,416

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-143

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 125:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-471-800-125

Query Match 48.3%; Score 42; DB 2; Length 33;
Best Local Similarity 54.5%; Pred. No. 3.4;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DMHYSSYIRP 11
DB 9 EWHRYSTILP 19

RESULT 10
US-08-471-068-125

Sequence 125, Application US/08471068
Patent No. 5948635

GENERAL INFORMATION:

APPLICANT: Kay, B. K.

TITLE OF INVENTION: Totally Synthetic Affinity Reagents

NUMBER OF SEQUENCES: 186

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,068

* FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,331
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-068-125

Query Match
Best Local Similarity 48.3%; Score 42; DB 2; Length 33;
54.5%; Pred. No. 3.4;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DWHYSSYIRP 11
|||:|
Db 9 EWHRYSYLLP 19

RESULT 11
US-08-459-146-3
Sequence 3, Application US/08459146
Patent No. 5866405
GENERAL INFORMATION:
APPLICANT: Choi, Gail HO
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Genetically Engineered Transmissible
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,146
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,117
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Roseman, Catherine R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8589
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3165 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Endothia parasitica (Cryptonecristia)
ORGANISM: parasitica
STRAIN: EP713
US-08-459-146-3

Query Match
Best Local Similarity 47.1%; Score 41; DB 2; Length 3165;
38.5%; Pred. No. 4.8e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 DWHYSSYIRP 14
|||:|
Db 2425 WHTHNOYVEKFIY 2437

RESULT 12
US-08-459-065-3
Sequence 3, Application US/08459065
Patent No. 5882642
GENERAL INFORMATION:
APPLICANT: Choi, Gail HO
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Genetically Engineered Transmissible
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,065
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,117
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Roseman, Catherine R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8589
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3165 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Endothia parasitica (Cryptonecristia)
ORGANISM: parasitica
STRAIN: EP713
US-08-459-065-3

Query Match
Best Local Similarity 47.1%; Score 41; DB 2; Length 3165;
38.5%; Pred. No. 4.8e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 DWHYSSYIRP 14
|||:|
Db 2425 WHTHNOYVEKFIY 2437

RESULT 13
US-08-600-430-5
Sequence 5, Application US/08600430
Patent No. 6124436
GENERAL INFORMATION:
APPLICANT: Mcclanahan, Terrill K.
APPLICANT: Gorman, Daniel M.
TITLE OF INVENTION: PURIFIED MAMMALIAN MONOCYTE ANTIGENS AND
TITLE OF INVENTION: RELATED REAGENTS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: DMAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,430
FILING DATE: 13-FEB-1996
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0517
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 160 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-600-430-5

Query Match 46.0%; Score 40; DB 3; Length 160;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DMHYSSYIRPAY 14
: 11 1 1 11
DB 123 EHLNDSYSGFAY 136

RESULT 14
US-08-822-774-45
Sequence 45, Application US/08822774
Patent No. 6183997
GENERAL INFORMATION:
APPLICANT: HOGREFE, Holly
TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: and Methods for Purifying and Identifying Same
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards &
STREET: 1200 G Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-822-774-45

Query Match 46.0%; Score 40; DB 4; Length 246;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 WHYSSY 8
: 11 1 1 11
DB 176 WHYFSY 182

RESULT 15
US-09-632-711-45
Sequence 45, Application US/09632711
Patent No. 6333165
GENERAL INFORMATION:
APPLICANT: HOGREFE, Holly
TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: and Methods for Purifying and Identifying Same
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards &
STREET: 1200 G Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/632,711
FILING DATE: 04-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/822,774
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide

•
; HYPOTHETICAL: YES
; SEQUENCE DESCRIPTION: SEQ ID NO: 45;
US-09-632-711-45

Query Match 46.0%; Score 40; DB 4; Length 246;
Best Local Similarity 71.4%; Pred. NO. 52;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 WHYYSSY 8
 |||: ||
DB 176 WHYFXSY 182

Search completed: February 25, 2003, 10:38:45
Job time : 3.56333 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 46.9933 Seconds
(without alignments) 469.543 Million cell updates/sec

Title: US-09-743-482A-18

Perfect score: 2835
Sequence: 1 MGWSCIILFLVATATGVHSD.....GGTKLEIKRTTSHHHHHHTS 532

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	19.6	113	1 KV2G_MOUSE	P01631 mus musculus
2	510.5	18.0	139	1 HV07_MOUSE	P01751 mus musculus
3	490	17.3	120	1 HV03_MOUSE	P01747 mus musculus
4	486	17.1	140	1 HV02_MOUSE	P01746 mus musculus
5	476	16.8	133	1 KV2E_HUMAN	P06310 homo sapien
6	470	16.6	117	1 HV52_MOUSE	P06327 mus musculus
7	468.5	16.5	137	1 HV11_MOUSE	P01755 mus musculus
8	458	16.2	138	1 HV48_MOUSE	P03980 mus musculus
9	457	16.1	113	1 KV2D_HUMAN	P01617 homo sapien
10	456	16.1	117	1 HV12_MOUSE	P01750 mus musculus
11	456	16.1	117	1 KV2E_HUMAN	P06309 homo sapien
12	454	16.0	117	1 HV06_MOUSE	P01750 mus musculus
13	454	16.0	117	1 HV13_MOUSE	P01757 mus musculus
14	452	15.9	113	1 KV2E_MOUSE	P03976 mus musculus
15	449	15.8	117	1 HV05_MOUSE	P01749 mus musculus
16	448.5	15.8	115	1 KV2A_HUMAN	P01614 homo sapien
17	448	15.8	113	1 KV2B_HUMAN	P01615 homo sapien
18	448	15.8	113	1 HV15_MOUSE	P01759 mus musculus
19	442.5	15.6	118	1 HV51_MOUSE	P06330 mus musculus
20	441	15.6	117	1 HV04_MOUSE	P01748 mus musculus
21	441	15.6	117	1 HV09_MOUSE	P01753 mus musculus
22	440	15.5	121	1 HV01_MOUSE	P01745 mus musculus
23	439.5	15.5	120	1 HV50_MOUSE	P06329 mus musculus
24	437	15.4	113	1 KV2F_MOUSE	P01630 mus musculus
25	436	15.4	117	1 HV49_MOUSE	P06328 mus musculus
26	432	15.2	112	1 KV2D_MOUSE	P01629 mus musculus
27	431	15.2	117	1 HV10_MOUSE	P01754 mus musculus
28	430	15.2	117	1 HV14_MOUSE	P01758 mus musculus
29	424.5	15.0	112	1 KV2C_HUMAN	P01616 homo sapien
30	392.5	13.8	147	1 HV1C_HUMAN	P01744 homo sapien
31	392	13.8	113	1 KV2C_MOUSE	P01628 mus musculus
32	391.5	13.8	134	1 KV4C_HUMAN	P06314 homo sapien
33	389.5	13.7	111	1 KV3H_MOUSE	P01660 mus musculus

34	388.5	13.7	114	1 KV4A_HUMAN	P01625 homo sapien
35	387	13.7	133	1 KV4B_HUMAN	P06313 homo sapien
36	383.5	13.5	108	1 KV1_CANFA	P01618 canis famill
37	383	13.5	131	1 KV3I_MOUSE	P01626 mus musculus
38	380	13.4	112	1 KV2A_MOUSE	P01626 mus musculus
39	378.5	13.4	111	1 KV3J_MOUSE	P01662 mus musculus
40	377	13.3	117	1 HV1B_HUMAN	P01743 homo sapien
41	376.5	13.3	111	1 KV3I_MOUSE	P01664 mus musculus
42	373.5	13.2	108	1 KV5P_MOUSE	P01649 mus musculus
43	373.5	13.2	111	1 KV3D_MOUSE	P01670 mus musculus
44	373	13.2	108	1 KV3D_MOUSE	P01636 mus musculus
45	373	13.2	132	1 KV3F_MOUSE	P01658 mus musculus

ALIGNMENTS

RESULT 1	KV2G_MOUSE	STANDARD:	PRT: 113 AA.
ID	KV2G_MOUSE		
AC	P01631:		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig kappa chain V-II region 26-10.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RM	[1]		
RP	SEQUENCE.		
RC	STRAIN-A/J;		
RX	MEDLINE=83178921; PubMed=6404298;		
RA	Novotny J, Margolies M.N.;		
RT	"Amino acid sequence of the light chain variable region from a mouse		
RT	anti-digoxin hybridoma antibody.";		
RT	Biochemistry 22:1153-1158(1983).		
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA		
CC	PROTEIN THAT BINDS DIGOXIN.		
DR	PIR: A01914; KIMS26.		
DR	HSSP: P80362; IMTL.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR003596; Ig_V.		
DR	Pfam: PF00047; 19; 1.		
DR	SMART: SM00406; IGV; 1.		
KW	Immunoglobulin V region; Monoclonal antibody; Hybridoma.		
FT	DOMAIN 1 23		
FT	DOMAIN 24 39		
FT	DOMAIN 40 54		
FT	DOMAIN 55 61		
FT	DOMAIN 62 93		
FT	DOMAIN 94 102		
FT	DOMAIN 103 112		
FT	DISULFID 23 93		
FT	NON_TER 113 113		
SO	SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;		
Query Match	19.6%; Score 555; DB 1; Length 113;		
Best local similarity	93.8%; Pred. No. 3; 1e-31;		
Matches 106; Conservative	5; Mismatches 2; Indels 0; Gaps 0;		
QY	409 ELYMTQPLSLPPLSLGQASISCRSSQSLVHSNGNTLHYLYLQKPGGPKLLIKVSNRF 468		
DB	1 DVMYTOPPLSLPPLSLGQASISCRSSQSLVHSNGNTLHYLYLQKPGGPKLLIKVSNRF 60		
QY	469 SGVDFRSGSGSGTFTLKISRVEAEDLGVFCSSQTHVPYTFGGGTKLEIKR 521		
DB	61 SGVDFRSGSGSGTFTLKISRVEAEDLGVFCSSQTHVPYTFGGGTKLEIKR 113		
RESULT 2			
HV07_MOUSE			
ID	HV07_MOUSE	STANDARD:	PRT: 139 AA.

```

Db      119 DYYGSSY---FDYWGGCTTLTVSS 139

RESULT 3
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Silevitz M., Gelfer M.L., Brodeur P., Riblet R.,
RA Marshall-Rochstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -I- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC PIR: A02028; HVM5G7.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
SQ SEQUENCE 120 AA; 13307 MW; FFO4EALA167B654AF CRC64;

Query Match 17.3%; Score 490; DB 1; Length 120;
Best Local Similarity 77.0%; Pred. No. 8,3e-27;
Matches 94; Conservative 10; Mismatches 16; Indels 2; Gaps 1

QY 143 VOLOOSGAELVPGSSVKRSKASGYTFTSYDMHMIKQDPNGMLEITGTYINGNGTKYN 202
DB 1 VOLOOSGAELVAGSSVKMSCKASGYTFTSYGINWVKORPGGLEIMIGINPGNYTKYN 60
QY :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 203 OKFNKGATLADKSSSTAYVQLSLTSEDSAVYFCARDMHHYSYTRFPAYVGCGTLTV 262
DB 61 EKFKGKTLLTVDKSSSTAYVQLRLSLTSEDSAVYFCARSYYGGSY--FDYWGGCTTLTV 118
QY 263 SS 264
DB 119 SS 120

RESULT 4
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/T;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabdlits T.H., Estess P., Slaughter C., Tucker P.W.,
RA "Genetic mutation in genes for the variable portion of the
RA kappa chain of immunoglobulin Kappa chains; Sequences from mouse

```



```

RT Immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: J00493; AAA38128.1; -.
DR PIR: A02028; HYMSG7.
DR HSSP: P01810; 2FBU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
KW Immunoglobulin V region; Antisense antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25AACBBE31DA5CE8 CRC64;

Query Match 17.1%; Score 486; DB 1; Length 140;
Best Local Similarity 72.9%; Pred. No. 1.8e-26;
Matches 94; Conservative 12; Mismatches 21; Indels 2; Gaps 1;

QY 136 SGGGGVOYVLOQSGAGELVKGSSVKTSCKASGYFTSYDMHWIKQKQNGLEWIGIYTPG 195
DB 14 TACVHSEVQLQDSGAEVLRAGSSVKMSCKASGYFTSYGINWVKQKQGLEWIGIYTPG 73
QY 196 NGNTKYNGKFKATLTADKSSSTAYWQLSLTSEDAVFCAKADWYYSYIRPFAYWG 255
DB 74 NGYINNEKFKGKTTLTVDKSSSTAYWQLSLTSEDAVFCAKADWYYSYIRPFAYWG 131
QY 256 QGTLVTVSS 264
DB 132 QGTPLTVSS 140

RESULT 5
KVZF_HUMAN
ID KVZF_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPM1 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III."
RL Nucleic Acids Res. 13:6499-6513(1985).
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CC -----
DR EMBL: J00493; AAA38128.1; -.
DR PIR: A02028; HYMSG7.
DR HSSP: P01810; 2FBU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25AACBBE31DA5CE8 CRC64;

Query Match 16.8%; Score 476; DB 1; Length 133;
Best Local Similarity 76.9%; Pred. No. 8.2e-26;
Matches 90; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 405 GGGSELYMTQTPSLPVSGLDQASISCRSSQSLVHSGNTLYLHWYLOKPGSPKLLIYKV 464
DB 17 GSSGDVYMTQSPSLPVTLCGPASISCRSSQSLVSDGNTLYLNMFOQRPQSPRLIYKV 76
QY 465 SNRPSGVDPDRSSGSGDFTLKISRVEADLGYVFCOSRHVYPTGCGTKLEIKR 521
DB 77 SNRPSGVDPDRSSGSGDFTLKISRVEADLGYVFCOSRHVYPTGCGTKLEIKR 133

RESULT 6
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH58 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85099340; PubMed=2578321;
RA Vancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT rearranged VH gene segments."
RL Cell 40:271-281(1985).
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CC -----
DR EMBL: M13787; AAA38499.1; -.
DR PIR: A02029; HYMSA1.
DR HSSP: P01810; 2FBU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH58 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.

```

[illegible]

Oy	1	MGMSCIIIELVATATGAGSDIQMGSPPASLSAPEIYITTCQASODIGNMLAWOQRPG	60
Dd	1	:	18
Oy	61	KSPOLLIVATSADGIPSRFSRSGSRTGYSLKISRLQVEDTGIYYCLORYSNPNTFGAG	120
Dd	19	-----	18
Oy	121	TKLELKGCGGGSGGGGGGSOVLOQSGAEIYMPGSSVKISCRASGTTFYSIDMHNIKQ	180
Dd	19	-----SOVOLQDGAEPKPGASVKKLSCKASGYTFYSILMHWNQ	58
Oy	131	QPNGLENWIMGWIPNGNMTKNYNOKENGKATLTADSSSTAAWOLSSLTSSEDSAVYFCARD	240
Dd	59	RPGRELEWIGRIDPNSGGTTYNENHRSKATLTIFDKPSSTAIAWOLSSLTSSEDSAVYFCAR-	117
Oy	241	WHYSSYIRPFAYWGQTLYTVSS 264	
Dd	118	--YRLG--RYFDYWQGTLTYVSS 137	
RESULT 8			
ID	HV48_MOUSE	STANDARD:	PRT: 138 AA.
AC	P03980:		
DT	23-OCT-1986 (Rel. 02, Created)		
DT	23-OCT-1986 (Rel. 03, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig heavy chain V region TEPC 1017 precursor.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCB1_Taxid=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84248078; Pubmed=6429663;		
RA	Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,		
RA	Tucker P.W.;		
RT	"Illegitimate recombination generates a class switch from C mu. to C		
RL	Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984)."		
DR	PIR: A02033; HVMST7.		
DR	HSSP: P01810; ZEBU.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR003596; Ig-V.		
DR	Pfam: PF00047; Ig: 1.		
KW	SMART: SM00406; IGV: 1.		
FT	Immunoglobulin V region: Signal.		
FT	SIGNAL	1	20
FT	CHAIN	21	138
FT	DOMAIN	21	54
FT	DOMAIN	50	49
FT	DOMAIN	55	68
FT	DOMAIN	69	85
FT	DOMAIN	86	117
FT	DOMAIN	118	127
FT	DOMAIN	128	138
FT	DISULFID	41	115
FT	NON_TER	138	138
SEQ	SEQUENCE	138 AA: 15576 MW; 748157E4C6907B8E CRC64;	
Query Match 16.2%; Score 458; DB 1; Length 138;			
Best Local Similarity 38.6%; Pred. No. 1.4e-24;			
Matches 102; Conservative 14; Mismatches 22; Indels 126; Gaps			
Oy	1	MGMSCIIPLVATGCVHSDIQMTGPSALSPERIVITTOASQDIGNMLAWOQRRG	60
Dd	1		18
Oy	61	KSPOLLIVATSADGIPSRFSRSGRTGYSLKISRLQVEDTGIYYCLORYSNPNTFGAG	120
Dd	19	-----	18

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OY 121 TKLEKGGGGGGGGGGGGGGGQVQLQSGAEIVKPGSSVAKISCKASGTFSTYDMHWIKQ 180
DB 19 -----SQQVQLQPGAEIVKPGASVQLSCKASGHTTNTNWIHWIKQ 58
OY 181 QPGNGLEWIGWYPGNGNTKYNQKENGKATLVADKSSSTAYWQLSLTSEDSAVYFCARD 240
DB 59 PFGGLEWIGEIVNPDRGRSNYEKFKKATLVADKSSSTAYWQLSLTSEDSAVYFCARD 118
OY 241 WHYSSYIRFAYWGQGLTVTVSS 264
DB 119 DGYIDW----FVYWGQGLTVTVSSA 138

RESULT 9
KV2D_HUMAN
ID KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
RX SEQUENCE (BENCE-JONES PROTEIN TEM).
RA PUTNAM F.W., WHITLEY E.J. JR., PAUL C., DAVIDSON J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
RT primary amyloidosis."
RL Biochemistry 12:3763-3780(1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEM).
RA MEDLINE=7316638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F.,
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
RT patient with plasma cell dyscrasia and amyloidosis."
RL J. Clin. Invest. 52:1276-1281(1973).
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC PIR: A01888; K2HUTW.
DR HSSP: P01607; 1REL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 16.1%; Score 457; DB 1; Length 113;
Best Local Similarity 76.1%; Pred. No. 1.3e-24;
Matches 86; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

OY 409 ELVMTQPLSLPYSLDQASISCRSSQSLVHSGNTYLVHWLKPQGSPLLYKYNRF 468
DB 1 DIVMTQPLSLPYTPDEPAPISICRSSQSLVHSGFDILNWLKPQGSPLLYALSNRA 60

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OY 469 SGVDFRFGSGSGTDFTLKISRVEADLGIVFCSSQTHVPYTFGGRKLEIKR 521
DB 61 SGVDFRFGSGSGTDFTLKISRVEADGVGYCCZALQAPITTFGGRLEIKR 113

RESULT 10
HVI2_MOUSE
ID HVI2_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RX SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RA MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains."
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC PIR: A02039; MHMS4E.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACEB47E47E1 CRC64;

Query Match 16.1%; Score 456; DB 1; Length 117;
Best Local Similarity 72.4%; Pred. No. 1.6e-24;
Matches 89; Conservative 8; Mismatches 20; Indels 6; Gaps 1;

OY 142 QVQLQSGAEIVKPGSSVAKISCKASGTFSTYDMHWIKQPGNGLEWIGWYPGNGNTKY 201
DB 1 QVQLQSGPELVKPGASVAKMSCKASGYTFDYKMKWKQSHGKSLIEWIGDIPNNGGTSY 60
OY 202 NQKFKGATLVADKSSSTAYWQLSLTSEDSAVYFCARDMHIYSSYIRFAYWGQGLTVT 261
DB 61 NQKFKGATLVADKSSSTAYWQLSLTSEDSAVYFCARDIWMY-----FDYWGAGTIVT 114
OY 262 VSS 264
DB 115 VSS 117

RESULT 11
KV2E_HUMAN
ID KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Gm607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
RX SEQUENCE FROM N.A.
RA MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;

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"Contribution of human V kappa II germ-line genes to light-chain diversity".
 Nature 309:73-76(1984).
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 CC
 CC EMBL: 200009; NOT_ANNOTATED_CDS.
 DR PIR: A01889; K2HUGM.
 DR HSSP: P80362; 1WTL.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_V.
 DR SMART: SM00406; IGV_1.
 KM Immunoglobulin V region; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 4
 FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
 FT DOMAIN 5 27 FRAMEWORK-1.
 FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 44 58 FRAMEWORK-2.
 FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 66 97 FRAMEWORK-3.
 FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 107 116 FRAMEWORK-4.
 FT DISULFID 27 97 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;
 Query Match 16.1%; Score 456; DB 1; Length 117;
 Best Local Similarity 75.2%; Pred. No. 1,6e-24;
 Matches 88; Conservative 10; Mismatches 19; Indels 0; Gaps 0;
 OY 405 GGSEELVMTQPLSLPYSLDQASISCRSSQSLHNSGNTLYLHWYLOKPGSPKLYIKV 464
 ID HV06_MOUSE STANDARD; PRT; 117 AA.
 AC P01750;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 102 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBITaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reich M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
 RT "Heavy chain variable region contribution to the NpB family of antibodies: somatic mutation evident in a gamma 2a variable region";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THIS GERM-LINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 DR PIR: A02032; HWS02.
 DR HSSP: P01810; 2FBU.
 DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_V.
 DR SMART: SM00406; IGV_1.
 KM Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 FRAMEWORK-3.
 FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-2.
 FT DISULFID 41 115 FRAMEWORK-4.
 FT NON_TER 117 117 BY SIMILARITY.
 SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCABC CRC64;
 Query Match 16.0%; Score 454; DB 1; Length 117;
 Best Local Similarity 41.2%; Pred. No. 2.2e-24;
 Matches 98; Conservative 8; Mismatches 10; Indels 122; Gaps 1;
 OY 1 MGWSCIILFLVATATGATGVSIDQMTQSPASLSASPEEIVITTCQASQDIGNWLAWYQKPG 60
 ID HV13_MOUSE STANDARD; PRT; 117 AA.
 AC P01757;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region J558.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBITaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80078170; PubMed=6765983;
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements in heavy chain V-region gene segments";
 RL Nature 283:35-40(1980).
 CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN THE D AND J SEGMENTS.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 DR PIR: A26242; MHMSJ5.
 DR HSSP: P01789; IMCP.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_V.
 DR SMART: SM00406; IGV_1.
 KM Immunoglobulin V region.
 FT DISULFID 22 96
 FT NON_TER 117 117 BY SIMILARITY.
 SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
 Query Match 16.0%; Score 454; DB 1; Length 117;
 Best Local Similarity 72.4%; Pred. No. 2.2e-24;
 Matches 89; Conservative 8; Mismatches 20; Indels 6; Gaps 1;

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QY 142 QVLOQSGAELVKPGSSVYKISKASGYTTSYDMHMKQOPNGLEWIGWYPGNGNTKY 201
DE :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
DB 1 EVOLQOSGPGLVKGASVYKMSCKASGYTFTDYKMKVQSHCKSLSEWIGDIPNNGGISTY 60
QY 202 NQKNGKATLTADKSSSTAYVQLSLSEDSAVVFCARDMHHYSSIRPFAYMGGTLVT 261
DB 61 NQKNGKATLTADKSSSTAYVQLSLSEDSAVVFCARDMHHYSSIRPFAYMGGTLVT 261
QY 262 VSS 264
DB 115 VSS 117

RESULT 14
KV2E_MOUSE
ID KV2E_MOUSE STANDARD: PRT: 113 AA.
AC P03976;

DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Hybridoma;
RX MEDLINE=85128968; PubMed=6441768;
RA "Abertsold R., Herbet H., Grutter T., Chang J.Y., Braun D.G.,
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide.";
RL Hoppe-Seiler's Z. Physiol. Chem. 365:1375-1383(1984)
CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
CC PIR: A01912; KMS17.
DR HSSP: P01607; IRE1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KM Immunoglobulin V region: Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 40 54 FRAMEWORK-2.
FT DOMAIN 4 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 62 93 FRAMEWORK-3.
FT DOMAIN 6 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 15.9%; Score 452; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 2.9e-24;
Matches 84; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

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DB 1 DIVMTQAVFNPVTLTGTSASISCRSSKSLHSNCTITLYLWYLPKPGSPOLLILQMSNLA 60
QY 469 SGVPDRFSGSGGTDTPLKISRVAEDLVGYFCSQSTHVPYFGGKLEIKR 521
DB 61 SGVPDRFSGSGGTDTPLKISRVAEDLVGYFCSQSTHVPYFGGKLEIKR 521

RESULT 15
HV05_MOUSE
ID HV05_MOUSE STANDARD: PRT: 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

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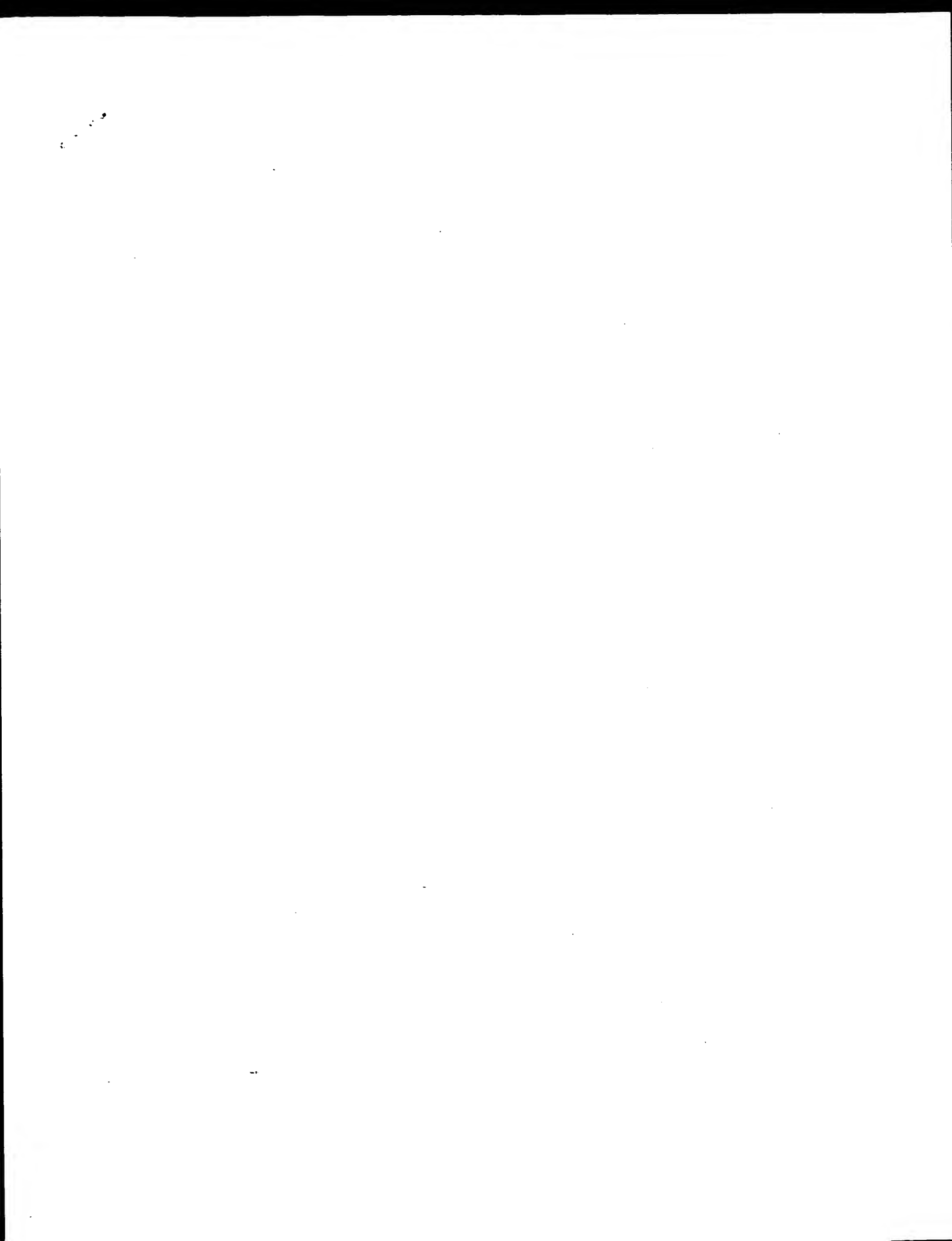
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 3 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC
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CC or send an email to license@sib.ch)
CC
CC EMBL: J00536; AAA38605.1; -.
DR PIR: A02031; HVMS3.
DR HSSP: P01810; ZEBU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KM Immunoglobulin V region: Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 30 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 55 FRAMEWORK-2.
FT DOMAIN 55 68 FRAMEWORK-3.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

Query Match 15.8%; Score 449; DB 1; Length 117;
Best Local Similarity 41.4%; Pred. No. 4.7e-24;
Matches 99; Conservative 6; Mismatches 12; Indels 122; Gaps 1;

QY 1 MGWSCIILFVATATGVSQDIQMTQSPASLSASPEIVTITCOASQDIGNMLAWYQKRG 60
DB 1 MGWSCIILFVATATGVSQDIQMTQSPASLSASPEIVTITCOASQDIGNMLAWYQKRG 60
QY 61 KSPOLLIVSATSLADGIPSRFSRSGSTQVSLKISRLQVEDTGIYCLQRYSNPTFGAG 120
DB 19 -----
QY 121 TKLELKGSGSGSGSGSGSGSGSOVLOQSGAELVKGSSVYKISKASGYTFTSYDMHMKQ 180
DB 19 -----SOVLOQSGAELVKGSSVYKISKASGYTFTSYDMHMKQ 58
QY 181 QPNGLEWIGWYPGNGNTKYNKFNGKATLTADKSSSTAYVQLSLSEDSAVVFCAR 239
DB 59 RFGGLEMIGWYPGNGNTKYNKFNGKATLTADKSSSTAYVQLSLSEDSAVVFCAR 117

Search completed: February 25, 2003, 10:37:34
Job time: 48.9933 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 67.3667 Seconds
(without alignments)
758.956 Million cell updates/sec

Title: US-09-743-482A-18

Perfect score: 2835
Sequence: 1 MGVSCILFLVATGCVHSD.....GGTKLEIKRTSHHHHHHS 532

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	824.5	29.1	249	2	SA1374
2	759	26.8	268	2	A56446
3	691	24.4	233	2	UC5322
4	669.5	23.6	287	4	PC4402
5	583	20.6	118	2	PT0359
6	579	20.4	112	2	E27887
7	578	20.4	131	2	B34904
8	574	20.2	131	2	C34904
9	573	20.2	112	2	S32189
10	571	20.1	131	2	B32513
11	571	20.1	131	2	B30577
12	570	20.1	112	2	D27887
13	570	20.1	112	2	S53750
14	569	20.1	115	2	SG6066
15	568	20.0	111	2	PL0257
16	568	20.0	112	2	A27887
17	568	20.0	113	2	B41940
18	567	20.0	115	2	S38715
19	565	19.9	112	2	B27887
20	563	19.9	112	2	B31485
21	562	19.8	112	2	C27887
22	562	19.8	131	2	D29380
23	562	19.8	131	2	D34904
24	562	19.8	131	2	G34903
25	559	19.7	132	2	PH0106
26	555	19.6	113	1	KVMS26
27	555	19.6	113	2	PL0205
28	555	19.6	219	2	SL6112
29	554	19.5	131	2	PT0178

30	552	19.5	112	2	A49715	Ig kappa chain V r
31	549	19.4	219	2	S38665	Ig kappa chain - m
32	547	19.3	131	2	B39276	Ig light chain pre
33	546	19.3	131	2	S52449	Ig kappa chain V r
34	545	19.2	112	2	A31807	Ig kappa chain V r
35	545	19.2	217	2	S42772	Ig kappa chain - m
36	544.5	19.2	130	2	C29380	Ig kappa chain pre
37	544	19.2	113	2	PL0203	anti-DNA autoantib
38	542	19.1	107	2	D32530	Ig kappa chain V r
39	542	19.1	219	2	PC4203	Ig kappa chain (mo
40	540	19.0	110	2	S26335	Ig kappa chain V r
41	538	19.0	219	2	S52028	Ig kappa chain - m
42	535	18.9	112	2	F27887	Ig kappa chain V r
43	532	18.8	138	2	S21810	Ig heavy chain V r
44	531	18.7	112	2	S38719	Ig light chain V r
45	531	18.7	114	2	A32967	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

SA1374

Single chain Fv antibody - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C:Accession: SA1374

R:Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

Submitted to the EMBL Data Library, January 1994

A:Description: Construction and functional characterization of a single chain Fv anti

A:Reference number: SA1374

A:Accession: SA1374

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-249 <Art>

A:Cross-references: EMBL:Z29480

Query Match

Best Local Similarity 29.1%; Score 824.5; DB 2; Length 249;

Matches 161; Conservative 39; Mismatches 47; Indels 5; Gaps 2;

QY	270	EVQLLESGAELARPGASVKLSCKASGTFETNGCLSMWKORPOVLEIGEVYPRGINAY	329
DB	1	QVQ-LQOQSAELVRRPGASVKLSCTASGFENFKDDYIMWVKORPEKLEWARIAPASGNVK	59
QY	330	YNEKFKAKATLPADKSSSTASMEIRSLTSEDSAVYFCARGSYDTNVDYFDWGGQTTV	369
DB	60	YVPRFDKATITPADTSSNTAYLLLSLTSEDITAVYYCARDDTLTSLGY----WGQGSTV	115
QY	390	TVSSGGGSGGGGGGSELVMTQPLSLPVSLGDAQSTICRSQSGLVHNSGNTYLHWY	449
DB	116	TVSSRGSGGGGGGGSGDIELTQSPVYVPGESVSTICRSKSLYSDSDSYLFWF	175
QY	450	LQPPGSPKILITKYKVNRFSGVDPFRFGSGGSDFTLTISRVAEDLDGVYFCOSQTHPY	509
DB	176	LQPPGSPKILITKYKVNRFSGVDPFRFGSGGSDFTLTISRVAEDLDGVYFCOSQTHPY	225
QY	510	TFGGGTLEIKR	521
DB	236	TFGGGTLEIKR	247

RESULT 2

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C:Accession: A56446

R:Yang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity diroxin-binding protein displayed on M13 is functionally ide

A:Reference number: A56446; PMID:7713873

A:Accession: A56446

C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: E27887
R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: E27887
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Experimental source: strain Balb/c
A:Note: this sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 20.4%; Score 579; DB 2; Length 112;
Best Local Similarity 98.2%; Pred. No. 6.7e-27;
Matches 110; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 409 ELVMTQTPLSPVSLGDOASISCRSSQSLVHNGNTYLHWYLOKPGSPKLLIKVSNR 468
Db 1 DVVMTQTPLSPVSLGDOASISCRSSQSLVHNGNTYLHWYLOKPGSPKLLIKVSNR 60

Oy 469 FSGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSSTHVPYTFGGGTKLEIK 520
Db 61 FSGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSSTHVPYTFGGGTKLEIK 112

RESULT 7
B34904
Ig kappa chain precursor V region (12-40 and 5-14) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C:Accession: B34904; H34903
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-rea
A:Reference number: A34903; MUID:90094387; PMID:2104617
A:Accession: B34904
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BED>
A:Cross-references: GB:M32384; GB:J05237; GB:J05238; NID:9639656; PIDN:AAAG1589.1; PID:9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 20.4%; Score 578; DB 2; Length 131;
Best Local Similarity 97.3%; Pred. No. 9.1e-27;
Matches 110; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 408 SELVMTQTPLSPVSLGDOASISCRSSQSLVHNGNTYLHWYLOKPGSPKLLIKVSNR 467
Db 19 SDVMTQTPLSPVSLGDOASISCRSSQSLVHNGNTYLHWYLOKPGSPKLLIKVSNR 78

Oy 468 FSGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSSTHVPYTFGGGTKLEIK 520
Db 79 FSGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSSTHVPYTFGGGTKLEIK 131

RESULT 8
C34904
Ig kappa chain precursor V region (3-24) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
C:Accession: C34904; I31485
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-rea
A:Reference number: A34903; MUID:90094387; PMID:2104617
A:Accession: C34904

A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BED>
R:Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J. Biol. Chem. 264, 1565-1569, 1989
A:Title: Comparison of variable region primary structures within an anti-fluorescein
A:Reference number: A31485; MUID:89109167; PMID:2492278
A:Accession: I31485
A:Status: preliminary
A:Molecule type: protein
A:Residues: 20-52 <BE2>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 20.2%; Score 574; DB 2; Length 131;
Best Local Similarity 96.5%; Pred. No. 1.5e-26;
Matches 109; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 408 SELVMTQTPLSPVSLGDOASISCRSSQSLVHNGNTYLHWYLOKPGSPKLLIKVSNR 467
Db 19 SDVMTQTPLSPVSLGDOASISCRSSQSLVHNGNTYLHWYLOKPGSPKLLIKVSNR 78

Oy 468 FSGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSSTHVPYTFGGGTKLEIK 520
Db 79 FSGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSSTHVPYTFGGGTKLEIK 131

RESULT 9
S32189
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S32189
R:Itzli, S.
submitted to the EMBL Data Library, February 1993
A:Reference number: S32185
A:Accession: S32189
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <IZU>
A:Cross-references: EMBL:X70094; NID:q288255; PIDN:CAA49699.1; PID:q288256
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 20.2%; Score 573; DB 2; Length 112;
Best Local Similarity 97.3%; Pred. No. 1.5e-26;
Matches 109; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 409 ELVMTQTPLSPVSLGDOASISCRSSQSLVHNGNTYLHWYLOKPGSPKLLIKVSNR 468
Db 1 DVVMTQTPLSPVSLGDOASISCRSSQSLVHNGNTYLHWYLOKPGSPKLLIKVSNR 60

Oy 469 FSGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSSTHVPYTFGGGTKLEIK 520
Db 61 FSGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSSTHVPYTFGGGTKLEIK 112

RESULT 10
B32513
Ig kappa chain precursor V region (MRL4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: B32513
R:Kotler, R.; Ströhal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization a
A:Reference number: A94689; MUID:88331394; PMID:3138286
A:Accession: B32513
A:Molecule type: DNA
A:Residues: 1-131 <KOR>
A:Cross-references: GB:M20828; NID:g196937; PIDN:AAA38843.1; PID:g196938

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 20.1% Score 571; DB 2; Length 131;
Best Local Similarity 96.5%; Pred. No. 2.3e-26;
Matches 109; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 408 SELVMTQPTPLSPVSLGDAQSISCRSSQSLVHNSGNTYLMHWLQKPGQSPKLLIKVSNR 467
D 19 SDVMTQPTPLSPVSLGDAQSISCRSSQSLVHNSGNTYLMHWLQKPGQSPKLLIKVSNR 78

OY 468 FSGVPRFSGSGSGDTFTLKISRVEAEDLGVFCFSQSTHVPYFGGCTLEIK 520
D 79 FSGVPRFSGSGSGDTFTLKISRVEAEDLGVFCFSQSTHVPYFGGCTLEIK 131

RESULT 11

Ig kappa chain precursor V region (MRL10) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 21-Jan-2000

C:Accession: B30577

R:Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theod

J.; Exp. Med. 161, 803-815, 1985

A:Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely relat

A:Reference number: A30577; MUID:85159423; PMID:3920343

A:Accession: B30577

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-131 <KOE>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 20.1% Score 571; DB 2; Length 131;
Best Local Similarity 96.5%; Pred. No. 2.3e-26;
Matches 109; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 408 SELVMTQPTPLSPVSLGDAQSISCRSSQSLVHNSGNTYLMHWLQKPGQSPKLLIKVSNR 467
D 19 SDVMTQPTPLSPVSLGDAQSISCRSSQSLVHNSGNTYLMHWLQKPGQSPKLLIKVSNR 78

OY 468 FSGVPRFSGSGSGDTFTLKISRVEAEDLGVFCFSQSTHVPYFGGCTLEIK 520
D 79 FSGVPRFSGSGSGDTFTLKISRVEAEDLGVFCFSQSTHVPYFGGCTLEIK 131

RESULT 12

D27887

Ig kappa chain V region (H36-2) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000

C:Accession: D27887

R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to a d

A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: D27887

A:Molecule type: DNA

A:Residues: 1-112 <CAT>

A:Experimental source: strain Balb/c

A:Note: This sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 20.1% Score 570; DB 2; Length 112;
Best Local Similarity 96.4%; Pred. No. 2.2e-26;
Matches 108; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 409 ELVMTQPTPLSPVSLGDAQSISCRSSQSLVHNSGNTYLMHWLQKPGQSPKLLIKVSNR 468

Db 1 DVVMTQPTPLSPVSLGDAQSISCRSSQSLVHNSGNTYLMHWLQKPGQSPKLLIKVSNR 60

OY 469 SGVPRFSGSGSGDTFTLKISRVEAEDLGVFCFSQSTHVPYFGGCTLEIK 520
D 61 SGVPRFSGSGSGDTFTLKISRVEAEDLGVFCFSQSTHVPYFGGCTLEIK 112

RESULT 13

antibody Fab Jcl 103 light chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000

C:Accession: S53750

R:Pokkuri, P.R.; Bouthillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M.

J. Mol. Biol. 243, 283-297, 1994

A:Title: Preparation, characterization and crystallization of an antibody Fab fragmen

A:Reference number: S53750; MUID:95018269; PMID:7523684

A:Accession: S53750

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 <POK>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 20.1% Score 570; DB 2; Length 112;
Best Local Similarity 97.3%; Pred. No. 2.2e-26;
Matches 109; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 409 ELVMTQPTPLSPVSLGDAQSISCRSSQSLVHNSGNTYLMHWLQKPGQSPKLLIKVSNR 468
D 1 DVVMTQPTPLSPVSLGDAQSISCRSSQSLVHNSGNTYLMHWLQKPGQSPKLLIKVSNR 60

OY 469 SGVPRFSGSGSGDTFTLKISRVEAEDLGVFCFSQSTHVPYFGGCTLEIK 520
D 61 SGVPRFSGSGSGDTFTLKISRVEAEDLGVFCFSQSTHVPYFGGCTLEIK 112

RESULT 14

S60066

Ig kappa chain V region (monoclonal antibody C3) (validated) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 23-Feb-1996 #sequence_revision 10-Oct-1997 #text_change 23-Mar-2001

C:Accession: S60066

R:Wien, M.W.; Filman, D.J.; Stura, E.A.; Guillot, S.; Delpeyroux, F.; Craignic, R.; Ho

Nat. Struct. Biol. 2, 232-243, 1995

A:Title: Structure of the complex between the Fab fragment of a neutralizing antibody

A:Reference number: S60066; MUID:95292109; PMID:7538711

A:Accession: S60066

A:Molecule type: mRNA

A:Residues: 1-115 <WIE>

A:Cross-references: EMBL:X84697; NID:q773226

R:Wien, M.W.; Hogle, J.M.

submitted to the Brookhaven Protein Data Bank, January 1995

A:Reference number: A52979; PDB:1EPT

A:Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 1-23, 'S', 25-11

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-95/Domain: immunoglobulin homology <IMM>

F:23-93/Disulfide bonds: #status experimental

Query Match 20.1% Score 569; DB 2; Length 115;
Best Local Similarity 96.5%; Pred. No. 2.6e-26;
Matches 109; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 409 ELVMTQPTPLSPVSLGDAQSISCRSSQSLVHNSGNTYLMHWLQKPGQSPKLLIKVSNR 468
D 1 DVVMTQPTPLSPVSLGDAQSISCRSSQSLVHNSGNTYLMHWLQKPGQSPKLLIKVSNR 60

OY 469 SGVPRFSGSGSGDTFTLKISRVEAEDLGVFCFSQSTHVPYFGGCTLEIK 521
D 61 SGVPRFSGSGSGDTFTLKISRVEAEDLGVFCFSQSTHVPYFGGCTLEIK 113

RESULT 15

PL0257

Ig kappa chain V region (anti-DNA, Dp1VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000

C:Accession: PL0257

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MIMD:90111618; PMID:2104919

A:Accession: PL0257

A:Molecule type: mRNA

A:Residues: 1-111 <SHL>

C:Superfamily: immunoglobulin V region: immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: Framework 1

F:16-95/Domain: immunoglobulin homology <IMM>

F:24-39/Region: complementarity-determining 1

F:40-54/Region: Framework 2

F:55-61/Region: complementarity-determining 2

F:62-83/Region: Framework 3

F:94-102/Region: complementarity-determining 3

F:103-111/Region: Framework 4

Query Match 20.0%; Score 568; DB 2; Length 111;

Best Local Similarity 97.3%; Pred. No. 2.9e-26;

Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 409 ELYVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLMHWYLOKPGOSPKLLIKVSNRF 468

Db 1 DVMVTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLMHWYLOKPGOSPKLLIKVSNRF 60

QY 469 SGVPDRFSGSGSGDFLTLSRVAEDLGVYFCSSGTHVPYTFGGGTKLEI 519

Db 61 SGVPDRFSGSGSGDFLTLSRVAEDLGVYFCSSGTHVPYTFGGGTKLEI 111

Search completed: February 25, 2003, 10:33:56
Job time : 68.3867 secs

20

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 134.773 Seconds
(without alignments)
813.344 Million cell updates/sec

Title: US-09-743-482a-18

Perfect score: 2835
Sequence: 1 KMWSCILFLVATGCVHSD.....GGTKLEIKRTTSHHHHHHS 532

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp._archaea:*
- 2: sp._bacteria:*
- 3: sp._fungi:*
- 4: sp._human:*
- 5: sp._invertebrate:*
- 6: sp._mammal:*
- 7: sp._mhc:*
- 8: sp._organelle:*
- 9: sp._phage:*
- 10: sp._plant:*
- 11: sp._rodent:*
- 12: sp._virus:*
- 13: sp._vertebrate:*
- 14: sp._unclassified:*
- 15: sp._virus:*
- 16: sp._bacteriap:*
- 17: sp._archeap:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	679	24.0	298	11	09QYFO mus musculu
2	678.5	23.9	241	11	0921A6 mus musculu
3	617	21.8	218	11	0925S1 mus musculu
4	578	20.4	238	11	08VC16 mus musculu
5	555	19.6	238	11	099M37 mus musculu
6	539	19.0	104	11	09JL82 mus musculu
7	512.5	18.1	473	11	09DB14 mus musculu
8	511	18.0	239	11	08VC55 mus musculu
9	502	17.7	463	11	0991C4 mus musculu
10	499	17.6	473	11	0991C5 mus musculu
11	499	17.6	481	11	091WT1 mus musculu
12	494	17.4	278	11	0921K1 mus musculu
13	487.5	17.2	145	11	0924Q7 mus musculu
14	487	17.2	146	11	0924R8 mus musculu
15	486	17.1	239	4	08TCD0 homo sapien
16	485	17.1	170	11	0925S2 mus musculu

17	480	16.9	146	11	0924Q3	0924Q3 mus musculu
18	478.5	16.9	145	11	0924Q6	0924Q6 mus musculu
19	477	16.8	146	11	0924Q8	0924Q8 mus musculu
20	476	16.8	613	11	08VCX7	08VCX7 mus musculu
21	473	16.7	489	11	08VCX4	08VCX4 mus musculu
22	472.5	16.7	145	11	0924R1	0924R1 mus musculu
23	471.5	16.6	145	11	0924R4	0924R4 mus musculu
24	469.5	16.6	141	11	0924Q4	0924Q4 mus musculu
25	468.5	16.5	145	11	0924Q9	0924Q9 mus musculu
26	468	16.5	140	11	0924P8	0924P8 mus musculu
27	467.5	16.5	143	11	0924Q0	0924Q0 mus musculu
28	467	16.5	117	11	09QYFO	09QYFO mus musculu
29	467	16.5	142	11	0924Q1	0924Q1 mus musculu
30	466	16.4	147	11	0925S3	0925S3 mus musculu
31	465.5	16.4	137	11	0924R6	0924R6 mus musculu
32	465.5	16.4	143	11	0924R0	0924R0 mus musculu
33	465	16.4	140	11	0924R2	0924R2 mus musculu
34	465	16.4	481	11	08VCV5	08VCV5 mus musculu
35	464.5	16.4	143	11	0924Q5	0924Q5 mus musculu
36	464.5	16.4	145	11	0924P7	0924P7 mus musculu
37	463.5	16.3	139	11	0924R5	0924R5 mus musculu
38	463.5	16.3	145	11	0924R3	0924R3 mus musculu
39	461	16.3	123	11	08VJL1	08VJL1 mus musculu
40	460.5	16.2	109	11	09JL75	09JL75 mus musculu
41	460	16.2	144	11	0924P5	0924P5 mus musculu
42	459.5	16.2	143	11	0924R7	0924R7 mus musculu
43	459.5	16.2	143	11	0924P9	0924P9 mus musculu
44	458	16.2	117	11	09QX69	09QX69 mus musculu
45	454.5	16.0	118	11	0921C4	0921C4 mus musculu

ALIGNMENTS

RESULT 1

Q9YFO PRELIMINARY; PRT. 298 AA.

AC Q9YFO; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE CN 8 scfv.

GN CN 8.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BAJB/C; TISSUE=SPLEEN;

RX MEDLINE=20183931; PubMed=10706631;

RA Shiohara N., Demura T., Fukuda H.;

RT "Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction method."

RT Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).

RL EMBL; AB036341; BAA8633.1; .

DR HSSP; P01607; IREI.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig_2.

DR SMART; SM00406; Ig_2.

SO SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match

Best Local Similarity 51.0%; Pred. No. 1.6e-38;

Matches 128; Conservative 41; Mismatches 72; Indels 10; Gaps 2;

QY 274 LEOGGAELARPGASVYKLSKASGYFTNYGLSVKORPQOVLEWIGEVPRIGNAYNEX 333

Db 43 LQSGGGLVKGPGSLKLSAASGSDPSRYWMSVROAPGKLEWIGELINDSSTINYPDS 102

QY 334 FKGAITLADKSSSTASMELRSLTSDSAVYFCARRGSTDTNDWTFDWGQGTIVTYS 393

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DR InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC
DR

DR InterPro: IPR003597; Ig_cl.
 DR InterPro: IPR003006; Ig_MHC

DR InTerPro: IPR003596; Ig-V.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IGcl; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 20.4%; Score 578; DB 11; Length 238;
 Best Local Similarity 97.4%; Pred. No. 8,7e-32;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 408 SELVMTQTPSLPVSIGDQASISCRSSQSLVHSGNTYLHWYLOKPGQSPKLLIKVSNR 467
 DB 19 SDVMTQTPSLPVSIGDQASISCRSSQSLVHSGNTYLHWYLOKPGQSPKLLIKVSNR 78
 QY 468 FSGVPRFSGSGGTDFTLKISRVEADLGIVFCGSGSTHVPYTFGGTKLEIKR 521
 DB 79 FSGVPRFSGSGGTDFTLKISRVEADLGIVFCGSGSTHVPYTFGGTKLEIKR 132

RESULT 5
 Q99M37 PRELIMINARY; PRT; 238 AA.

AC Q99M37;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hypothetical 26.3 kDa protein.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC002035; AA02035.1;
 DR HSSP: P01679; 2FBJ.
 DR InterPro: IPR003599; 19.
 DR InterPro: IPR003597; 19-cl.
 DR InterPro: IPR003600; 19-like.
 DR InterPro: IPR003006; 19_MHC.
 DR InterPro: IPR003596; 19-V.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IGcl; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 19.6%; Score 555; DB 11; Length 238;
 Best Local Similarity 92.1%; Pred. No. 3.2e-30;
 Matches 105; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 408 SELVMTQTPSLPVSIGDQASISCRSSQSLVHSGNTYLHWYLOKPGQSPKLLIKVSNR 467
 DB 19 SDVMTQTPSLPVSIGDQASISCRSSQSLVHSGNTYLHWYLOKPGQSPKLLIKVSNR 78
 QY 468 FSGVPRFSGSGGTDFTLKISRVEADLGIVFCGSGSTHVPYTFGGTKLEIKR 521
 DB 79 FSGVPRFSGSGGTDFTLKISRVEADLGIVFCGSGSTHVPYTFGGTKLEIKR 132

RESULT 6
 Q99L82 PRELIMINARY; PRT; 104 AA.
 ID Q99L82;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Anti-myosin immunoglobulin light chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C;
 RX MEDLINE=20448942; PubMed=10992488;
 RA Makiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin";
 RL Infect. Immun. 68:5803-5808(2000).
 DR EMBL: AF206024; AAF69322.1;
 DR HSSP: P01607; 1REI.
 DR InterPro: IPR003006; 19_MHC.
 DR InterPro: IPR003596; 19-V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 104
 SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBD5F0A1AE CRC64;

Query Match 19.0%; Score 539; DB 11; Length 104;
 Best Local Similarity 98.1%; Pred. No. 1.4e-29;
 Matches 102; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 417 LSLPVSIGDQASISCRSSQSLVHSGNTYLHWYLOKPGQSPKLLIKVSNRFGVDDRS 476
 DB 1 LSLPVSIGDQASISCRSSQSLVHSGNTYLHWYLOKPGQSPKLLIKVSNRFGVDDRS 60
 QY 477 GSGSGTDFTLKISRVEADLGIVFCGSGSTHVPYTFGGTKLEIKR 520
 DB 61 GSGSGTDFTLKISRVEADLGIVFCGSGSTHVPYTFGGTKLEIKR 104

RESULT 7

Q9DBL4 PRELIMINARY; PRT; 473 AA.

AC Q9DBL4;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 181006009Rik protein.
 DE IGH-1 OR 181006009Rik.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-C57BL/6J; TISSUE-PANCREAS;
 RX MEDLINE=21085650; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaide M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guslincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK007918; BAB25349.1; -
 DR HSSP: P01842; 7FAB.
 DR MGD: MGI:96443; 1gh-1.
 DR InterPro: IPR003599; 1g.
 DR InterPro: IPR003597; 1g-cl.
 DR InterPro: IPR003600; 1g-like.
 DR InterPro: IPR003006; 1g_MHC.
 DR InterPro: IPR003596; 1g_v.
 DR Pfam: PF00047; 1g; 2.
 DR SMART: SM00409; 1g; 2.
 DR SMART: SM00407; 1gcl; 3.
 DR SMART: SM00406; 1g; 1.
 DR SMART: SM00410; 1g-like; 1.
 DR PROSITE: PS00290; 1g_MHC; 1.
 DR PROSITE: PS00290; 1g_MHC; 1.
 SQ SEQUENCE 473 AA; 51699 MW; 9DE057A514475FBB CRC64;

Query Match 18.18; Score 512.5; DB 11; Length 473;
 Best Local Similarity 61.8%; Pred. No. 5; 9e-27;
 Matches 110; Conservative 13; Mismatches 36; Indels 19; Gaps 4;

QY 136 SGGGSGVQVQOQSGAEIVKPGSSVKISCKASGYTFYSYDMHWIKOOPGNGLEWIGIYIP 195
 Db 14 TAGHCVQVQLKQSAELVKGASVYKISCKASGYTFDYIMVWKORPGGLEWIGIKIGF 73
 QY 196 NGNTKYNQKFNKATLTADKSSSTAYMQLSLSSEDSAVYFCAR-----DMHYSSYIRP 250
 Db 74 SGTYYNEKFKGKATLTADKSSSTAYMQLSLSSEDSAVYFCARSGYDIDM----- 124
 QY 251 FAYWGQTLTVSSG--GGSEVQLLEQSGAELARPGASVKISCKASGYTFYNYGLSW 306
 Db 125 FAYWGQTLTVSAARTAPSVYPLAPVCG--GTTGSSVTLGCLVKGYPPEVTLTW 179

RESULT 8
 O8VC55 PRELIMINARY; PRT; 239 AA.
 AC O8VC55;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, last sequence update)
 DE 01-JUN-2002 (TREMblrel. 21, last annotation update)
 DE Hypothetical 26.3 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC021781; AAH21781.1; -
 DR InterPro: IPR003599; 1g.
 DR InterPro: IPR003597; 1g-cl.
 DR InterPro: IPR003006; 1g_MHC.
 DR InterPro: IPR003596; 1g_v.
 DR Pfam: PF00047; 1g; 2.
 DR SMART: SM00409; 1g; 2.
 DR SMART: SM00407; 1gcl; 1.
 DR SMART: SM00406; 1g; 1.
 DR PROSITE: PS00290; 1g_MHC; 1.
 DR PROSITE: PS00290; 1g_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26303 MW; C16119CACAC25C337 CRC64;

Query Match 18.08; Score 511; DB 11; Length 239;
 Best Local Similarity 80.7%; Pred. No. 3; 1e-27;
 Matches 96; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
 QY 403 SGGGSELVMTQTPSLVSGDASTSCRSSQSVINSGTYIHWYIQLKPGSGPKLLIY 462
 Db 15 SPASSDVVLTQTPSLPVPVNIQDASISCKSKSLNSDGTYYLDWYIQLKPGSGPKLLIY 74

QY 463 KVSNRFSGVPDRFSGSGGTDFTLKISRVEAEGLGYFPCSSQSHVRYTGCGKLEIKR 521
 Db 75 LVSNRFSGVPDRFSGSGGTDFTLKISRVEAEGLGYFPCSSQSHVRYTGCGKLEIKR 133

RESULT 9
 O99LC4 PRELIMINARY; PRT; 463 AA.
 AC O99LC4;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
 DE 01-JUN-2002 (TREMblrel. 21, last annotation update)
 DE Similar to RIKEN CDNA 1810060009 gene.
 GN 1gh-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC003435; AAH03435.1; -
 DR HSSP: P01842; 7FAB.
 DR MGD: MGI:96446; 1gh-4.
 DR InterPro: IPR003599; 1g.
 DR InterPro: IPR003597; 1g-cl.
 DR InterPro: IPR003600; 1g-like.
 DR InterPro: IPR003006; 1g_MHC.
 DR InterPro: IPR003596; 1g_v.
 DR Pfam: PF00047; 1g; 4.
 DR SMART: SM00409; 1g; 2.
 DR SMART: SM00407; 1gcl; 2.
 DR SMART: SM00406; 1g; 1.
 DR SMART: SM00410; 1g-like; 1.
 DR PROSITE: PS00290; 1g_MHC; 1.
 DR PROSITE: PS00290; 1g_MHC; 1.
 SQ SEQUENCE 463 AA; 51007 MW; EAA674C6B8C30783 CRC64;

Query Match 17.78; Score 502; DB 11; Length 463;
 Best Local Similarity 59.3%; Pred. No. 3e-26;
 Matches 102; Conservative 21; Mismatches 45; Indels 4; Gaps 3;

QY 135 SGGGSGVQVQOQSGAEIVKPGSSVKISCKASGYTFYSYDMHWIKOOPGNGLEWIGIYIP 134
 Db 13 GTAGHSGVQVQLKQSAELARPGASVYKISCKASGYTFYGVSWVKRIGGLEWIGETIY 72
 QY 195 NGNTKYNQKFNKATLTADKSSSTAYMQLSLSSEDSAVYFCARDHWYSSYIRPFAWY 254
 Db 73 SGTYYNEKFKGKATLTADKSSSTAYMQLSLSSEDSAVYFCARS--SYSYDL--FAWY 129
 QY 255 GGGTLTVVSSGGSEVQLLEQSGAELARPGASVKISCKASGYTFYNYGLSW 306
 Db 130 GGGTLTVVSA-AKTPPSVYPLAPGSAOINSMVTLGCLVKGYPPEVTLTW 180

RESULT 10
 O99L25 PRELIMINARY; PRT; 473 AA.
 AC O99L25;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
 DE 01-JUN-2002 (TREMblrel. 21, last annotation update)
 DE Similar to RIKEN CDNA 1810060009 gene.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC003888; AAH03888.1; -

FT NON_TER 145 145
 SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match 17.2%; Score 487.5; DB 11; Length 145;
 Best Local Similarity 77.2%; Pred. No. 6.6e-26;
 Matches 95; Conservative 9; Mismatches 16; Indels 3; Gaps 1;

OY 142 QVQLQSGAEIVKPGSSVKISCKASGYTFTSYDMHWIKQDPNGLEWIGMYPGNGNTKY 201
 DB 1 QVQLQSGAEIVKPGASVKSCKASGYTFTSYDMHWIKQDPNGLEWIGRIDPNSGITY 60

OY 202 NQKFNKATLTADKSSSTAYVQLSLTSDSAVYFCARDHWYSSYIRPFAYWGQTLVT 261
 DB 61 NEKFKSKATLTVDKPSSTAYVQLSLTSDSAVYFCARDYDYGSSY---FDYWGQCTLT 117

OY 262 VSS 264
 DB 118 VSS 120

RESULT 14

ID Q924R8 PRELIMINARY; PRT; 146 AA.

AC Q924R8; 01-DEC-2001 (TREMUREL. 19, Created)

DT 01-DEC-2001 (TREMUREL. 19, Last sequence update)

DT 01-MAR-2002 (TREMUREL. 20, Last annotation update)

DE WH186.2-D-J-C mu protein (Fragment).

OS Mus musculus (mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP STRAIN=C57BL/6;

RA Kozono Y., Kozono H., Azuma T.;

RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals

RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-

RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB067781; BAB63266.1;

DR InterPro: IPR003006; I9_MHC.

DR Pfam: PF00447; I9; 1.

FT NON_TER 1 1

FT NON_TER 146 146

SQ SEQUENCE 146 AA; 16216 MW; 92460F1FDF1B7538 CRC64;

Query Match 17.2%; Score 487; DB 11; Length 146;
 Best Local Similarity 76.4%; Pred. No. 7.2e-26;
 Matches 94; Conservative 9; Mismatches 18; Indels 2; Gaps 1;

OY 142 QVQLQSGAEIVKPGSSVKISCKASGYTFTSYDMHWIKQDPNGLEWIGMYPGNGNTKY 201
 DB 1 QVQLQSGAEIVKPGASVKSCKASGYTFTSYDMHWIKQDPNGLEWIGRIDPNSGITY 60

OY 202 NQKFNKATLTADKSSSTAYVQLSLTSDSAVYFCARDHWYSSYIRPFAYWGQTLVT 261
 DB 61 NEKFKSKATLTVDKPSSTAYVQLSLTSDSAVYFCARDYDYGSSY---YDYGSSLYFDYWGQCTLT 118

OY 262 VSS 264
 DB 118 VSS 121

RESULT 15

ID Q8TCD0 PRELIMINARY; PRT; 239 AA.

AC Q8TCD0; 01-JUN-2002 (TREMUREL. 21, Created)

DT 01-JUN-2002 (TREMUREL. 21, Last sequence update)

DT 01-JUN-2002 (TREMUREL. 21, Last annotation update)

DE [protein] 26.2 kDa protein.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP STRAIN=FROM N.A.

RA Straussberg R.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC023362; AAH22362.1;

DR Hypothetical protein 26234 MW; FACEPC3A3B03871D CRC64;

SQ SEQUENCE 239 AA; 26234 MW; FACEPC3A3B03871D CRC64;

Query Match 17.1%; Score 486; DB 4; Length 239;
 Best Local Similarity 76.7%; Pred. No. 1.6e-25;
 Matches 92; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

OY 405 GGSSELVMTQTPLSLPVSLGDAISCSRSSQSLVHSNNTYTLHWYLOKPGSPKLLIKY 464
 DB 17 GSSGIVMTQSPSLPVTLLGQPASISCKSTQSLVSDGNTYLNMFQKPGSPKRLIKY 76

OY 465 SNRFGVDPDRFSGSGSGTDFTLKISRVEAEDLGVYFCQSSTHVPYFEGGKLEIKRTTS 524
 DB 77 SNRDSGVDPDRFSGSGSGTDFTLKISRVEAEDLGVYFCQSGTHVPYFEGGKLEIKRTVA 136

Search completed: February 25, 2003, 10:36:36
 Job time : 136.773 secs

Db 421 GSOVLOOOSGPELVPRGASVYKLSCKASGVTFTSYMMNNVQRRPDEGLEWIGHRIDPYDSFT 180
 QY 200 KYNOKFNGKATLTADKSSSTAYMQLSLTSEDSAVYFCARDWHYSSYTRPAYMGQTL 259
 Db 181 HYNOKFKDKALITVDKASASTAYMQLSLTSEDSAVYCAKMDY-----SFDYMGQTT 234
 QY 260 VYSSGGGSEVQLLEQSGAELARPGASVYKLSCKASGVTFTSYMMNNVQRRPDEGLEWIGH 319
 Db 235 VYSSGGGSEVQLLEQSGAELARPGASVYKLSCKASGVTFTSYMMNNVQRRPDEGLEWIGH 294
 QY 320 EYPRIGNAYNEKFKATLTADKSSSTAYMQLSLTSEDSAVYFCARDWHYSSYTRPAYMGQTL 379
 Db 235 EYPRIGNAYNEKFKATLTADKSSSTAYMQLSLTSEDSAVYFCARDWHYSSYTRPAYMGQTL 354
 QY 380 FDVWGQTTVYSSGGGSEVQLLEQSGAELARPGASVYKLSCKASGVTFTSYMMNNVQRRPDEGLEWIGH 439
 Db 355 FDVWGQTTVYSSGGGSEVQLLEQSGAELARPGASVYKLSCKASGVTFTSYMMNNVQRRPDEGLEWIGH 414
 QY 440 SNGNTYLMHWYLOKPGOSPKLLIYKVNRFSGVPPDRFSGSGGTFTLKISRVEAEDLGVY 499
 Db 415 SNGNTYLMHWYLOKPGOSPKLLIYKVNRFSGVPPDRFSGSGGTFTLKISRVEAEDLGVY 474
 QY 500 FCSQSTHVPYTFGGGTKLEIKRTTSHNNHNTS 532
 Db 475 FCSQSTHVPYTFGGGTKLEIKRTTSHNNHNTS 507

RESULT 3
 AAU72860
 ID AAU72860 standard; Protein: 510 AA.
 AC AAU72860:
 DT 26-FEB-2002 (first entry)
 DE Human p53 tetramerisation domain.
 XX Human; NKG2D receptor complex; cancer; infectious disease; tumour;
 KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
 KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
 KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; EV;
 KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI0;
 KW helminth; cytotoxic; antimicrobial; immunomodulatory; 1182D10; 6H7E7;
 KW 8G7C10; 6E5A7x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
 KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
 KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
 XX Homo sapiens.
 OS
 XX
 PN WO200117005-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 26-MAR-2001: 2001WO-EP03414.
 XX
 PR 24-MAR-2000: 2000EP-0106467.
 XX
 PA (KUEF/) KUEF P.
 PI Kufner P, Rietmuelier G, Lutterbuese R, Borschert K, Kischel R;
 PI Mayer M, Hofmeister R;
 XX
 DR MPI: 2002-055119/07.
 DR N-PSDB: AAS97134.
 XX
 XX Multifunctional polypeptides comprising binding sites that specifically
 PT recognise extracellular groups of the NKG2D receptor complex and
 PT domains which function as receptors or ligands, useful for treating
 PT cancers and infectious diseases -
 XX
 PS Example 7: Fig 16: 11app: English.
 CC The invention relates to a multifunctional polypeptide comprising a

CC domain with a binding site that specifically recognises an extracellular
 CC group of the NKG2D receptor complex and a second domain which functions
 CC as a receptor or ligand. The polypeptide and its associated
 CC polynucleotide are used for the preparation of a pharmaceutical
 CC composition for the treatment of cancer, infections and/or autoimmune
 CC conditions. The cancer may be a tumour of the head and neck, stomach,
 CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
 CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
 CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
 CC The infectious diseases can be caused by viruses, bacteria, fungi,
 CC protozoa or helminths. The autoimmune diseases include multiple
 CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
 CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
 CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
 CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
 CC receptor and the polypeptides of the invention.
 CC
 SQ Sequence 510 AA:
 Query Match 74.9%; Score 2124.5; DB 23; Length 510;
 Best Local Similarity 78.4%; Pred. No. 6, 3e-116;
 Matches 402; Conservative 38; Mismatches 70; Indels 3; Gaps 2;
 QY 20 DIQMTGSPASLSAPEIYITTCQASQDINWLMYQOKPKSPOLLIYATSLADGPS 79
 Db 1 DIQMTGSPASLSAPEIYITTCQASQDINWLMYQOKPKSPOLLIYATSLADGPS 60
 QY 80 RFSGSRSQIOYSLKISLQVEDTGYICLORISNPTFGAGTKLELKGSGSGSGSGG 139
 Db 61 RFSGSRSQIOYSLKISLQVEDTGYICLORISNPTFGAGTKLELKGSGSGSGSGG 120
 QY 140 GSOVLOOOSGAEVLYKPSVYKISCKASGVTFTSYMMNNVQRRPDEGLEWIGH 199
 Db 121 GSOVLOOOSGAEVLYKPSVYKISCKASGVTFTSYMMNNVQRRPDEGLEWIGH 179
 QY 200 KYNOKFNGKATLTADKSSSTAYMQLSLTSEDSAVYFCARDWHYSSYTRPAYMGQTL 259
 Db 180 KYNOKFNGKATLTADKSSSTAYMQLSLTSEDSAVYFCARDWHYSSYTRPAYMGQTL 237
 QY 260 VYSSGGGSEVQLLEQSGAELARPGASVYKLSCKASGVTFTSYMMNNVQRRPDEGLEWIGH 319
 Db 238 VYSSGGGSEVQLLEQSGAELARPGASVYKLSCKASGVTFTSYMMNNVQRRPDEGLEWIGH 297
 QY 320 EYPRIGNAYNEKFKATLTADKSSSTAYMQLSLTSEDSAVYFCARDWHYSSYTRPAYMGQTL 379
 Db 298 EYPRIGNAYNEKFKATLTADKSSSTAYMQLSLTSEDSAVYFCARDWHYSSYTRPAYMGQTL 357
 QY 380 FDVWGQTTVYSSGGGSEVQLLEQSGAELARPGASVYKLSCKASGVTFTSYMMNNVQRRPDEGLEWIGH 439
 Db 358 FDVWGQTTVYSSGGGSEVQLLEQSGAELARPGASVYKLSCKASGVTFTSYMMNNVQRRPDEGLEWIGH 417
 QY 440 SNGNTYLMHWYLOKPGOSPKLLIYKVNRFSGVPPDRFSGSGGTFTLKISRVEAEDLGVY 499
 Db 418 SNGNTYLMHWYLOKPGOSPKLLIYKVNRFSGVPPDRFSGSGGTFTLKISRVEAEDLGVY 477
 QY 500 FCSQSTHVPYTFGGGTKLEIKRTTSHNNHNTS 532
 Db 478 FCSQSTHVPYTFGGGTKLEIKRTTSHNNHNTS 510

RESULT 4
 AAU72859
 ID AAU72859 standard; Protein: 510 AA.
 AC AAU72859:
 DT 26-FEB-2002 (first entry)
 DE Human; NKG2D receptor complex; cancer; infectious disease; tumour;
 KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
 KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;

CC The invention relates to a multifunctional polypeptide comprising a
CC domain with a binding site that specifically recognises an extracellular
CC group of the NKGD2 receptor complex and a second domain which functions
CC as a receptor or ligand. The polypeptide and its associated
CC polynucleotide are used for the preparation of a pharmaceutical
CC composition for the treatment of cancer, infections and/or autoimmune
CC conditions. The cancer may be a tumour of the head and neck, stomach,
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma
CC The infectious diseases can be caused by viruses, bacteria, fungi,
CC protozoa or helminths. The autoimmune diseases include multiple
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC autoimmune hepatitis. Sequences AAU72820-AAU72815 represent the NKGD2
CC receptor and the polypeptides of the invention.

Sequence 510 AA:
XX

[illegible]

DE Amino acid sequence of the bscCD19xCD3 antibody.
XX
XX bscCD19xCD3 antibody; bispecific single-chain fragment; CD19 antigen;
KW CD3 antigen; CD19-positive target cell; T-cell stimulation;
KW cytotoxic T-lymphocyte; B-cell malignancy; myasthenia gravis;
KW B-cell mediated autoimmune disease; Morbus Basedow;
KW Hashimoto thyroiditis; Goodpasture syndrome; B-cell depletion;
KW non-Hodgkin lymphoma; gene therapy; cancer; viral disease.
XX
XS Synthetic.

Key	Location/Qualifiers
FT Peptide	1..19
FT Peptide	/note= "signal peptide"
FT Peptide	28..138
FT Peptide	/note= "VL-CD19 peptide"
FT Peptide	154..277
FT Peptide	/note= "VH-CD19 peptide"
FT Peptide	283..401
FT Peptide	/note= "VH-CD3 peptide"
FT Peptide	420..525
FT Peptide	/note= "VL-CD3 peptide"
FT Peptide	526..531
FT Peptide	/note= "His tag"
PN	WO954440-A1.
PD	28-OCT-1999.
PF	21-APR-1999; 99WO-EP02693.
PR	21-APR-1998; 98EP-0107269.
PA	(DOER/) DOERKEN B.
PA	(RIET/) RIETHMUELLER G.
PI	Kuifer P, Luterbuese R, Bargou R, Loeffler A;
DR	WPI: 2000-013241/01.
DR	N-PSDB; AAZ30332.
PT	Novel multifunctional polypeptide for treating B-cell malignancies
PT	especially non-Hodgkin lymphoma
PS	Example 2; Fig 8; 91pp; English.

CC The present sequence represents a bscCD19xCD3 antibody. This antibody
 CC is a bispecific single-chain polypeptide comprising domains providing
 CC binding-site of immunoglobulin chains or antibodies specifically
 CC recognizing CD19 and CD3 antigen. The polypeptide destroys CD19-positive
 CC target cells without any need of T-cell pre and/or co-stimulation, by
 CC recruiting cytotoxic T-lymphocytes and so specific lysis by T-cells
 CC rather than a direct effect by an antibody is achieved. The bispecific
 CC single-chain polypeptides, or nucleotides encoding them, are used for
 CC the treatment of B-cell malignancies, B-cell mediated autoimmune
 CC diseases like myasthenia gravis, Morbus Basedow, Hashimoto thyroiditis
 CC or Goodpasture syndrome or for the depletion of B-cells and more
 CC particularly non-Hodgkin lymphoma in mammals preferably human. They can
 CC also delay the pathological conditions caused by these diseases, and
 CC can be used for detecting these diseases. The polynucleotide is used
 CC for gene therapy. The polypeptides are also used for identifying
 CC compounds modulating B-cell/T-cell mediated immune response with can in
 CC turn be used for treating cancer, its related diseases and also for
 CC inhibiting viral diseases by preventing viral infection.

XX Sequence 531 AA:

Query Match 61.2%; Score 1735.5; DB 21; Length 531;
 Best Local Similarity 62.8%; Pred. No. 2.7e-93;
 Matches 346; Conservative 63; Mismatches 101; Indels 41; Gaps 10;

QY 1 MCMSCILFLVATATGVS-----DIQMTQSPASISASPEELVITTCASQDI---- 48
 DB 1 MCMSCILFLVATATGVSVDKDDDDKDLQTPSPASISASVIGQRTTISCKASQSDVYDG 60
 QY 49 GNMILWYQOQPKSPQQLLYSATSLADGIPSRFGSGSGTQYSLKISRLQVEDTGIYCL 108
 DB 61 DSYLWYQOQIPQOPKLLIYDASNLVSGIPRFGSGSGTDETLNHPEKVDAAHYHQC 120
 QY 109 QRYSNPTFGACTKLELKGSGSGSGSGSGSOVLOOQSGAELVKGSSVATSCASGY 168
 DB 121 QSTEDPTWTFGGCTKLEIKGSGSGSGSGSOVLOOQSGAELVKGSSVATSCASGY 180
 QY 169 PTTSYDMHVKQOPGNGLEWIMIGYNGNTRYNCKFNKATLTADKSSSTAYMQLSLT 228
 DB 181 AFSSTWMNVKQRPQGLIEMIQIWPQDDPTNYNGFKKATLTADSSSTAYMQLSLT 240
 QY 229 SEDSAVYFCAR-----DMHYSSYIRPPAWGQGLTVSSGGSGSEVOLQSGAELA 282
 DB 241 SEDSAVYFCARRETTVGRYYA-----MDYWGQGLTVTVSSGGSGSDIK-LQOQSGAELA 294
 QY 283 RFGASVKSLSKASGYFTFTYGLSWKQRGVLEWIGEYPRRGNAVYNKEKFKATLT 342
 DB 295 RFGASVKSLSKASGYFTFTYGLSWKQRGVLEWIGEYPRRGNAVYNKEKFKATLT 354
 QY 343 DKSSSTASMEKSLTSEDSAVYFCARGSYDTWYFDVWQGTTVTVSS--GGGSG 399
 DB 355 DKSSSTAYMQLSLTSEDSAVYFCAR--YDDHY--CLDWGQGLTVTVSSVGGSGSG 410
 QY 400 GGGSGSGSELVMTQPLSPVSLGQASISCRSSQSLVHNGNTYLIHWLQKPGQSPKL 459
 DB 411 GSGSGSGVDIDQLTQSPALISASPEKVTMTCRASSV-----SYAMWYQOKSGTSPKR 464
 QY 460 LIYKVSNRSGVDRFSGSGSGDTFLKISRVAEDLGYFCSOSTNVPRTFGGKTL 519
 DB 465 WITDTSKVAQVPRFSGSGSGTSLTSSMEADATATYCCQWSSNPLTFAGTKLEL 524
 QY 520 KRTTSHHHHH 530
 DB 525 K-----HHHHH 531

RESULT 6
 AAE22193

ID AAE22193 standard; protein; 495 AA.

XX AAE22193;

DT 25-JUL-2002 (First entry)

XX Murine CCR5xCD3 bispecific single chain antibody construct.
 DE
 XX Chemokine construct; human immunodeficiency virus 1; allergic disease;
 KW skin disease; immunological disorder; autoimmune disease; psoriasis;
 KW multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;
 KW diabetes; skin inflammation; atopic dermatitis; inflammatory disease;
 KW inflammatory renal disease; HIV-1; transplant rejection; CCR5xCD3;
 KW antibody; chemokine receptor 5; CD3 antigen; chimeric; murine.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - unidentified.
 XX
 PN WO200220615-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-EP10433.
 XX
 PR 08-SEP-2000; 2000EP-0119694.
 XX
 PR 05-SEP-2001; 2001US-0948004.
 XX
 PA (MICR-) MICROMET AG.
 XX
 PI Mack M, Schloendorff D, Spring M;
 XX
 DR WPI: 2002-362240/39.
 DR N-PSDB: MAD35252.

XX Use of an antibody and/or chemokine construct that binds to a chemokine
 PT receptor, for eliminating cells latently infected with primate
 PT immunodeficiency virus, or treating, preventing and alleviating immune
 PT disorders
 XX
 PS Claim 29; Page 52; 117pp; English.

XX The invention relates to the use of an antibody and/or chemokine
 CC construct that binds a chemokine receptor for preparing a pharmaceutical
 CC composition for eliminating cells latently infected with a primate
 CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1). They
 CC are used in gene therapy and as vaccines. The antibody and/or chemokine
 CC construct is also used for preparing a pharmaceutical composition for
 CC treating, preventing and/or alleviating immunological disorders
 CC including autoimmune diseases (e.g. multiple sclerosis, type 1 diabetes
 CC and rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin
 CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases
 CC such as inflammatory joint diseases (chronic arthritis), inflammatory
 CC renal diseases and inflammatory bowel diseases and graft versus host
 CC and transplant rejections. The present sequence is CCR5xCD3 bispecific
 CC single chain antibody construct. This antibody construct comprises
 CC light chain variable domain (VL) and heavy chain variable (VH) domains
 CC of murine MC-1 antibody specific for human chemokine receptor 5 (CCR5)
 CC and VH and VL domains of an antibody specific for a CD3 antigen joined
 CC by a peptide linker.
 XX
 XX Sequence 495 AA:

Query Match 59.8%; Score 1695; DB 23; Length 495;
 Best Local Similarity 64.4%; Pred. No. 5.6e-91;
 Matches 331; Conservative 62; Mismatches 99; Indels 22; Gaps 7;

QY 20 DIQMTQSPASISASPEELVITTCASQDIDGMILWYQOQPKSPQQLLYSATSLADGIPS 79
 DB 1 DIVLTQSPASISASVGEVITTCRASENIVSYLWYQOQKQKSPQLLYNKTLTLEGVPS 60
 QY 80 RFGSSRGSTQYSLKISRLQVEDTGIYCLQYNSNPFGACTKLELKGSGSGSGSG 139
 DB 61 RFGSGSGTQPSLKTINSIQPDGNYGQHHTYPRFTFGGKTLKIRGSGSGSGSGSG 120
 QY 140 GSQVLOOQSGAELVKGSSVATSCASGYFTFTYGLSWKQRGVLEWIGEYPRRGNAV 199
 DB 121 GSQVLOOQPGAGRVPRFASVATSCASGYFTFTYGLSWKQRGVLEWIGEYPRRGNAV 180


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OY 200 KYNQKFNKATLTADKSSSTAYMQLSLTSEDSAVYFCARDMHHYSSYRPFAYGQGL 259
DB 181 RLNQKFNDRATLTVDKYSTAYTQLSSPTSEDSAVYCARGYIYGI----FDWAGQGT 236
OY 260 VYVSSGGGSEVQLLEQSGAELARPGASVKLSCKASGTFITNYGLSWKQKRPQVLEWIG 319
DB 237 VYVSSGGGSDIK-LQOQSGAELARPGASVKMSCKTSYTFITRYTMHWKQKRPQGLWIG 295
OY 330 EYVPRIGNAYNEKFKGATLTADKSSSTAYMQLSLTSEDSAVYFCARDSSYDPRNDWY 379
DB 296 YINPGRGTNNQKFKDKATLTLDKSSSTAYMQLSLTSEDSAVYCAR--YIDHW--C 351
OY 380 FDWAGQGTIVYSS---GGGSGGGGSGGGSELVMTQPTSLPYSLDQASISCRSSQS 436
DB 332 LDWYRGQTTLTIVSSVEGSGGSGGGGSGVDIQLTQSPAIMASDPGEKVTMTCRASSS 411
OY 437 LVHNSGNITLYLHMYLQKPGQSPKLLTYKYSNRFSGVPRDFSSGSGGTDTLTISRVEADL 496
DB 412 V-----SYMNYQOKSGTSPKRWITDTSKVASGVPRFSGSGGTSLTISSEMAEDA 465
OY 497 GYVPCSGSTHVPYTFGGGKLEIKRTTSHHHHH 530
DB 466 ATYYCOQWSSNPRTFGAGTKLEK----HHHHH 495

RESULT 7
AAU72875
ID AAU72875 standard; Protein: 505 AA.
XX
AC AAU72875:
XX
DT 26-FEB-2002 (first entry)
XX
DE Human NKG2D polypeptide.
XX
KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI0;
KW helminth; cytosolic; antimicrobial; immunomodulatory; 1182D10; 6H7E7;
KW p4-15; p5-2; p5-9; p5-10; p5-11; p5-23; 3B10xP4-3; 3B10xP4-14;
KW p53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
XX
OS Homo sapiens.
XX
PN WO200171005-A2.
XX
PD 27-SEP-2001.
XX
PE 26-MAR-2001; 2001MO-EP03414.
XX
PR 24-MAR-2000; 2000EP-0106467.
XX
PA (KUFE/) KUFER P.
XX
PI Kufer P, Riettmueller G, Lutterbuese R, Borschert K, Kischel R;
PI Mayer M, Hofmeister R;
XX
DR WPI: 2002-055119/07.
DR N-PSDB: AAS97158.
XX
XX
PT Multifunctional polypeptides comprising binding sites that specifically
PT recognise extracellular groups of the NKG2D receptor complex and
PT domains which function as receptors or ligands, useful for treating
PT cancers and infectious diseases -
XX
XX
PS Example 1; Fig 1; 114pp: English.
XX
XX
CC The invention relates to a multifunctional polypeptide comprising a
CC domain with a binding site that specifically recognises an extracellular
CC group of the NKG2D receptor complex and a second domain which functions

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CC as a receptor or ligand. The polypeptide and its associated
CC polynucleotide are used for the preparation of a pharmaceutical
CC composition for the treatment of cancer, infections and/or autoimmune
CC conditions. The cancer may be a tumour of the head and neck, stomach,
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
CC The infectious diseases can be caused by viruses, bacteria, fungi,
CC protozoa or helminths. The autoimmune diseases include multiple
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
CC receptor and the polypeptides of the invention.
XX
SQ Sequence 505 AA:
XX
Query Match 56.2%; Score 1594; DB 23; Length 505;
Best Local Similarity 58.7%; Pred. No. 4.2e-85;
Matches 307; Conservative 71; Mismatches 115; Indels 30; Gaps 9;
OY 20 DIQMTQ----SPASLSASPEIYVITTCQASODIGN----WLAWYQOKRPSQPLIYSA 70
DB 1 DIQMTQAFSPNPVTLGTS----ASISCRSSKSLHNSGITLYLWYLQKRGQSPQLIYQM 56
OY 71 TSLADGIPSRFSRSGRGTQYSLKISRLQYEDPDGITYCLOIRSNPNTFGAGTKLEKGGG 130
DB 57 SNLASGVPRDFSSGSGGTDTLTISRVEADGVYVCAQNLPLPRTFGGKLEIKRTTSHHHHH 116
OY 131 SGGGSGGGGGGSOYLOQSGAELVKKPGSSVYKISCKASGYFTSYDMHMIKQPGNLEWIG 190
DB 117 SGGGSGGGGGGSOYLOQSGPELKKPGETVYKISCKASGYFTSYDMHMIKQPGNLEWIG 176
OY 191 WITPYGNKTKYNNQKFNKATLTADKSSSTAYMQLSLTSEDSAVYFCARDMHHYSSYLRP 250
DB 177 WITPYGNKTKYNNQKFNKATLTADKSSSTAYMQLSLTSEDSAVYFCARDMHHYSSYLRP 229
OY 251 FAYWGGTLVTVSSGGGSEVQLLEQSGAELARPGASVKLSCKASGYFTNYGLSWKQKRP 310
DB 230 -DYGCGGTIVYSSGGGSEVQLLE-SGGGLVQPGGSLKLSAAGCFDFSRKYSMWVQDA 287
OY 311 PGQVLEWTEYVPRIGNAYNEKFKGATLTADKSSSTAYMQLSLTSEDSAVYFCARG 370
DB 288 PGKLEWTEYVPRIGNAYNEKFKGATLTADKSSSTAYMQLSLTSEDSAVYFCARG 347
OY 371 SYDTNVDWYFDWAGQGTIVTVSSGGGSGGGGSELVMTQPTSLPYSLDQASIS 430
DB 348 QMG-----YFDWAGQGTIVTVSSGGGSGGGGSELVMTQPTSLPYTAGERYWMS 402
OY 431 CRSSGSLVHS-NGNTYLYLHMYLQKPGQSPKLLTYKYSNRFSGVPRDFSSGSGGTDTLTISR 489
DB 403 CRSSGSLVHS-NGNTYLYLHMYLQKPGQSPKLLTYKYSNRFSGVPRDFSSGSGGTDTLTISR 462
OY 490 RVEADLVYPCSGSTHVPYTFGGGKLEIKRTTSHHHHH 530
DB 463 SVQAEADVAYYQNDYSYPLTFGAGTKLEIKRTTSHHHHH 505

RESULT 8
AAU72873
ID AAU72873 standard; Protein: 503 AA.
XX
AC AAU72873:
XX
DT 26-FEB-2002 (first entry)
XX
DE 3B10xP5-2 bispecific single chain Fv.
XX
XX
KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI0;

```


KW helminth; cytosolic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
 KM 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
 KM P4-15; P5-2; P5-3; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
 KM p53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
 OS Homo sapiens.
 PN WO200171005-A2.
 XX
 XX
 PD 27-SEP-2001.
 XX
 XX
 PF 26-MAR-2001; 2001WO-EP03414.
 XX
 PR 24-MAR-2000; 2000EP-0106467.
 XX
 PA (KUFE/) KUFEER P.
 PI Kufer P, Riettmueller G, Lutterbuese R, Borschert K, Kischel R;
 PI Mayer M, Hofmeister R;
 XX
 DR WPI: 2002-055119/07.
 DR N-PSDB; AAS97147.
 XX
 PT Multifunctional polypeptides comprising binding sites that specifically
 PT recognise extracellular groups of the NKG2D receptor complex and
 PT domains which function as receptors or ligands, useful for treating
 PT cancers and infectious diseases -
 XX
 XX
 PS Example 5; Fig 16; 114pp: English.
 XX
 XX The invention relates to a multifunctional polypeptide comprising a
 CC domain with a binding site that specifically recognises an extracellular
 CC group of the NKG2D receptor complex and a second domain which functions
 CC as a receptor or ligand. The polypeptide and its associated
 CC polynucleotide are used for the preparation of a pharmaceutical
 CC composition for the treatment of cancer, infections and/or autoimmune
 CC conditions. The cancer may be a tumour of the head and neck, stomach,
 CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
 CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
 CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
 CC The infectious diseases can be caused by viruses, bacteria, fungi,
 CC protozoa or helminths. The autoimmune diseases include multiple
 CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
 CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
 CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
 CC autoimmune hepatitis. Sequences AAU72820-AAU7875 represent the NKG2D
 CC receptor and the polypeptides of the invention.
 XX
 XX Sequence 503 AA:
 SQ
 Query Match 55.1%; Score 1562; DB 23; Length 503;
 Best local Similarity 56.7%; Pred. No. 3.1e-83;
 Matches 296; Conservative 77; Mismatches 119; Indels 30; Gaps 9;
 QY 20 DIQMTQ---SPASLSASPEEIVTTCQASQDIGN---WLAWYQKPGKSPQLLIYSA 70
 DB 1 DIVTQQAFAFNPVLIGTS---ASISCRSSKSLHNSGITYLWYLRKPGSQPLLIIYQM 56
 QY 71 TSLADGIPRSRSRSGSGYQYSLKISRLOVEDTGIYCLQKRSNPTFPAGKLEKGGG 130
 DB 57 SNLASGVDPDRSSSGSGTDFLTRISRYAEEDVGYCAQNELPRTFPGKLEKGGG 116
 QY 131 SGGGSGGGGGSOVOLOOGSGAELVKKPGSSVKSISKASGYTFTSYDHHWTKQOPGNLEWIG 190
 DB 117 SGGGSGGGGGSOVOLOOGSGPELKKRGETVKISCRASGYTFTYNGKNNWKKQARKGFKMG 176
 QY 191 WIYFGNGTKYNQKFNCKATLTADKSSSTAYWQSLTSEDSAVYFCARDWHYSSYLRP 250
 DB 177 WINTYTGPTGYGDFKFGFAFSLETSASTAYLQIINLNKNEPTATYFCAR-----FTSP 229
 QY 251 FAYWGGGLTVYVSSGGGSEVOLLLEQSGAELARPGASVKSCKASGYTFTWYGLSWVQR 310
 DB 230 -DIWGGGTVTVSSGGGSEVOLLLE-SGGGLVQPGSLKLSCAASGDFPSRYWMSWVQDA 287

QY 311 PGQVLEWIGEYVPRIGNAYVNEKFKKATLTADKSSSTASMELRSLTSEDSAVYFCARG 370
 DB 288 PGKGLEWIGELINPDSSITINTPSLDKRFLISRDNKNTLYLQMSKVRBEDTALTYFCAR- 346
 QY 371 SYDTNYDMYFDVWGGGTVTVSSGGGSGGGSGGSELYWYOTPLSLPVSLGQASIS 430
 DB 347 SYGSSYDMYFDVWGGGTVTVSSGGGSGGGSGGSELYWYOTPLSLPVSLGQASIS 406
 QY 431 CRSSGSLVHNSGNTLYLHMYLQKPGSKPLLYKYVNSRSGVDPDRSSGSGTDFLTRKIS 490
 DB 407 CRASENIV-----SYLAWYQKQKSPQLLVYNAKTLAEGVPSRSSSGSGTQFSLKINS 461
 QY 491 VEAEIDIGVYFCSSQSTHVPYTFGGGKLEIKRTTS--HHNNH 530
 DB 462 LQPEDFGSYTCOHNGTFLTFGAGTKLEIKRTTSSGHHNNH 503
 RESULT 9
 AAU72874
 ID AAU72874 standard; Protein: 503 AA.
 XX
 XX AAU72874:
 AC
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE 3B10xP5-23 bispecific single chain Fv.
 XX
 XX Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
 KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
 KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
 KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
 KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI10;
 KW helminth; cytosolic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
 KM 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
 KW P4-15; P5-2; P5-3; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
 KW p53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
 OS Homo sapiens.
 PN WO200171005-A2.
 XX
 XX
 PD 27-SEP-2001.
 XX
 PF 26-MAR-2001; 2001WO-EP03414.
 XX
 PR 24-MAR-2000; 2000EP-0106467.
 XX
 PA (KUFE/) KUFEER P.
 PI Kufer P, Riettmueller G, Lutterbuese R, Borschert K, Kischel R;
 PI Mayer M, Hofmeister R;
 XX
 DR WPI: 2002-055119/07.
 DR N-PSDB; AAS97148.
 XX
 PT Multifunctional polypeptides comprising binding sites that specifically
 PT recognise extracellular groups of the NKG2D receptor complex and
 PT domains which function as receptors or ligands, useful for treating
 PT cancers and infectious diseases -
 XX
 XX
 PS Example 5; Fig 16; 114pp: English.
 XX
 XX The invention relates to a multifunctional polypeptide comprising a
 CC domain with a binding site that specifically recognises an extracellular
 CC group of the NKG2D receptor complex and a second domain which functions
 CC as a receptor or ligand. The polypeptide and its associated
 CC polynucleotide are used for the preparation of a pharmaceutical
 CC composition for the treatment of cancer, infections and/or autoimmune
 CC conditions. The cancer may be a tumour of the head and neck, stomach,
 CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
 CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
 CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.


```

Db 348 VVAP-----FDYWGOGITVTVSSGGGSGGGGSELVWTOSSLSLAGEVSLT 402
QY 431 CRSSQSLVHNSGNTYLHWYLOKPGSPKLLIYKVNRFSGVPPDRFSGSGSTDFLTKSR 490
Db 403 CRAQDIDSS-----LNLQOEPDGTIRKLIYATSSLDSPKRRSGSRSGSDYSLTSS 457
QY 491 VEADLGVYFCQSSTHVPYTFGCGTKLEIKRTTS--HHNNHH 530
Db 458 LESEDFVDYCYCLOYAASSPYTFGCGTKLEIKRTTSSGHHNNH 499

RESULT 11
AAG67499
ID AAG67499 standard; Protein: 533 AA.
AC AAG67499;
XX
XX 26-NOV-2001 (first entry)
XX
XX Amino acid sequence of a murine antibody L chain.
XX
XX Apoptosis: nucleated blood cell; integrin-associated protein; IAP;
XX erythrocyte agglutination; blood disease; leukemia; myeloma;
XX Hodgkin's disease; non-Hodgkin's lymphoma.
XX
XX Mus sp.
XX MO20016737-A1.
XX
XX 13-SEP-2001.
XX
XX 12-MAR-2001; 2001WO-JP01912.
XX
XX 10-MAR-2000; 2000US-0523095.
XX 17-APR-2000; 2000JP-0115246.
XX 20-OCT-2000; 2000JP-0321822.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Fukushima N, Tsuchiya M, Oh-eda M, Uno S, Kikuchi Y;
XX WPI: 2001-570772/64.
XX DR N-PSDB; AAH78156.
XX
XX Reconstituted polypeptide induces apoptosis in nucleated blood cells
XX that contain integrin-associated protein (IAP), is useful for the
XX treatment of blood diseases such as leukemia
XX
XX Example 6; Page 123-126; 141pp; Japanese.
XX
XX The specification describes a reconstituted polypeptide, which
XX induces apoptosis in nucleated blood cells that contain
XX integrin-associated protein (IAP). The polypeptide binds to IAP
XX without causing agglutination of erythrocytes. The polypeptide
XX contains at least two H chain V domains and at least two L chain
XX V domains of a monoclonal antibody which induces apoptosis in
XX nuclear blood cells having IAP. The reconstituted polypeptide is used
XX for the treatment of blood diseases such as acute or chronic myeloid
XX leukemia, acute or chronic lymphoid leukemia, adult T-cell leukemia,
XX multiple myeloma, mixed leukemia, hairy cell leukemia, Hodgkin's
XX disease or non-Hodgkin's lymphoma. The present sequence represents a
XX a murine monoclonal antibody L chain, which is used in the course of
XX the invention.
XX
XX Sequence 533 AA:
XX
XX Query Match 51.8%; Score 1468.5; DB 22; Length 533;
XX Best Local Similarity 47.1%; Pred. No. 8.8e-78;
XX Matches 311; Conservative 32; Mismatches 42; Indels 275; Gaps 5;
QY 1 MGWSCILFLVATATGVHSDIQMTQSPASLSASPEIIVITTCQASODIGMNLAWYQKPG 60
Db 1 MGWSCILFLVATATGV----- 17

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QY 61 KSPOLLIVSATSLADGIPSRFSGSRSGTOYSLKISRLQVEDPRTGYICLORTSNPNTFGAG 120
Db 18 ----- 17
QY 121 TKLELKGSGSGSGSGGSGGSOVOLQOQSGAELVFKPSSVYKISCKASGYTFSDMHMIO 180
Db 18 -----DSOYLOQSGPELVYKPKASVYKMSCKASGYTFANHVHVKQ 58
QY 181 QPQNGLEWIGWIPGNGNTYKQKFNKATLTPADKSSSTAYVQLSLTSSDAVYFCARD 240
Db 59 KPGQGLEWIGWITYPYNDGTAKYNEKFKDKATLTSDKSTTAYVMDLSLASEDAVYVYCARG 118
QY 241 WHYVSSYIRPFAYWGQGLVTVYSSGGG----- 268
Db 119 GYY-----TYDWDGQGTTLTVSSGGGSGGSGGSDVVMQSPSLPVLGQDAST 172
QY 269 ----- 268
Db 173 SCRSSQSLVHNSGNTYLHWYLOKPGSPKLLIYKVNRFSGVPPDRFSGSGSVTDFTLMTS 232
QY 269 -----SEVOLLQSGAE 280
Db 233 RVEADLGVYFCQSSTHVPYTFGCGTKLEIKGSGSGGSGGSGGSDVSOVO-LQOSGPE 291
QY 281 LARPGASVYKLSCKASGYTFETNYGLSMVKORPGQVLEWIGEYVPRIGNATYNEKFKGATL 340
Db 292 LKVPASVYKMSCKASGYTFANHVHVKQPGQGLEWIGYIIPYNDGTAKYNEKFKDKATL 351
QY 341 TADKSSSTASMEIARSLTSEDSAVYFCARSGSYDTYVDWYFDVWGQGTTLTVSSGGSGSG 400
Db 352 TSDKSSSTAYVMDLSLASEDAVYVYCARGYVT-----YDWMGQGTTLTVSSGGSGSG 405
QY 401 GSGSGGSELVWTFOTPLSLPVSILGQASTISCRSSQSLVHNSGNTYLHWYLOKPGSPKLL 460
Db 406 GSGSGGSDVVMQSPSLPVSILGQASTISCRSSQSLVHNSGNTYLHWYLOKPGSPKLL 465
QY 461 IYKVNRFSGVPPDRFSGSGSTDFTLKISRVAEDLGVYFCQSSTHVPYTFGCGTKLEIK 520
Db 466 IYKVNRFSGVPPDRFSGSGSVTDFTLMTSRVAEDLGVYFCQSSTHVPYTFGCGTKLEIK 525

RESULT 12
ABG35317
ID ABG35317 standard; Protein: 533 AA.
AC ABG35317;
XX
XX 30-JUL-2002 (first entry)
XX
XX Thrombopoietin agonist antibody associated protein #11.
XX
XX Modified antibody; thrombopoietin; TPO; agonist;
XX TPO receptor; platelet reduction-associated blood disease;
XX thrombocytopenia; cancer chemotherapy; leukemia; signal transduction.
XX
XX Mus sp.
XX WO200233072-A1.
XX
XX 22-OCT-2001; 2001WO-JP09259.
XX
XX 20-OCT-2000; 2000JP-0321821.
XX 17-APR-2001; 2001WO-JP03286.
XX 12-SEP-2001; 2001JP-0277314.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Tsuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;
XX WPI: 2002-383513/41.
XX

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DR N-PSDB; ABK71335.
 XX
 PT Degraded thrombopoietin agonist antibodies containing H and L chain V
 PT domains of monoclonal antibody, useful in preventives and/or remedies
 PT for blood diseases, thrombocytopenia following cancer chemotherapy or
 PT leukaemia
 XX
 XX
 PS Disclosure: Page 161-165; 213pp; Japanese.
 XX
 CC The invention describes a modified antibody comprising at least 2 heavy
 CC chain variable domains and 2 or more light chain variable domains of an
 CC antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing
 CC the TPO receptor to crosslink. The antibodies are useful in preventives
 CC and/or remedies for platelet reduction-associated blood diseases,
 CC thrombocytopenia following cancer chemotherapy or leukaemia. The
 CC antibody can act as a TPO signal transduction agonist by transducing a
 CC signal into cells by crosslinking a TPO receptor to exert TPO agonism.
 CC This is the amino acid sequence of a thrombopoietin (TPO) agonist
 CC antibody associated protein.
 XX
 SO Sequence 533 AA:
 Query Match 51.8%; Score 1468.5; DB 23; Length 533;
 Best Local Similarity 47.1%; Pred. No. 8.8e-78;
 Matches 311; Conservative 32; Mismatches 42; Indels 275; Gaps 5;
 OY 1 MGNSCILLFLVATGTVHSDIQMTQSPASLSASPEELVITTCASODIGNMLAWQOKPG 60
 DB 1 MGNSCILLFLVATGTVHSDIQMTQSPASLSASPEELVITTCASODIGNMLAWQOKPG 17
 OY 61 KSPOLLIVSATSLADGIPSRFSGSRGTQYSLKISRLQVEDTGIVYCLQRYSNPTFCAG 120
 DB 18 ----- 17
 OY 121 TKLELKGSGGSGGG 180
 DB 18 -----DSQVQLQDGGSLYVKGASVMSCKASGYTFANHHVHWKQ 58
 OY 181 QPENGLEMGIVYPCNGNTKYNOKENGKATLTADKSSSTAYMOLSLTSEDSAVYFCARD 240
 DB 59 KPGGLEMGIVYPCNGNTKYNOKENGKATLTADKSSSTAYMOLSLTSEDSAVYFCARG 118
 OY 241 WHYSSYIRPFAWGGTLVTVSSGGG----- 268
 DB 119 GY-----TYDWDGQGTTLTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 172
 OY 269 ----- 268
 DB 173 SCRSSQSLVHNSNGKTYLHWYLOKPGSPKLLITKYNRFSGVDPDRFSGSGVTDFLMTIS 232
 OY 269 -----SEVQLLEDSGAE 280
 DB 233 RVEAEDLGIVFCQSTHVPYTFGGGKTLKKGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 291
 OY 281 LARGASVAKLSCKASGYTFNNGYLSWYKORPGVLEWIGEVYPRICNAYNEKFKATL 340
 DB 292 LVKPGASVKMSCKASGYTFNHHVHWKORPGGLEWIGEVYPRNDGKTKNEKFKATL 351
 OY 341 TADSSSTASMEKSLTSEDSAVYFCARGSDYDNTDYMVGOGCTTVVSSGGGGSGG 400
 DB 352 TSDSSSTTAAMDLSLSEDSAVYFCARGGYT-----TDDWGQGTTLTVSSGGGGSGG 405
 OY 401 GSGSGGSELMVQTPLSLPSLDQASISCRSSQSLVHNSNGNTYLMHWYLOKPGSPKLL 460
 DB 406 GSGSGGSDVMTQSPSLPSLDQASISCRSSQSLVHNSNGNTYLMHWYLOKPGSPKLL 465
 OY 461 IYKVNRFSGVDPDRFSGSGGTFTTLKISRVEAEDLGIVFCQSTHVPYTFGGGKLEIK 520
 DB 466 IYKVNRFSGVDPDRFSGSGGTFTTLKISRVEAEDLGIVFCQSTHVPYTFGGGKLEIK 525
 RESULT 13
 AAM47637

ID AAM47637 standard; Protein; 533 AA.
 XX
 AC AAM47637;
 XX
 DT 28-FEB-2002 (first entry)
 XX
 DE Murine MABL-2 #6.
 XX
 KW Murine; cytotatic; antinflammatory; antinaemic; vasotropic;
 KW antibody; signal transduction; cancer; inflammation; hormonal disorder;
 KW leukaemia; lymphoma; aplastic anaemia; skeletal malformation.
 XX
 OS Mus sp.
 PN W020019494-A1.
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-JP03288.
 XX
 PR 17-APR-2000; 2000JP-0115246.
 PR 20-OCT-2000; 2000JP-0321821.
 PR 20-OCT-2000; 2000JP-0321822.
 PR 12-MAR-2001; 2001WO-JP01912.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Fukushima N, Tsuchiya M, Oheda M, Uno S, Kikuchi Y, Ontomo T;
 DR WPI: 2002-06368/09.
 DR N-PSDB; ABK04532.
 XX
 PT Antibodies for treatment of diseases associated with cell
 PT proliferation, hormonal disorders and cytokines comprise agonist
 PT activity to signal transmission across cell membranes -
 XX
 PS Disclosure: Page 141-145; 173pp; Japanese.
 XX
 CC The present invention relates to modified antibodies. The antibodies
 CC contain two or more H chain V domains and two or more L chain V domains
 CC of a monoclonal antibody (MAb) which is capable of transmitting a signal
 CC across the cell membrane by cross-linking a cell surface molecule, where
 CC the antibodies can serve as signal transmission agonists. The antibodies
 CC are useful for treatment and prevention of a broad range of disorders in
 CC which signal transmission is implicated, such as cancer, inflammation,
 CC hormonal disorders, leukaemia, malignant lymphoma, aplastic anaemia, and
 CC skeletal malformations. The present sequence was used to illustrate the
 CC present invention.
 CC
 SO Sequence 533 AA:
 Query Match 51.8%; Score 1468.5; DB 23; Length 533;
 Best Local Similarity 47.1%; Pred. No. 8.8e-78;
 Matches 311; Conservative 32; Mismatches 42; Indels 275; Gaps 5;
 OY 1 MGNSCILLFLVATGTVHSDIQMTQSPASLSASPEELVITTCASODIGNMLAWQOKPG 60
 DB 1 MGNSCILLFLVATGTVHSDIQMTQSPASLSASPEELVITTCASODIGNMLAWQOKPG 17
 OY 61 KSPOLLIVSATSLADGIPSRFSGSRGTQYSLKISRLQVEDTGIVYCLQRYSNPTFCAG 120
 DB 18 ----- 17
 OY 121 TKLELKGSGGSGGG 180
 DB 18 -----DSQVQLQDGGSLYVKGASVMSCKASGYTFANHHVHWKQ 58
 OY 181 QPENGLEMGIVYPCNGNTKYNOKENGKATLTADKSSSTAYMOLSLTSEDSAVYFCARD 240
 DB 59 KPGGLEMGIVYPCNGNTKYNOKENGKATLTADKSSSTAYMOLSLTSEDSAVYFCARG 118
 OY 241 WHYSSYIRPFAWGGTLVTVSSGGG----- 268

```

Db  119 GY-----TYDWMGGCTTLTVSSGGGGGGGGGGSDVVMQSPVSLPVLGDAQSI 172
Qy  269 -----268
Db  173 SCRSGSLVHNSGKTYLHWYLOKPGQSPKLLIKVSNRFGSDVDFSSGVTDTLTMS 232
Qy  269 -----SEVOLLQSGAE 280
Db  233 RVEADLGVFCSTHVPYTFGGGKLEIKGGGGGGGGGGSSVDSQV-LQOQSGPE 291
Qy  281 LARGASVKLSCKASGYFTNYGLSMVKORPGOVLEWIGEVPRIGNAYNKEFKGKATL 340
Db  292 LVKPGASVKKSCASGTFPAHNVHVMVQKPGQGLEMIGITPYDGTNRKNEKFKDKATL 351
Qy  341 TADKSSSTASMELSLTSEDSAVVFCARRGSYDTNYDFVMGCGTTVTVSSGGGGSGG 400
Db  352 TSDKSTTAYWDLSSLASEDSAVVYCARGYKT-----YDWMGGCTTLTVSSGGGGSGG 405
Qy  401 GGGGGGSELVMTQTPVSLPVLGDAQSISCRSSQSLVHNSGNTYLAHWYLOKPGQSPKLL 460
Db  406 GGGGGGGSDVVMQSPVSLPVLGDAQSISCRSSQSLVHNSGKTYLHWYLOKPGQSPKLL 465
Qy  461 IYKSNRFGSDVDFSSGSGTDFLTKSRVREADLGVFCSTHVPYTFGGGKLEIK 520
Db  466 IYKSNRFGSDVDFSSGSGVTDFLTMTSRVREADLGVFCSTHVPYTFGGGKLEIK 525

RESULT 14
AAR56967
ID  AAR56967 standard; Protein: 553 AA.
AC  AAR56967;
XX  14-FEB-1995 (first entry)
DT  CC49 VL-L-VH-L-VH-L-VL.
DE  CC49 VL-L-VH-L-VH-L-VL.
XX  Multivalent single chain antibody; antigen binding site;
KM  diagnosis; peptide linker; variable; light; heavy; VL; VH;
KM  CC antibody; tumour-associated glycoprotein 72 antigen;
KM  TAg-72.
XX  Mus musculus.
OS  Mus musculus.
XX  Key
FH  Location/Qualifiers
FT  Peptide
FT  1..22
FT  /label= sig-peptide
FT  Region
FT  23
FT  /note= "start of VL region"
FT  Region
FT  161
FT  /note= "start of VH region"
FT  Region
FT  301
FT  /note= "start of VH region"
FT  Region
FT  441
FT  /note= "start of VL region"
XX  WO9413806-A.
XX  PN 23-JUN-1994.
XX  PD 23-JUN-1994.
XX  PF 10-DEC-1993; 93WO-US12039.
XX  PR 11-DEC-1992; 92US-0990263.
XX  PA (DOMC ) DOM CHEM CO.
XX  PI Gouille BB, Mezes PS;
XX  WP1; 1994-217882/26.
XX  DR N-PSDB; AAO68660.
XX  PT Multivalent single chain antibodies with two or more active
PT antigen binding sites - are used for use in diagnosis and

```

```

PT therapeutics, reaching their target tissue more rapidly and are
PT cleared more quickly from the body
PS Disclosure: Fig 7; 48pp; English.
XX Multivalent single chain antibodies are formed by using a peptide
CC linker to covalently link two or more single chain antibodies, each
CC single chain antibody having a variable light (VL) domain linked to a
CC variable heavy (VH) chain domain by a peptide linker.
CC The VL and VH domains are pref. obtained from a series of CC
CC antibodies against tumour-associated glycoprotein 72 antigen
CC (TAg-72), eg. see AAO68657 for VL of CC49 and AAO68658 for VH of CC49.
CC The linker is pref. based on the helical linker designated 205C,
CC eg. see AAR56963.
CC Two plasmids were constructed to produce multivalent single
CC chain antibodies. The sequences of p49LHLH and p49LHLH are
CC given in AAO68659-60.
XX SQ Sequence 553 AA;
XX
Query Match 51.3%; Score 1453; DB 15; Length 553;
Best Local Similarity 55.0%; Pred. No. 7.3e-77;
Matches 307; Conservative 63; Mismatches 124; Indels 64; Gaps 9;
Qy 10 LVATATGVHSDIQMTQSPASLSASPEEITVTCQASQDI-----GNMLAWYQOKPGKSP 63
Db 13 ILLAQPMADIVMSQSPSLPVSVEKVTLSCKSSQSLVSGNKNYLAHWYQOKPGQSP 72
Qy 64 QLLIYSAISLADGIRSRFSRSGTQYSLKISRLQVEDTGITYICLQIRSNPMTFGAGTKL 123
Db 73 KLLIYASARRESGVDPDRFTGSGSDTDFLTLSISVKTEDLAVVYCOQYYSYPLTFAGTKL 132
Qy 124 ELKGGGGSGGGGGG-----OVOLQOAGELVKGSSYKISCKASGYFTNY 173
Db 133 VLKSLADDAKKAADAKKDDAKKDDAKKDEVLQOQDAELVKGASVYKISCKASGYFTNH 192
Qy 174 DMHWIKQOPNGLEWIGITYPGNGNTKYNQKENGKATLTADKSSSTAYVQLSLTSEDSA 233
Db 193 AIHWKQNPDEQGLEWIGYFSPGNDPFKYNERRKATLTADKSSSTAYVQLSLTSEDSA 252
Qy 234 VYFCARDMHIYSYTRPFAVYNGGTLVYSSGGGG-----EVLQ 273
Db 253 VYFCRSLN-----MAVWGGGTSTVYVSSLSADDAKKAADAKKDDAKKDEVLQ- 303
Qy 274 LEQSGAELARPGASVKLSCKASGYFTNYGLSMVKORPGOVLEWIGEVPRIGNAYNKE 333
Db 304 LQOQDAELVKGASVYKISCKASGYFTDHAITHVMVQKPGQGLEMIGYFSPGNDPFKYNR 363
Qy 334 FKGAATLTADKSSSTASMELSLTSEDSAVVFCARRGSYDTNYDFVMGCGTTVTVSS 393
Db 364 FKGAATLTADKSSSTAYVQLSLTSEDSAVVFCR--SLNMAV-----WGCGTSTVYSS 415
Qy 394 GGGGGGGGGGGG-----ELVMTQTPVSLPVLGDAQSISCRSSQSLVHNS-NG 442
Db 416 LSADDAKKAADAKKDDAKKDDAKKDDIYVMSQSPSSLPVSGEKVYLTSCSSQSLVYSGNQ 475
Qy 443 NTYLAHWYLOKPGQSPKLLIKVSNRFGSDVDFSSGSGTDFLTKSRVREADLGVFCPS 502
Db 476 KNYLAHWYLOKPGQSPKLLIYMASARESGVDPDRFTGSGGSDTFTLSSVKTEDLAVYCO 535
Qy 503 OSTHVPYTFGGGKLEIK 520
Db 536 QYYSYPLTFGAGTKLVK 553

RESULT 15
AAY05763
ID  AAY05763 standard; Protein: 553 AA.
AC  AAY05763;
XX  19-JUL-1999 (first entry)
XX  DT

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:36:42 ; Search time 43.4467 Seconds
(without alignments)
380.447 Million cell updates/sec

Title: US-09-743-482A-18

Perfect score: 2835
Sequence: 1 MGNSCILFLVATATGVHSD.....GKTKLEIKRTSHHHHHHTS 532

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	949.5	33.5	532	9 US-09-887-853-4	Sequence 4, Appl1
2	867	30.6	535	9 US-09-968-851-38	Sequence 38, Appl1
3	842.5	29.7	249	9 US-10-237-667-18	Sequence 18, Appl1
4	842.5	29.7	249	9 US-09-984-186-18	Sequence 18, Appl1
5	827.5	29.2	256	9 US-10-247-488-2	Sequence 2, Appl1
6	827.5	29.2	258	9 US-10-247-488-4	Sequence 4, Appl1
7	815	28.7	245	9 US-09-991-470-27	Sequence 27, Appl1
8	806.5	28.4	244	9 US-09-940-391-1	Sequence 1, Appl1
9	798	28.1	443	9 US-10-006-771A-2	Sequence 1, Appl1
10	798	28.1	443	9 US-10-006-773-2	Sequence 18, Appl1
11	792	27.9	302	10 US-09-813-659-18	Sequence 18, Appl1
12	791	27.9	302	10 US-09-813-659-32	Sequence 32, Appl1
13	789.5	27.8	249	9 US-09-956-086-2	Sequence 2, Appl1
14	789.5	27.8	249	9 US-09-956-087-2	Sequence 2, Appl1
15	789.5	27.8	601	10 US-09-480-236-1	Sequence 1, Appl1
16	788.5	27.8	257	9 US-09-985-442-2	Sequence 2, Appl1
17	788.5	27.8	257	10 US-09-791-578-4	Sequence 4, Appl1
18	788.5	27.8	257	10 US-09-791-540-4	Sequence 4, Appl1
19	788.5	27.8	257	10 US-09-983-580-2	Sequence 2, Appl1

20	788.5	27.8	269	9 US-09-985-442-4	Sequence 4, Appl1
21	788.5	27.8	269	10 US-09-983-580-4	Sequence 4, Appl1
22	784.5	27.7	274	10 US-09-813-659-30	Sequence 30, Appl1
23	783.5	27.6	241	10 US-09-791-578-6	Sequence 6, Appl1
24	783.5	27.6	241	10 US-09-791-540-6	Sequence 2, Appl1
25	781.5	27.6	246	10 US-09-791-578-2	Sequence 2, Appl1
26	781.5	27.6	246	10 US-09-791-540-2	Sequence 2, Appl1
27	775	27.3	267	10 US-09-766-543-10	Sequence 10, Appl1
28	769.5	27.1	239	10 US-09-808-037-6	Sequence 6, Appl1
29	769	27.1	239	10 US-09-818-247-22	Sequence 22, Appl1
30	766	27.0	269	12 US-10-027-770-5	Sequence 5, Appl1
31	756.5	26.7	240	10 US-09-976-787-28	Sequence 28, Appl1
32	756.5	26.7	240	10 US-09-865-198-27	Sequence 27, Appl1
33	752.5	26.5	238	10 US-09-976-787-29	Sequence 29, Appl1
34	752.5	26.5	238	10 US-09-865-198-28	Sequence 28, Appl1
35	752.5	26.5	269	9 US-09-749-873-109	Sequence 109, Appl1
36	752	26.5	243	10 US-09-924-099-10	Sequence 10, Appl1
37	747	26.3	269	12 US-10-027-770-2	Sequence 2, Appl1
38	737.5	26.0	381	10 US-09-822-658A-5	Sequence 5, Appl1
39	735	25.9	240	9 US-09-968-561A-2	Sequence 2, Appl1
40	735	25.9	240	10 US-09-192-854-2	Sequence 2, Appl1
41	732	25.8	491	12 US-10-011-125-2	Sequence 12, Appl1
42	728	25.7	276	10 US-09-766-543-12	Sequence 12, Appl1
43	728	25.7	669	9 US-09-807-721-2	Sequence 2, Appl1
44	716	25.3	237	10 US-09-924-099-9	Sequence 9, Appl1
45	715.5	25.2	252	10 US-09-971-543-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-887-853-4
Sequence 4, Application US/09887853
Patent No. US20020168375A1

GENERAL INFORMATION:
APPLICANT: Huscon, James S.
Houston, L. L.
Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins for
Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESS: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887,853
FILING DATE: 21-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-887-853-4

Query Match 33.5% Score 949.5; DB 9; Length 252;
Best Local Similarity 74.7%; Pred. No. 1.3e-37;
Matches 189; Conservative 24; Mismatches 33; Indels 7; Gaps 4;

QY 270 EVQLLESGAELVPGASVKSLCKASGYSFTNYGSLWVKQRPGVLEWIGEVPRIGMAY 329
DB 2 EVQLLESGAELVPGASVKSLCKASGYSFTNYGSLWVKQRPGVLEWIGEVPRIGMAY 329
QY 330 YNEFKKATLTADKSSSTASMEIRSLTSDSAVYFCARGSDYDNDVYEDWVGQSTTV 389
DB 61 YNEFKKATLTADKSSSTASMEIRSLTSDSAVYFCARGSDYDNDVYEDWVGQSTTV 389
QY 390 TVSSGGGGSGGSGGSELMVTQPTPLSLPVSLGDAISICRSSQSLVHSGNTYLMNY 449
DB 117 TVSS--SGSSSSSSSSGSDVMTQPTPLSLPVSLGDAISICRSSQSLVHSGNTYLMNY 449
QY 450 LQKPGSPKLLIYKVSNGFVDPDRFGSGSGDTFTLKISRVEAEDLGYFCGSTHVPY 509
DB 175 LQKAGSPKLLIYKVSNGFVDPDRFGSGSGDTFTLKISRVEAEDLGYFCGSTHVPY 509
QY 510 TFGGGRKLEIKRT 522
DB 235 TFGGGRKLEIKRS 247

RESULT 2

US-09-968-851-38
Sequence 38, Application US/09968851
Publication No. US20020193561A1
GENERAL INFORMATION:

APPLICANT: CONSEILLER, EMMANUEL

BRACCO, LAURENT

TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &

DUNNER, LLP

STREET: 1300 I Street, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/968,851

FILING DATE: 03-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/983,035

FILING DATE: 20-Feb-1998

APPLICATION NUMBER: PCT/FR96/01111

FILING DATE: 17-Jul-1996

APPLICATION NUMBER: FR 95/08729

FILING DATE: 19-Jul-1995

ATTORNEY/AGENT INFORMATION:

NAME: Strauss, William L.

REGISTRATION NUMBER: 47,114

REFERENCE/DOCKET NUMBER: 03804.0142

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-968-851-38

Query Match 30.6% Score 867; DB 9; Length 535;
Best Local Similarity 46.4%; Pred. No. 1.5e-33;
Matches 178; Conservative 30; Mismatches 40; Indels 136; Gaps 2;

QY 141 SOVQLDQGAELVPGSSSVKISKASGYFTSDYDMHMIKQPGNGLEWIGWTPGNGNTK 200
DB 2 AOVQLDQGAELVPGSSSVKISKASGYFTSDYDMHMIKQPGNGLEWIGWTPGNGNTK 200
QY 201 YNEFKKATLTADKSSSTASMEIRSLTSDSAVYFCARDMHYSSYIRPPAWGQSTLV 260
DB 62 YNEFKKATLTADKSSSTASMEIRSLTSDSAVYFCARDMHYSSYIRPPAWGQSTLV 260
QY 261 TVSSGGGGSEVQLLESGAELVPGASVKSLCKASGYFTNYGSLWVKQRPGVLEWIG 320
DB 99 -----NFYGA-----L 105
QY 321 YPRIGMAYNEFKKATLTADKSSSTASMEIRSLTSDSAVYFCARGSDYDNDVY 380
DB 99 -----NFYGA-----L 105
QY 381 DVMGQSTTVTVSSGGGGSGGSGGSELMVTQPTPLSLPVSLGDAISICRSSQSLVHS 440
DB 106 DVMGQSTTVTVSSGGGGSGGSGGSDVMTQPTPLSLPVSLGDAISICRSSQSLVHS 440
QY 441 NGNTYLHWYLOKPGSPKLLIYKVSNGFVDPDRFGSGSGDTFTLKISRVEAEDLGY 500
DB 166 DGTLYLWMLQKPGSPKLLIYKVSNGFVDPDRFGSGSGDTFTLKISRVEAEDLGY 500
QY 501 CSQSTHWPTFGGGRKLEIKRTTS 524
DB 226 CSQSTHWPTFGGGRKLEIKRAA 249

RESULT 3

US-10-237-667-18
Sequence 18, Application US/10237667
Publication No. US20030022308A1
GENERAL INFORMATION:

APPLICANT: Fleer, Reinhard

Fournier, Alain

Guitton, Jean-Dominique

Jung, Gerard

Yeh, Patrice

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,

PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION

CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Atcola Road, 3C43

CITY: Collegeville

STATE: PA

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: Macintosh

SOFTWARE: Word 5.1 (Patentin)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/237,667

FILING DATE: 10-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/797,689

FILING DATE: 31-Jan-1997


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;
;      OPERATING SYSTEM: System 7.1
;      SOFTWARE: word 5.1 (Patentin)

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ORGANISM: Humanus
US-10-247-486-2

Db 4 QVQV-LOOSDAELVPCGASVKISCKASGYFTDHAHWHKQPEQGLEMGVSPGNDIK 62
QY 330 YNEKFKGKATLTADKSSSTASMLRLTSDSDAVYFCARGSDYDNDWMVWGQSTV 389
Db 63 YNEKFKGKATLTADKSSSTAYMOLNLTSDSAVYFCKR--SYG-NDY---WGQSTV 115
QY 390 TVSSGGGSGGSGGSGGSELMVMTQPLSLPVSIGDQASISCRSSQSLVHNGNTLHMV 449
Db 116 TVSSGGGSGGSGGSGGSDILTLQSPALLSVSPGERVNSCRASQNI-----GTSIMV 170
QY 450 LQPGGSPKLLIYKVSNRFSGVPDRFSGSGGTDFLTKISRVEADLGVYFCGSDTHVPY 509
Db 171 QQRTNSPRLIKYASVSAGVPSRFRSGSGGTDFLTLSNVESEDYADYCCQHTNSMPT 230
QY 510 TFGGCTKLEIK 520
Db 231 TFGGCTKLEIK 241

RESULT 9
US-10-006-771A-2
Sequence 2, Application US/10006771A
Patent No. US20020165360A1
GENERAL INFORMATION:
APPLICANT: Jungmans, Richard P.
TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
FILE REFERENCE: 002
CURRENT APPLICATION NUMBER: US/10/006, 771A
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 60/250, 090
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 443
TYPE: PRT
ORGANISM: Homo sapiens
US-10-006-771A-2

Query Match 28.1%; Score 798; DB 9; Length 443;
Best Local Similarity 57.4%; Pred. No. 1.9e-30;
Matches 155; Conservative 39; Mismatches 60; Indels 16; Gaps 4;
QY 1 MGMSCTILFLVATATGVSHTDQMTQSPASISASPEIYVTTTCOASODIGNMLAWYQKPG 60
Db 1 MGMSCTILFLVATATGVSHTDQMTQSPASISASVGDRTYTTCKASQDVGTSVAMVQKPG 60
QY 61 KSPQLIYSATSLADGIPSRFSRSGTQYSLKISRLOVEDTGIYVCLQRYSNPTFGAG 120
Db 61 KAPRLIYMTSTRHTGVPSRFSRSGGTDFTTTISLQPEDIATYYC-QQYSLYRSFGG 119
QY 121 TKLELK-GGGGSGGSGGSGGSGGVQLOQSGAELVPCGSSVYKISCKASGYFTSDMHMK 179
Db 120 TKVEIKRGSGSGGSGGSEVQLVESGGGVQVQPSRLSLCSASGDFDTTWMSVVR 179
QY 180 QQPGNGLEWIMWIYPCGNKNTYKNOFKNGKATLTADKSSSTAYMOLNLTSDSAVYFCAR 239
Db 180 QAPKGKLEWIGEIHDPDSSTINVAPELKDRTFISRDNAKNTFLQMDSLRPEDTGVYFCAS 239
QY 240 -----DMHYSSYIRPFAYMGQGLTVYSS 264
Db 240 LYFGFPW-----FAYMGQGLTVYSS 260

RESULT 10
US-10-006-773-2
Sequence 2, Application US/10006773
Patent No. US20020132983A1
GENERAL INFORMATION:
APPLICANT: Jungmans, Richard P.
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Ant
FILE REFERENCE: 003
CURRENT APPLICATION NUMBER: US/10/006, 773

CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/250, 089
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 443
TYPE: PRT
ORGANISM: Homo sapiens and Mus sp.
US-10-006-773-2

Query Match 28.1%; Score 798; DB 12; Length 443;
Best Local Similarity 57.4%; Pred. No. 1.9e-30;
Matches 155; Conservative 39; Mismatches 60; Indels 16; Gaps 4;
QY 1 MGMSCTILFLVATATGVSHTDQMTQSPASISASPEIYVTTTCOASODIGNMLAWYQKPG 60
Db 1 MGMSCTILFLVATATGVSHTDQMTQSPASISASVGDRTYTTCKASQDVGTSVAMVQKPG 60
QY 61 KSPQLIYSATSLADGIPSRFSRSGTQYSLKISRLOVEDTGIYVCLQRYSNPTFGAG 120
Db 61 KAPRLIYMTSTRHTGVPSRFSRSGGTDFTTTISLQPEDIATYYC-QQYSLYRSFGG 119
QY 121 TKLELK-GGGGSGGSGGSGGSGGVQLOQSGAELVPCGSSVYKISCKASGYFTSDMHMK 179
Db 120 TKVEIKRGSGSGGSGGSEVQLVESGGGVQVQPSRLSLCSASGDFDTTWMSVVR 179
QY 180 QQPGNGLEWIMWIYPCGNKNTYKNOFKNGKATLTADKSSSTAYMOLNLTSDSAVYFCAR 239
Db 180 QAPKGKLEWIGEIHDPDSSTINVAPELKDRTFISRDNAKNTFLQMDSLRPEDTGVYFCAS 239
QY 240 -----DMHYSSYIRPFAYMGQGLTVYSS 264
Db 240 LYFGFPW-----FAYMGQGLTVYSS 260

RESULT 11
US-09-813-659-18
Sequence 18, Application US/09813659
Patent No. US20020012989A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden, Martha S.
APPLICANT: Lindsey, Peter S.
APPLICANT: Bajorth, Jürgen
APPLICANT: Gilliland, Lisa K.
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
FILE REFERENCE: 30436, 18USD2
CURRENT APPLICATION NUMBER: US/09/813, 659
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 09/549, 067
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 08/539, 436
PRIOR FILING DATE: 1995-10-05
PRIOR APPLICATION NUMBER: 08/121, 054
PRIOR FILING DATE: 1993-09-13
PRIOR APPLICATION NUMBER: 08/013, 420
PRIOR FILING DATE: 1993-02-01
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 302
TYPE: PRT
ORGANISM: Homo sapiens
US-09-813-659-18

Query Match 27.9%; Score 792; DB 10; Length 302;
Best Local Similarity 58.0%; Pred. No. 2.6e-30;
Matches 174; Conservative 32; Mismatches 74; Indels 20; Gaps 6;

QY 6 ILFLVATATGCHS---DIQMTQSPASISAPETIYITTCASODIGNMLAMYOQKPKGS 62
 Db 7 IFSEFLIASVIMSRGVDIQMTQTTSSLSASLDGRVITISCRASDIRNYLWMOQKPKGT 66
 QY 63 POLLIVATSLADGIPSRFSSRSCTGYSLKISRLQVEDTGICLYCLQRYSNPNTFGAGTK 122
 Db 67 VKLLIYTTSLRHSVSPRFSGSGSDTSLTIANLPEDATYFCQCGNTLPMTFGGGK 126
 QY 123 LELEK---GGGGSGGGSGGGGS--QVOLOOGAELVKGSSVSKISCKASGYFTSYDMHW 177
 Db 127 LVTKRELGGGGSGGGSGGGGSIDEVQLOOGPELVKPGASMTWSCASGYFTGYIVNW 186
 QY 178 IKQOPNGLEWIGIYTGNGNTKYNOKFNGKATLTADKSSSTAYMQLSSTSEDSAVYFC 237
 Db 187 LKOSHGNLEWIGILINPWKGLTYYNOKFKGKATLVKSSSTAYMELLSITSEDSAVYFC 246
 QY 238 ARDWHYSS--YIRPFAYGCGTLVTSSGGGSEVQLLEQSGAELAPGASVLSCKAS 295
 Db 247 ARSGYIGSDMY---FDVWAGTCTVSSPFS-----DQSNSEAKKEAKKEAKKS 296

RESULT 12

US-09-813-659-32
 : Sequence 32, Application US/09813659
 : Patent No. US20020012989A1
 : GENERAL INFORMATION:
 : APPLICANT: Ledbetter, Jeffrey A.
 : APPLICANT: Hayden, Martha S.
 : APPLICANT: Linsley, Peter S.
 : APPLICANT: Rajorath, Jürgen
 : APPLICANT: Pell, H. Perry
 : APPLICANT: Gilliland, Lisa K.
 : TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BIOLOGICALLY ACTIVE FUSION PROTEINS
 : TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
 : FILE REFERENCE: 30436.18USD2
 : CURRENT APPLICATION NUMBER: US/09/813.659
 : FILING DATE: 2001-03-21
 : PRIOR APPLICATION NUMBER: 09/549.067
 : FILING DATE: 2000-04-13
 : PRIOR APPLICATION NUMBER: 08/539.436
 : FILING DATE: 1995-10-05
 : PRIOR APPLICATION NUMBER: 08/121.054
 : FILING DATE: 1993-09-13
 : PRIOR APPLICATION NUMBER: 08/013.420
 : FILING DATE: 1993-02-01
 : NUMBER OF SEQ ID NOS: 32
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO: 32
 : LENGTH: 302
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-09-813-659-32

Query Match 27.9%; Score 791; DB 10; Length 302;

Best Local Similarity 58.0%; Pred. No. 2.9e-30;

Matches 174; Conservative 32; Mismatches 74; Indels 20; Gaps 6;

QY 6 ILFLVATATGCHS---DIQMTQSPASISAPETIYITTCASODIGNMLAMYOQKPKGS 62
 Db 7 IFSEFLIASVIMSRGVDIQMTQTTSSLSASLDGRVITISCRASDIRNYLWMOQKPKGT 66
 QY 63 POLLIVATSLADGIPSRFSSRSCTGYSLKISRLQVEDTGICLYCLQRYSNPNTFGAGTK 122
 Db 67 VKLLIYTTSLRHSVSPRFSGSGSDTSLTIANLPEDATYFCQCGNTLPMTFGGGK 126
 QY 123 LELEK---GGGGSGGGSGGGGS--QVOLOOGAELVKGSSVSKISCKASGYFTSYDMHW 177
 Db 127 LVTKRELGGGGSGGGSGGGGSIDEVQLOOGPELVKPGASMTWSCASGYFTGYIVNW 186
 QY 178 IKQOPNGLEWIGIYTGNGNTKYNOKFNGKATLTADKSSSTAYMQLSSTSEDSAVYFC 237
 Db 187 LKOSHGNLEWIGILINPWKGLTYYNOKFKGKATLVKSSSTAYMELLSITSEDSAVYFC 246

QY 238 ARDWHYSS--YIRPFAYGCGTLVTSSGGGSEVQLLEQSGAELAPGASVLSCKAS 295
 Db 247 ARSGYIGSDMY---FDVWAGTCTVSSPFS-----DQSNSEAKKEAKKEAKKS 296

RESULT 13

US-09-956-086-2
 : Sequence 2, Application US/09956086
 : Patent No. US20020155498A1
 : GENERAL INFORMATION:
 : APPLICANT: FILPULA, DAVID
 : APPLICANT: WANG, MAOLIANG
 : APPLICANT: SHORR, ROBERT
 : APPLICANT: WHITLOW, MARC
 : LEE, LIHSYNG S.

TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS

CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF

NUMBER OF SEQUENCES: 33

ADDRESS/SEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/956.086

FILING DATE: 20-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/069.821

FILING DATE: <Unknown>

APPLICATION NUMBER: US 60/063.074

FILING DATE: 27-OCT-1997

APPLICATION NUMBER: US 60/050.472

FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/044.449

FILING DATE: 30-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0977.2280003

TELEPHONE: (202)371-2600

TELEFAX: (202)371-2540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 249 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-956-086-2

Query Match 27.8%; Score 789.5; DB 9; Length 249;

Best Local Similarity 61.0%; Pred. No. 3e-30;

Matches 155; Conservative 32; Mismatches 50; Indels 17; Gaps 3;

QY 20 DIQMTQSPASISAPETIYITTCASODI-----GNMLAMYOQKPKSPOLLIVATSL 73
 Db 1 DYVMSQSPSSLPVSGKATVLSCKSSQSLXSGNOKNYLANYOQKPKQSRKLLITYMASAR 60
 QY 74 ADGIPSRFSSRSCTGYSLKISRLQVEDTGICLYCLQRYSNPNTFGAGTKLELG---GGC 130
 Db 61 ESGVDPDRFTSGSGCTDFTLSISSVKTEDLAVVYCOQYYSVPLRFGAGTKLVKSGTSGSG 120
 QY 131 SGGGSGGGSGGQVOLOOGAELVKGSSVSKISCKASGYFTSYDMHWIKQOPNGLEWIG 190

Oy 393 SCG 395
: 1
Db 399 TRG 401

Search completed: February 25, 2003, 10:57:22
Job time : 45.4467 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58; Search time 59.4067 Seconds
(without alignments)
263,489 Million cell updates/sec

Title: US-09-743-482A-18

Perfect score: 2835
Sequence: 1 MGWSCIPLFLVATATGVHSD.....GCKLEIKRTTHHHHHHTS 532

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents, AA:*
1: /cgn2.6/ptodata/1/aa/5A.COMB.pep:*
2: /cgn2.6/ptodata/1/aa/5B.COMB.pep:*
3: /cgn2.6/ptodata/1/aa/6A.COMB.pep:*
4: /cgn2.6/ptodata/1/aa/6B.COMB.pep:*
5: /cgn2.6/ptodata/1/aa/PCITUS.COMB.pep:*
6: /cgn2.6/ptodata/1/aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1453	51.3	553	2	US-08-263-911-9 Sequence 9, Appl1
2	1172.5	41.4	553	2	US-08-661-052-16 Sequence 16, Appl1
3	1172.5	41.4	553	4	US-09-188-082-16 Sequence 16, Appl1
4	1172.5	41.4	553	4	US-09-364-088-16 Sequence 16, Appl1
5	1172.5	41.4	553	4	US-09-102-716-16 Sequence 85, Appl1
6	1112	39.2	541	4	US-09-485-737B-85 Sequence 19, Appl1
7	1102	38.9	483	2	US-08-392-338A-19 Sequence 19, Appl1
8	1102	38.9	483	3	US-09-166-750-19 Sequence 19, Appl1
9	1102	38.9	483	3	US-09-166-093-19 Sequence 19, Appl1
10	1102	38.9	483	3	US-09-172-019-19 Sequence 19, Appl1
11	1102	38.9	483	3	US-09-166-094-19 Sequence 19, Appl1
12	1057	37.3	553	2	US-08-263-911-7 Sequence 7, Appl1
13	1057	37.3	553	2	US-08-263-911-7 Sequence 7, Appl1
14	995.5	35.1	711	4	US-09-485-737B-90 Sequence 90, Appl1
15	976.5	34.4	269	4	US-09-070-408-132 Sequence 132, App
16	949.5	33.5	252	1	US-08-133-804-4 Sequence 4, Appl1
17	949.5	33.5	252	1	US-08-461-838-4 Sequence 4, Appl1
18	948.5	33.5	252	2	US-08-461-838-4 Sequence 4, Appl1
19	948.5	33.5	252	2	US-08-461-838-4 Sequence 4, Appl1
20	948.5	33.5	252	2	US-08-461-838-4 Sequence 4, Appl1
21	926	32.7	288	4	US-09-423-439-38 Sequence 38, Appl1
22	912.5	32.2	260	4	US-08-447-402-1 Sequence 1, Appl1
23	888	31.3	673	4	US-09-423-439-32 Sequence 32, Appl1
24	879.5	31.0	263	2	US-08-752-844-66 Sequence 66, Appl1
25	873.5	30.8	247	4	US-09-227-693-34 Sequence 34, Appl1
26	873.5	30.8	248	1	US-08-331-398A-34 Sequence 34, Appl1
27	873.5	30.8	248	2	US-08-331-397B-34 Sequence 34, Appl1

28	873.5	30.8	248	2	US-08-759-804A-34 Sequence 34, Appl1
29	869.5	30.7	366	3	US-08-875-811-53 Sequence 53, Appl1
30	869.5	30.7	366	3	US-08-875-811-53 Sequence 55, Appl1
31	867	30.6	535	4	US-08-983-035A-38 Sequence 38, Appl1
32	863	30.4	495	4	US-08-828-741B-4 Sequence 4, Appl1
33	863	30.4	495	4	US-09-160-567-4 Sequence 4, Appl1
34	843.5	29.8	281	4	US-09-025-769B-178 Sequence 178, App
35	842.5	29.7	249	2	US-08-797-689-18 Sequence 18, Appl1
36	841.5	29.7	273	2	US-08-403-853-18 Sequence 18, Appl1
37	836.5	29.5	243	1	US-08-230-843-4 Sequence 4, Appl1
38	836.5	29.5	243	2	US-08-636-936-4 Sequence 4, Appl1
39	835.5	29.5	244	2	US-08-553-497A-20 Sequence 20, Appl1
40	831.5	29.3	599	1	US-08-463-163-3 Sequence 3, Appl1
41	830	29.3	239	4	US-08-279-772A-8 Sequence 8, Appl1
42	830	29.3	239	4	US-08-902-486-11 Sequence 11, Appl1
43	830	29.3	355	3	US-08-875-811-41 Sequence 41, Appl1
44	830	29.3	355	3	US-08-875-811-49 Sequence 49, Appl1
45	830	29.3	355	3	US-08-875-811-64 Sequence 64, Appl1

ALIGNMENTS

RESULT 1
US-08-263-911-9
; Sequence 9, Application US/08263911
; Patent No. 5877291

GENERAL INFORMATION:

APPLICANT: Mezes, Peter S
APPLICANT: Courille, Brian B

TITLE OF INVENTION: MULTIVALENT SINGLE CHAIN ANTIBODIES

NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967

CITY: Midland
STATE: MI

COUNTRY: US
ZIP: 48641-1967

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/263,911
FILING DATE: 21-JUN-1994

CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/990,263
FILING DATE: 11-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: Ulmer, Duane C

REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-41, 014

TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: Protein

LOCATION: 23
US-08-263-911-9

Query Match 51.3%; Score 1453; DB 2; Length 553;
Best Local Similarity 55.0%; Pred. No. 1,7e-94;
Matches 307; Conservative 63; Mismatches 124; Indels 64; Gaps 9;

QY 10 LVATATGVHSDIOMTOSFASLSASBPDELIVTTTCASODI-----GNLWATYQKPKGSP 63

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; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-661-052-16

Query Match
Best Local Similarity 41.4%; Score 1172.5; DB 2; Length 553;
Matches 260; Conservative 86; Mismatches 158; Indels 75; Gaps 18;

1 MGSCLIFLAVATGATVSHDIDMTOSPASLSAPEIYITTCQASODI--GNMLAWYQOK 58
1 MGSCLIFLAVATGATVSHDIDLVESGGV--VQPSRLRLSCSSSGFIISDNMYWYRQA 59
59 PKSPQLIY-----SATSLADGIPRSRSGSRGTQYS--LKISRLQVEDTGTYCLORY 111
60 PKGLEWATTISDGSSTYTPDYSVGRFTISRDNKNTLFLQMDSLRPEDTGFFCARGY 119
112 ----SNPRTFGAGTKLEL-KGGGSGSGSGSGGSGGSOVLOOGAEL-VKPSYSKISCKA 165
120 YREBAMDWGOGTYVTVSSGGGSGSGSGGSGGSDIDLTSPSSLSASVGDRTYITCKS 179
166 SGYFTSYD---MMIKQOPNGLEWIGWYKPGNTRYNOKFNKATLTADKSSSTAY 221
180 SQSVLYSSNOKMYLAWYQOKPGKAPKLITY--MASRREGSVRSRSGS-----SGTDF 232
222 MQLSLTSEDSNVYFCADMHYSSYIRPEAWGQGLTVY----SSGGGSEVOLLQOS 277
233 FTISLQPEDATYTYCHQ---YLSMT-----FQGTKEVLEKSSCGGSGSDIK-LQOS 283
278 GAELARPASVYKLSKASGYTFYNGLSVWKORPGOVLEWIGEYPRIGNAYYKFKGK 337
284 GAELVRSSTVYKLSGASGFNIKDSYMHMLRQGEGLWIGMIDPENGDIEYAPKQOK 343
338 ATLTDKSSSTASMEIQLTSEDSAVYFCARGSYDTNYDWYFDWOGGTYTVSSGGG 397
344 ATFTTDTSSNTAYLQSLTSEDTAYVYCC--NEGTPTPGY--YFDYWGOGTYTVSSGGG 400
398 SGGGSGGSGSELVMTQPLSLPVSLDQASISCRSSOSLVHNSGNTYLMYLOKPGOSP 457
401 SGGGSGGSGSENVLTQSPALMSAPGKVTITTSASSSV-----SYMHPQOKPGTSP 454
458 KLIYKVSNRFSGVPDRFSGSGGTDFTLKISRVEADLVGYFCSQSTHYPTFGGCTKL 517
455 KLWYISTNLASGVPARFSGSGSTSYSLTISRMEADATAYYCOQSSVPLTFGAGTKL 514
518 EIKRT-----TSIHNNH 530
515 ELKRAAGSGGGGSDIAAEOKLISEEDLNGAAHHNNH 553

; RESULT 3
; US-09-188-082-16
; Sequence 16, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Grazianno
; APPLICANT: Chezia Somsundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Bech E.
; REGISTRATION NUMBER: 35,430

```

```

; RESULT 2
; US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Grazianno
; APPLICANT: Chezia Somsundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Bech E.
; REGISTRATION NUMBER: 35,430

```


STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-188-082-16

Query Match 41.4%; Score 1172.5; DB 4; Length 553;
Best Local Similarity 44.9%; Pred. No. 8,1e-75;
Matches 260; Conservative 86; Mismatches 158; Indels 75; Gaps 18;

QY 1 MGSCTILFLVATATGVSDIOMQSPASLSPEEIVITTOASODI--GNLWLMYQOK 58
DB 1 MGSCTILFLVATATGVSDIQLVESGGGV-VQPGSLRLSSGSGFISDMYMWVRA 59
QY 59 PGKSPOLLY-----SATSLADGIPSRFSGSRSTQYS--LKISRLOVEDTGYYCLQRY 111
DB 60 PGKGLEWATISDGSYYTPDVKRGFTISRNSKNTFLQMDSLRPEDTGVYFCARG 119
QY 112 ----SNPTFGAGTKLEL-KGGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 165
DB 120 YRECAMYWGQGTPTVYSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 179
QY 166 SGYTFISYD---MHMIOQPGNGLEWIGMITYGNGNTKYNOKFNKATLTADKSSSTAY 221
DB 180 SOSVLVSSNOKNYLAWYQOKPGKAPKLLY--WASTRESGVPSRFGSG-----SGTDFT 232
QY 222 MQLSLTSEDSAVYFCARDMHHYSSYIRPFAYWGGTTLTVY-----SSGGGSEVOLLEOS 277
DB 233 FTISSLQPEDIAITYCHQ---YLSMT-----FGGKTVEIKSSCGSGGGGSDIK-LQOS 283
QY 278 GAELARPGASVKSCKASGYTFTNYGLSWVKQRPQGVLEWIGEVYPRIGMAYNEKFKG 337
DB 284 GAELVRSSTSVKLSCTASGFNIKDSYHMLRQGPQGLEWIGIDPENGDTVYAPRFOGK 343
QY 338 ATLTDKSSSTASMLRSLTSEDSAVYFCARGSYDTNTDMYFDWGGGTTVYSSGGGG 397
DB 344 ATFTDTSNTAYLQLSLTSEDTAVYVC--NEGTPTPPY--YEDYWGQGTITVYSSGGGG 400
QY 398 SGGGSGGGGGSELVMTQPLSLPVSLGDQASISCRSSQSLVHNSNGTYLHWLQKGGP 457
DB 401 SGGGSGGGGGSENVLTQSAIAMSABGEKVTITCSASSV-----SYHMHVQOKRGTSP 454
QY 458 KLLIVKSNRFGVDRPDRFSGSGGTDFTLKISRVEAEDGAGVYFCGSSTHPVPTFGGKTL 517
DB 455 KLMTVSTSLASGVARFARFSGSGGTSYSLTISRMEADAATAYYCCQGRSSYPLTFGAGTKL 514
QY 518 ELKRT-----TSHHHHH 530
DB 515 ELKRAAGSGGGGSDIAAEOKLISEEDLNGAHHHHH 553

RESULT 4
US-09-364-088-16

Sequence 16, Application US/09364088
Patent No. 6365161

GENERAL INFORMATION:

APPLICANT: Yashwant M. Deo, et al.

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED

TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street, 24th floor

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/364,088

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/188,082

FILING DATE: 07-JUNE-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/484,172

FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Remillard, Jane E.

REGISTRATION NUMBER: 38,872

REFERENCE/DOCKET NUMBER: MXI-043CP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-7414

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-364-088-16

Query Match 41.4%; Score 1172.5; DB 4; Length 553;
Best Local Similarity 44.9%; Pred. No. 8,1e-75;
Matches 260; Conservative 86; Mismatches 158; Indels 75; Gaps 18;

QY 1 MGSCTILFLVATATGVSDIOMQSPASLSPEEIVITTOASODI--GNLWLMYQOK 58
DB 1 MGSCTILFLVATATGVSDIQLVESGGGV-VQPGSLRLSSGSGFISDMYMWVRA 59
QY 59 PGKSPOLLY-----SATSLADGIPSRFSGSRSTQYS--LKISRLOVEDTGYYCLQRY 111
DB 60 PGKGLEWATISDGSYYTPDVKRGFTISRNSKNTFLQMDSLRPEDTGVYFCARG 119
QY 112 ----SNPTFGAGTKLEL-KGGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 165
DB 120 YRECAMYWGQGTPTVYSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 179
QY 166 SGYTFISYD---MHMIOQPGNGLEWIGMITYGNGNTKYNOKFNKATLTADKSSSTAY 221
DB 180 SOSVLVSSNOKNYLAWYQOKPGKAPKLLY--WASTRESGVPSRFGSG-----SGTDFT 232
QY 222 MQLSLTSEDSAVYFCARDMHHYSSYIRPFAYWGGTTLTVY-----SSGGGSEVOLLEOS 277
DB 233 FTISSLQPEDIAITYCHQ---YLSMT-----FGGKTVEIKSSCGSGGGGSDIK-LQOS 283
QY 278 GAELARPGASVKSCKASGYTFTNYGLSWVKQRPQGVLEWIGEVYPRIGMAYNEKFKG 337
DB 284 GAELVRSSTSVKLSCTASGFNIKDSYHMLRQGPQGLEWIGIDPENGDTVYAPRFOGK 343

ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/166,750
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/392,338
 FILING DATE: 22-FEB-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/989,846
 FILING DATE: 20-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/796,936
 FILING DATE: 25-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Goldstein, Jorge A.
 REGISTRATION NUMBER: 29,021
 REFERENCE/DOCKET NUMBER: 0977.003000C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 483 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-166-750-19

Query Match 38.9%; Score 1102; DB 3; Length 483;
 Best Local Similarity 47.4%; Pred. No. 6.1e-70;
 Matches 237; Conservative 45; Mismatches 74; Indels 144; Gaps 7;

20 DIOMTOSPASISASPEEIVITTCASODI-----GNWLAWYQOKPGKSPOLITYATSU 73
 1 DVWMSQSPSSLPVSGEYVTLSCSSOSLYSGNOKNYLAWYQOKPGKSPKLLITYWASAR 60
 74 ADGIPSRFSRSGTQYSLKISRLQVEDTGIIYCLORYSNPMTFGAGTLELEKGGGSGG 133
 61 ESGVPRFTGSGGDTFTLSSSVKTEDLAVYYCOQYISYPLTFAGTKLYLK -GSTSGS 119
 134 GSGGGGSGVOLOQSGAEVLKPGSSVKISCKASGYTFTSYDMHWIKOOPGNGLEWIGIT 193
 120 GKSSGKGQVLOQSDALVPGASVKISCKASGYTFDHAIHWKONPEOGLWIGIFS 179
 194 PGNGTKYKQKFNKATLTADKSSSTAYMOLSLTSEDSAVYFCARDMHHYSSYIRPFAY 253
 180 PGNDKFNKFNKATLTADKSSSTAYVOLNSLTSEDSAVYFCSTRLN-----MAY 231
 254 WGQGTLYTVSS----- 264
 232 WGQGTLYTVSSDVWMSQSPSSLPVSGEYVTLSCSSOSLYSGNOKNYLAWYQOKPGS 291
 265 -----GGGSGSEVL----- 273
 292 PKLLIYMASARESVPDRFTGSGSGDTFTLSSSVKTEDLAVYYCOQYISYPLTFAGTK 351
 274 -----LEQSGAEIARPGASVKISCKASGYTFTNYGLSNWKORPG 312
 352 LVLKSTGSGKSGSGKQVLOQSDALVPGASVKISCKASGYTFDHAIHWKONPE 411
 313 QVLEWIGEVYPRIGMAVYNEFKKATLTADKSSSTAYMELRSLTSEDSAVYFCARRGSY 372
 412 OGLMIGIFSGNDKFNKFNKATLTADKSSSTAYVOLNSLTSEDSAVYFCSTR--SL 469
 373 DTNDWTFDVGQGTLYTVSS 392
 470 NMAY-----WGQGTLYTVSS 483

RESULT 9
 US-09-166-093-19

; Sequence 19, Application US/09166093
 ; Patent No. 6027725

GENERAL INFORMATION:

APPLICANT: Whilow, Marc

APPLICANT: Wood, James F.

APPLICANT: Hardman, Karl

APPLICANT: Bird, Robert

APPLICANT: Rolence, David

TITLE OF INVENTION: Multivalent Antigen-Binding Proteins

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

STREET: Sterne, Kessler, Goldstein & Fox P.L.L.C.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/166,093

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/392,338

FILING DATE: 22-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/989,846

FILING DATE: 20-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/796,936

FILING DATE: 25-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Goldstein, Jorge A.

REGISTRATION NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 0977.003000B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 483 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-166-093-19

Query Match

Best Local Similarity 38.9%; Score 1102; DB 3; Length 483;
 Matches 237; Conservative 45; Mismatches 74; Indels 144; Gaps 7;

20 DIOMTOSPASISASPEEIVITTCASODI-----GNWLAWYQOKPGKSPOLITYATSU 73
 1 DVWMSQSPSSLPVSGEYVTLSCSSOSLYSGNOKNYLAWYQOKPGKSPKLLITYWASAR 60
 74 ADGIPSRFSRSGTQYSLKISRLQVEDTGIIYCLORYSNPMTFGAGTLELEKGGGSGG 133
 61 ESGVPRFTGSGGDTFTLSSSVKTEDLAVYYCOQYISYPLTFAGTKLYLK -GSTSGS 119
 134 GSGGGGSGVOLOQSGAEVLKPGSSVKISCKASGYTFTSYDMHWIKOOPGNGLEWIGIT 193
 120 GKSSGKGQVLOQSDALVPGASVKISCKASGYTFDHAIHWKONPEOGLWIGIFS 179
 194 PGNGTKYKQKFNKATLTADKSSSTAYMOLSLTSEDSAVYFCARDMHHYSSYIRPFAY 253

Db 180 PGNDFFKYNREKFKATLTADKSSSTAYVOLNLSLSEDSAVYFCTRLN-----MAY 231
QY 254 WGGTTLTVSS----- 264
Db 232 WGGTSTVSSDVVMSQSPSSLPVSGEKVTLCKSSQSLISGNQKNLAWYQKPGQS 291
QY 265 -----GGGSEVOL----- 273
Db 292 PKLLIYMASARESGVPDRFTGSGSCTDFTLSSSVKTEDLAVYCCQYYSYPLTFGAGTK 351
QY 274 -----LEQSGAELARPGASVKLSCKASGYTFNTNGLSWKQRP 312
Db 352 LVLKSTSGSGKSEKSGQVQLQSDAELVKGASVKISCKASGYTFDHAHWKQNP 411
QY 313 QVLEWIGEVYPRIGNAYNNEKFKATLTADKSSSTASMEKLSLSEDSAVYFCARRGSY 372
Db 412 QGLEWIGYFSGNDFFKYNREKFKATLTADKSSSTAYVOLNLSLSEDSAVYFCTRLN-----SL 469
QY 373 DTNYDMYEDVWGQGTTVTS 392
Db 470 NMAY-----WGGTSTVTS 483

RESULT 10
US-09-172-019-19
; Sequence 19, Application US/09172019
; Patent No. 6103889
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
; TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/172.019
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-172-019-19
Query Match 38.9% Score 1102; DB 3; Length 483;
Best Local Similarity 47.4%; Pred. No. 6.1e-70;
Matches 237; Conservative 45; Mismatches 74; Indels 144; Gaps 7;
QY 20 DIOMTQSPASLASPEEIVTTTCQASQDI-----GNMLAWYQKPGKSPOLLISATS 73
Db 1 DVMSQSPSSLPVSGEKVTLCKSSQSLISGNQKNLAWYQKPGKSPKLLIYMASAR 60
QY 74 ADGIPRFSRSGRSTQYSLKISRLQVEDTGIYCLQRYSNPNTFCAGTKLEKGGGSGG 133
Db 61 EGVGDRFTGSGSCTDFTLSSSVKTEDLAVYCCQYYSYPLTFGAGTKLYLK-GSTSGS 119
QY 134 GSGGSGSOVQLQSDAELVKGASVKISCKASGYTFNTNGLSWKQRP 193
Db 120 GKSSGKGOVQLQSDAELVKGASVKISCKASGYTFDHAHWKQNP 179
QY 194 PGNDFFKYNREKFKATLTADKSSSTAYVOLNLSLSEDSAVYFCARRGSY 253
Db 180 PGNDFFKYNREKFKATLTADKSSSTAYVOLNLSLSEDSAVYFCTRLN-----MAY 231
QY 254 WGGTTLTVSS----- 264
Db 232 WGGTSTVSSDVVMSQSPSSLPVSGEKVTLCKSSQSLISGNQKNLAWYQKPGQS 291
QY 265 -----GGGSEVOL----- 273
Db 292 PKLLIYMASARESGVPDRFTGSGSCTDFTLSSSVKTEDLAVYCCQYYSYPLTFGAGTK 351
QY 274 -----LEQSGAELARPGASVKLSCKASGYTFNTNGLSWKQRP 312
Db 352 LVLKSTSGSGKSEKSGQVQLQSDAELVKGASVKISCKASGYTFDHAHWKQNP 411
QY 313 QVLEWIGEVYPRIGNAYNNEKFKATLTADKSSSTASMEKLSLSEDSAVYFCARRGSY 372
Db 412 QGLEWIGYFSGNDFFKYNREKFKATLTADKSSSTAYVOLNLSLSEDSAVYFCTRLN-----SL 469
QY 373 DTNYDMYEDVWGQGTTVTS 392
Db 470 NMAY-----WGGTSTVTS 483

RESULT 11
US-09-166-094-19
; Sequence 19, Application US/09166094
; Patent No. 6121424
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rolence, Michelle
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166.094
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

[illegible]

```
Db      366 DRFTGSGSGTDFTLSSSVKTEDLAVYYCQQYSPPLTFGAGTKLVLK 413
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RESULT 13
US-09-485-737B-90
Sequence 00 Application US/09485737B

Query Match	35.1%	Score 995.5	DB 4	Length 711
Best Local Similarity	31.4%	Pred. NO. 2.8e-62		
Matches 223	Conservative 56	Mismatches 83	Indels 349	Gaps 5

QY	141	SOVOLQOAGALVYRGSSVKTISCKASGYTFPSYMHNTIKOOPGGLMIGIMTIPGNTK	200
Db	20	SOVOLVQSGSELKPRGASVKISCKASGYTFPDYGMNWKQAPRGGLKMWGMINTYGEEST	79
QY	201	YNQFNCKATLTADKSSSTAYMOLSLTSEDSAYVFCARIDNHYYSXIRFPAYWGQSTLV	260
Db	80	YVDPEKGRFVPSLDTSVSAAYLQISLKAEDTATYFCARRFY-----AMDWQGGSTTV	133
QY	261	TVSSG-----	265
Db	134	TVSSASTKGPVFPFLAPSSKSTSGTALGCLVNDYPERPVTVSMNSGALSGVHTPRAY	133
QY	266	-----	265
Db	194	LOSSGLYSLSSVTVTPSSLSGTQTYICNVNHPKPSNTYVDKRVKPPSCDKTHTPCPRAPE	253
QY	266	-----	265
Db	254	LLGGPVFLFPKPKDPLIMISRTPEYVCYVVDVSHEDREYKFNKYVGVGEVHNNAKTKPRE	313
QY	266	-----	265
Db	314	EQYNSTYRVVSVLTVLHODMVLNGKEFKCKVSNKALPASIEKTISSAKAGPREPOVYTLPR	373
QY	266	-----	265
Db	374	SREEMTKNQVSLTCLVLNGEYPSDIAVEMESNGORENNYKTTTPRYLSDSGSFILYSKLTVLD	433
QY	266	-----GGSEVQLLEQSGAELTARPGASVKL	290
Db	434	KSRRQAGVNFSCSYMHNELHNHTYQKSLSPKGLGGGSOYOLV-QSGSELKPRGASVKI	422
QY	291	SCKASGYTFPTYGLSWVKQRPQGVLEWIGEYYPRIQNAUYNEKEKFKATLTADKSSSTAS	350
Db	493	SCKASGYTFPTYGMNWKQAPRGGLKMWGMINTYGEESTVVDPEKGRFVPSLDTSVSAAY	552
QY	351	MELASLTSEDSAYVFCARRGSYDTINPTWYEDWQGGSTTVVSSGGGGGGGGGGGGGSEL	410

[illegible]

RESULT 14
US-09-070-408-132
; Sequence 132, Application US/09070408
Reference: 6100341

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1  COMPUTER READABLE FORM:
2
3  MEDIUM TYPE: Floppy disk
4
5  COMPUTER: IBM PC compatible
6
7  OPERATING SYSTEM: PC-DOS/MS-DOS
8
9  SOFTWARE: PatentIn Release #1.0, Version #1.30
10
11 CURRENT APPLICATION DATA:

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? INFORMATION FOR SEQ ID NO: 132
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 269 amino acids
?
? TYPE: amino acid
?
? STRADEDNESS:
?
? TOPOLOGY: linear
?
US-09-070-408-132

```

Query Match	34.4%	Score 976.5:	DB 4:	Length 269;
Best Local Similarity	69.6%	Pred No. 2e-61:		
Matches 190;	Conservative 29;	Mismatches 37;	Indels 17;	Caps 4

Oy	270	EVLLEGGAGELARPGASVUKISCSAGTTPFNNGYSWKOPGGOVLMEIGEVYRISNAY	3228
Dd	2	EVO--LQSGPELVKRGASVRSSSGSITFDFFYNWNRQSHGSALDITGITSPYSCVTG	60
Oy	330	YNEFKKGATLTLPADSSSTASMELRLTSEDSAVYFCARGSYDTNYDFWVGOGCTJV	389
Dd	61	YNOKFKGATILTVDKSSSTAYMELRLTSEDSAVYYCA--GS--SGKNMADTWGHGASV	116
Oy	390	TVSGGGSGSGGGGSELMTOTPLSLPVSJGDQASISCRSSOSLYVNSNGWTJLHMY	449
Dd	117	TVSSGGGSGSGGGGSDIVLTQTPEPSLPVSLGDAQTISRSSOSLYVNSNGWTJLANMT	176

QY 450 LKPGOSPKLLIYVSNFSGVDPDRFSGSGSGTDTFTLKISRVEAEDLGVFCOSQTHVPY 509
Db 177 LKAGOSPKLLIYVSNFSGVDPDRFSGSGSGTDTFTLKISRVEAEDLGVFCOSQTHVP 236
QY 510 TFGGSKLEIKRT-----SHHHH 530
Db 237 TFGGSKLEIKRTASQPELAPEDPEDEHHHH 269

Db 235 TFGGSKLEIKRS 247

Search completed: February 25, 2003, 10:38:48
Job time : 62.4067 secs

RESULT 15
US-08-133-804-4
; Sequence 4, Application US/08133804
; Patent No. 5534254
GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ. ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-133-804-4

Query Match 33.5%; Score 949.5; DB 1: Length 252;
Best Local Similarity 74.7%; Pred. No. 1.5e-59;
Matches 189; Conservative 24; Mismatches 33; Indels 7; Gaps 4;

QY 270 EYLLQSGAELARPGASVYKLSKASGYFTNYGLSWKQRPQOVLEWIGEVYPRIGNAV 329
Db 2 EYQ-LQSGPELVKPGASVYKLSKASGYFTDFYMWVWQSHGKSLDYIGYISPYSGVTG 60
QY 330 YNEKFKATLTADKSSSTYASWELSLTSEDAVYFCARAGSYDTNYDYFDVWGQTTV 389
Db 61 YNOKFKATLTVDKSSSTATWELSLTSEDAVYVYCA--GS--SGNKWAMDYWGCHASV 116
QY 390 TVSSGGGSGGGGSELVMTQPLSLPYSLGDAISICRSSOSLVHSGNTYLMWY 449
Db 117 TVSS--SGSSSSSSSSSDVDMTQPLSLPYSLGDAISICRSSOSLVHSGNTYLMWY 174
QY 450 LKPGOSPKLLIYVSNFSGVDPDRFSGSGSGTDTFTLKISRVEAEDLGVFCOSQTHVPY 509
Db 175 LKAGOSPKLLIYVSNFSGVDPDRFSGSGSGTDTFTLKISRVEAEDLGVFCOSQTHVP 234
QY 510 TFGGSKLEIKRT 522

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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:30:10 : Search time 46 Seconds
(without alignments)
20.899 Million cell updates/sec

Title: US-09-743-482a-8
Perfect score: 59
Sequence: 1 GYTFSTYDMH 10

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_73:*
2: pir1:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	40.7	10	2	D61440 polygalacturonase
2	20	33.9	9	2	A24244 adipokinetic hormo
3	20	33.9	10	2	S74176 gluconokinase (EC
4	19	32.2	10	1	SPPGNK neuromedin K - pig
5	18	30.5	9	2	A61230 calsequestrin, car
6	18	30.5	9	2	S36850 Ig heavy chain V r
7	18	30.5	9	2	G85802 hypothetlcal prote
8	18	30.5	10	2	S62208 polyferredoxin - M
9	17	28.8	7	2	A60139 fatty-acid synthas
10	17	28.8	7	2	S11078 glucose-6-phosphat
11	16	27.1	8	2	S08996 hypertrehalosemic
12	16	27.1	8	2	B49823 adipokinetic hormo
13	16	27.1	8	2	B44960 neuropeptide led-C
14	16	27.1	8	2	A33995 adipokinetic hormo
15	16	27.1	8	2	PH0803 T-cell receptor al
16	16	27.1	9	2	PT0231 Ig heavy chain CDR
17	16	27.1	10	2	JC1416 hypertrehalosemic
18	16	27.1	10	2	S09138 hypertrehalosemic
19	16	27.1	10	2	A31571 hypertrehalosemic/
20	16	27.1	10	2	B33995 hypertrehalosemic/
21	16	27.1	10	2	B61440 polygalacturonase
22	15	25.4	6	2	PT0693 T-cell receptor be
23	15	25.4	8	2	J50315 leucokinin V - Mad
24	15	25.4	9	2	A11497 fructose-bisphosph
25	15	25.4	9	2	A28924 thrombospondin 2 -
26	15	25.4	10	2	C45474 sperm-activating p
27	15	25.4	10	2	E60589 S-layer protein -
28	15	25.4	10	2	A60476 triose-phosphate 1
29	15	25.4	10	2	A27617

30	15	25.4	10	2	C61440 polygalacturonase
31	15	25.4	10	2	S62880 polygalacturonase
32	14	23.7	5	3	JT0870 phytoosulfoxine alp
33	14	23.7	6	2	A61411 amelelin - rat
34	14	23.7	7	1	NP67 hypothalamic hepta
35	14	23.7	7	1	A56695 leghemoglobin III
36	14	23.7	8	2	S20162 inulinase (EC 3.2.
37	14	23.7	8	2	PT0030 neuropeptide calla
38	14	23.7	8	2	D47393 cytochrome-c oxida
39	14	23.7	8	2	S65381 MHC class I histoc
40	14	23.7	8	2	A59028 bradykinin-like pe
41	14	23.7	9	2	A61358 Thr-6 bradykinin -
42	14	23.7	9	2	A61057 bradykinin-like pe
43	14	23.7	9	2	A26744 bradykinin-like pe
44	14	23.7	9	2	A60579 ornitho-kinin - ch
45	14	23.7	9	2	B60246

ALIGNMENTS

RESULT 1

D61440 polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
C:Species: Aspergillus sp.
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 06-Dec-1996
C:Accession: D61440
R:Stratillova, E.; Markovic, O.; Skrivinova, D.; Rexova-Benkova, L.; Jorvall, H.
J. Protein Chem. 12, 15-22, 1993
A:Title: Pectinase Aspergillus sp. polygalacturonase: multiplicity, divergence, and s
A:Reference number: A61440; MUID:93151562; PMID:8427629
A:Accession: D61440
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <STR>
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match

Best Local Similarity 40.7% Score 24; DB 2; Length 10;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TFRSYD 8
|||||
DB 4 TFRSAD 9

RESULT 2

A24244 adipokinetic hormone - bollworm
N:Alternate names: Hez-AKH
C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C:Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C:Accession: A24244
R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridg
Biochem. Biophys. Res. Commun. 135, 622-628, 1986
A:Title: Isolation and primary structure of a peptide from the corpora cardiaca of He
A:Reference number: A24244; MUID:86186794; PMID:3964263
A:Accession: A24244
A:Molecule type: protein
A:Residues: 1-9 <JAF>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match

Best Local Similarity 33.9% Score 20; DB 2; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TFRS 6
|||||
DB 3 TFRS 6

RESULT 3

S74176
C:Species: Escherichia coli
C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999
C:Accession: S74176
R:Izu, H.; Adachi, O.; Yamada, M.
FEBS Lett. 394, 14-16, 1996
A:Title: Purification and characterization of the Escherichia coli thermoresistant glucoc
A:Reference number: S74176; MUID:97074194; PMID:8923917
A:Accession: S74176
A:Molecule type: protein
A:Residues: 1-10 <IZU>
A:Experimental source: strain K-12
C:Genetics:
A:Gene: gntK
C:Keywords: dimer; phosphotransferase

Query Match

33.9%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 TSYDMH 10
| : | : |
DB 3 TNNDHH 8

RESULT 4

SPGKNK

C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 23-Aug-1996
C:Accession: A01560
R:Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.
Biochem. Biophys. Res. Commun. 114, 533-540, 1983
A:Title: Neuropeptide K: a novel mammalian tachykinin identified in porcine spinal cord.
A:Reference number: A01560; MUID:83282812; PMID:6576785
A:Accession: A01560
A:Molecule type: protein
A:Residues: 1-10 <KAN>
A:Note: The structure of the peptide was confirmed by synthesis
C:Comment: The biological source of this peptide is spinal cord. It stimulates smooth mu
C:Superfamily: neuropeptide B precursor
C:Keywords: amidated carboxyl end; hormone; spinal cord
F:10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

32.2%; Score 19; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 DMH 10
| | |
DB 1 DMH 3

RESULT 5

A61230

C:Species: Rana pipiens (northern leopard frog)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C:Accession: A61230
R:McLeod, A.C.; Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.
Circ. Res. 69, 344-359, 1991
A:Title: Frog cardiac calsequestrin. Identification, characterization, and subcellular d
rdium.

A:Reference number: A61230; MUID:91316784; PMID:1860177

A:Accession: A61230

A:Molecule type: protein

A:Residues: 1-9 <MCL>

C:Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding protei
C:Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to d

C:Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in
C:Superfamily: calsequestrin
C:Keywords: calcium binding; cardiac muscle; glycoprotein; heart; phosphoprotein; ske

Query Match

30.5%; Score 18; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GYFTSY 7
| : | : |
DB 3 GINFPY 9

RESULT 6

S36850

Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
C:Accession: S36850
R:Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitroph
A:Reference number: S35024
A:Accession: S36850
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-9 <JAC>
A:Cross-references: EMBL:X67387; NID:950113; PIDN:CAAN7799.1; PID:es1594; PID:g133387
C:Keywords: heterodimer; immunoglobulin

Query Match

30.5%; Score 18; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 YFTSY 7
| : | : |
DB 3 YDGSY 8

RESULT 7

G85802

hypothetical protein Z2947 [imported] - Escherichia coli (strain O157:H7, substrain E
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: G85802
R:Penna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; DiMalanca, E.; Potamoudis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85802
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-9 <STO>
A:Cross-references: GB:AE005174; NID:g12515957; PIDN:AAG56883.1; GSPDB:GNO0145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z2947

Query Match

30.5%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YTF 4
| | |
DB 3 YTF 5

RESULT 8

S62208

polyferredoxin - Methanosarcina barkeri (fragment)
C:Species: Methanosarcina barkeri
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 31-Mar-1997

C:Accession: S62208
 R:Vorholt, J.A.; Vaupel, M.; Thauer, R.K.
 Eur. J. Biochem. 236, 309-317, 1996
 A:Title: A polyferredoxin with eight [4Fe-4S] clusters as a subunit of molybdenum formyl
 A:Reference number: S62194; MUID:96184912; PMID:8617280
 A:Accession: S62208
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <VOR>

Query Match 30.5%; Score 18; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 TSYD 8
 |||
 DB 3 TSYD 6

RESULT 9

A60139
 fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-May-2000
 C:Accession: A60139
 R:Hardie, D.G.; Dewar, K.B.; Aitken, A.; McCarthy, A.D.
 Biochem. Biophys. Acta 828, 380-382, 1985
 A:Title: Amino acid sequence around the reactive serine residue of the thioesterase doma
 A:Reference number: A60139; MUID:85175165; PMID:3921056
 A:Accession: A60139
 A:Molecule type: protein
 A:Residues: 1-7 <HAR>

C:Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I hom
 ydrolyase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein] S
 C:Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enz
 F:5/Modified site: Ser (of oleoyl-[acyl-carrier-protein] hydrolyase) #status experimental

Query Match 28.8%; Score 17; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYTF 4
 |||
 DB 3 GYSY 6

RESULT 10

S11078
 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - yeast (Pichia jadinii) (fragment)
 C:Species: Pichia jadinii, Candida utilis
 C:Date: 30-Jun-1991 #sequence_revision 30-Sep-1991 #text_change 05-Aug-1994
 C:Accession: S11078
 R:Egstad, B.; Estonius, M.; Danielsson, O.; Persson, B.; Cederlund, E.; Kaiser, R.; Hol
 FEBS Lett. 269, 194-196, 1990
 A:Title: Fast atom bombardment mass spectrometry and chemical analysis in determinations
 A:Reference number: S11074; MUID:90355571; PMID:2387402
 A:Accession: S11078
 A:Molecule type: protein
 A:Residues: 1-8 <EGE>

A:Note: the source is designated as Pichia jadinii
 C:Keywords: acetylated amino end; oxidoreductase; pentose phosphate pathway
 F:1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 28.8%; Score 17; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 SYD 8
 |||
 DB 1 SYD 3

RESULT 11

S08996
 hypertrihaloemic hormone II - oriental cockroach
 N:Alternate names: Pea-CAH-II
 C:Species: Blatta orientalis (oriental cockroach)
 C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
 C:Accession: S08996
 R:Gaede, G.; Rinehart, K.L.
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hypertrihaloemic neuropeptides isolated from the cor
 entails and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bomb
 A:Reference number: S08995; MUID:90253659; PMID:2340112
 A:Accession: S08996
 A:Molecule type: protein
 A:Residues: 1-8 <GAE>

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we h
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 27.1%; Score 16; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTF 5
 |||
 DB 3 TTF 5

RESULT 12

B49823
 adipokinetic hormone II - American cockroach
 N:Alternate names: neuropeptide M-II; periplanetin CC-1
 C:Species: Periplaneta americana (American cockroach)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
 C:Accession: B49823; A05170
 R:Scardoroug, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller,
 Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
 A:Title: Isolation and primary structure of two peptides with cardioacceleratory and
 A:Reference number: A49823; MUID:84298179; PMID:6591205
 A:Accession: B49823
 A:Molecule type: protein
 A:Residues: 1-8 <SCA>

R:Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr.,
 Biochem. Biophys. Res. Commun. 124, 350-358, 1984
 A:Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment
 A:Reference number: A90118; MUID:85046530; PMID:6548628
 A:Accession: A05170
 A:Molecule type: protein
 A:Residues: 1-8 <WIT>

C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglut
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 27.1%; Score 16; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTF 5
 |||
 DB 3 TTF 5

RESULT 13

B44960
 neuropeptide Ied-CC-II - Colorado potato beetle
 C:Species: Leptinotarsa decemlineata (Colorado potato beetle)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: B44960
 R:Gaede, G.; Kellner, R.
 Peptides 10, 1287-1289, 1989
 A:Title: The metabolic neuropeptides of the corpus cardiaca from the potato beetle a

Job time : 46 secs

A:Reference number: A44960; MUID:90160053; PMID:2576128
 A:Accession: B44960

A:Molecule type: protein

A:Residues: 1-8 <GAE>

C:Superfamily: adipokine hormone

C:Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match

27.1%; Score 16; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TFF 5

DB 3 TFF 5

RESULT 14

A33995 adipokine hormone - black horse fly

C:Species: Tabanus atratus (black horse fly)

C>Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997

C:Accession: A33995

R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang,

Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989

A:Title: Primary structure of two neuropeptide hormones with adipokine and hypotrehal

A:Reference number: A33995; MUID:90046758; PMID:2813385

A:Accession: A33995

A:Molecule type: protein

A:Residues: 1-8 <JAF>

C:Superfamily: adipokine hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F:8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match

27.1%; Score 16; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TFF 5

DB 3 TFF 5

RESULT 15

PH0803 T-cell receptor alpha chain (J2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PH0803

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-I

allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:9207846; PMID:1836010

A:Accession: PH0803

A:Molecule type: mRNA

A:Residues: 1-8 <CAS>

A:Cross-references: EMBL:X60912

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match

27.1%; Score 16; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTF 4

DB 4 GTF 7

Search completed: February 25, 2003, 11:33:59

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:49:02; Search time 30 Seconds

(Without alignments)
13.731 Million cell updates/sec

Title: US-09-743-482A-12
87
Sequence: 1 DMHYSSYIRPEAY 14

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 103252

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents-AA:
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	37.9	6	2	US-09-146-402-1
2	32	36.8	14	1	US-08-321-625-49
3	32	36.8	14	4	US-09-181-083-49
4	30	34.5	10	2	US-08-556-597-155
5	29	33.3	7	3	US-08-990-664-44
6	29	33.3	8	2	US-08-361-517-8
7	29	33.3	8	2	US-08-361-517-11
8	29	33.3	8	3	US-08-990-664-28
9	29	33.3	8	4	US-09-573-962-27
10	29	33.3	8	4	US-09-245-680-27
11	29	33.3	8	4	US-09-198-806C-27
12	29	33.3	8	4	US-09-352-191-27
13	29	33.3	8	4	US-09-012-400-27
14	29	33.3	8	4	US-09-264-563-27
15	29	33.3	8	5	PCT-US93-07964-8
16	29	33.3	8	5	PCT-US93-07964-11
17	29	33.3	9	2	US-08-361-517-7
18	29	33.3	9	4	US-09-644-600-53
19	29	33.3	9	5	PCT-US93-07964-7
20	29	33.3	9	6	5492893-3
21	29	33.3	10	2	US-08-556-597-83
22	29	33.3	10	2	US-08-361-517-10
23	29	33.3	10	2	US-08-361-517-12
24	29	33.3	10	2	US-08-361-517-18
25	29	33.3	10	2	US-08-361-517-22
26	29	33.3	10	5	PCT-US93-07964-10
27	29	33.3	10	5	PCT-US93-07964-12

28	29	33.3	10	5	PCT-US93-07964-18	Sequence 18, Appl
29	29	33.3	10	5	PCT-US93-07964-22	Sequence 22, Appl
30	29	33.3	11	2	US-08-361-517-5	Sequence 5, Appl
31	29	33.3	11	5	PCT-US93-07964-5	Sequence 5, Appl
32	29	33.3	12	2	US-08-361-517-4	Sequence 4, Appl
33	29	33.3	12	2	PCT-US93-07964-4	Sequence 4, Appl
34	29	33.3	13	1	US-08-464-531-108	Sequence 108, App
35	29	33.3	13	2	US-08-461-598-108	Sequence 108, App
36	29	33.3	13	2	US-08-361-517-3	Sequence 3, Appl
37	29	33.3	13	3	US-08-322-137-108	Sequence 108, App
38	29	33.3	13	4	US-08-582-333A-44	Sequence 44, Appl
39	29	33.3	13	5	PCT-US93-07964-3	Sequence 3, Appl
40	29	33.3	14	2	US-08-361-517-2	Sequence 2, Appl
41	29	33.3	14	2	US-08-361-517-6	Sequence 6, Appl
42	29	33.3	14	5	PCT-US93-07964-2	Sequence 2, Appl
43	29	33.3	14	5	PCT-US93-07964-6	Sequence 6, Appl
44	28.5	32.8	12	1	US-08-318-970B-11	Sequence 11, Appl
45	28.5	32.8	12	1	US-08-190-788A-167	Sequence 167, App

ALIGNMENTS

```
RESULT 1
; Sequence 1, Application US/09146402
; Patent No. 5994310
; GENERAL INFORMATION:
; APPLICANT: Buetner, Joseph A.
; APPLICANT: Davis, June P.
; TITLE OF INVENTION: Peptide ligands for Affinity Purification of Human
; FILE REFERENCE: 5043
; CURRENT APPLICATION NUMBER: US/09/146,402
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(6)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Random peptide
; US-09-146-402-1

Query Match      37.9%; Score 33; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WHY 5
Db 1 WHY 4

RESULT 2
US-08-321-625-49
; Sequence 49, Application US/08321625
; Patent No. 5639860
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Takeo
; APPLICANT: MORISHITA, Yoshikazu
; APPLICANT: MAKINO, Mika
; APPLICANT: CHIBA, Shigeru
; APPLICANT: KAWAMOTO, Isao
; APPLICANT: TSUKUDA, Ei-ji
; APPLICANT: YOSHIDA, Mayumi
; APPLICANT: BANDO, Chieko
; APPLICANT: YAMAGUCHI, Kazuo
; APPLICANT: MATSUDA, Yuzuru
```

TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 No. 5639860th Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,625
FILING DATE: 12-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-321-625-49

Query Match 36.8%; Score 32; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DMHY 5
Db 9 DMNY 13

RESULT 3
US-09-181-083-49
Sequence 49, Application US/09181083
Patent No. 6194195
GENERAL INFORMATION:
APPLICANT: TANAKA, Takeo
APPLICANT: MORISHITA, Yoshiakazu
APPLICANT: MAKINO, Mika
APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Isao
APPLICANT: TSUKUDA, Eiji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko
APPLICANT: YAMAGUCHI, Kazuo
APPLICANT: MATSUDA, Yuzuru
TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 No. 6194195th Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,083
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/321,625
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-09-181-083-49

Query Match 36.8%; Score 32; DB 4; Length 14;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DMHY 5
Db 9 DMNY 13

RESULT 4
US-08-556-597-155
Sequence 155, Application US/08556597
Patent No. 5877155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
HUMAN PLATELET GLYCOPROTEIN Ib/IX
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600

INFORMATION FOR SEQ ID NO: 155:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-155

Query Match 34.5%; Score 30; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 WHYSSYIRP 11
11111
Db 5 WH---YIRP 10

RESULT 5

US-08-990-664-44
Sequence 44, Application US/08990664
Patent No. 6110895

GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
APPLICANT: dizegega, Gere
TITLE OF INVENTION: METHOD OF PROMOTING HEALING
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,664

CLASSIFICATION:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,310
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: USC012.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:

INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-990-664-44

Query Match 33.3%; Score 29; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YIRPF 12
11111
Db 3 YIRPF 7

RESULT 6

US-08-361-517-8
Sequence 8, Application US/08361517
Patent No. 5916876

GENERAL INFORMATION:
APPLICANT: George A. Heavner and Leon A. Epps
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
ADHESION
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: and No. 5916876rls
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,517
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated
US-08-361-517-8

Query Match 33.3%; Score 29; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSSSY 8
11111
Db 3 YSSSY 7

RESULT 7

US-08-361-517-11
Sequence 11, Application US/08361517
Patent No. 5916876

GENERAL INFORMATION:
APPLICANT: George A. Heavner and Leon A. Epps
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
ADHESION
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: and No. 5916876rls
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,517
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated
US-08-361-517-11

Query Match 33.3%; Score 29; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRSSY 8
DB 4 YRSSY 8

RESULT 8
US-08-990-664-28
Sequence 28, Application US/08990664
Patent No. 6110895
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
APPLICANT: dizerega, Gere
TITLE OF INVENTION: METHOD OF PROMOTING HEALING
TITLE OF INVENTION: IN SKIN GRAFTS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,664
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,310
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: USC012,001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502

TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-990-664-28

Query Match 33.3%; Score 29; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YIRPF 12
DB 4 YIRPF 8

RESULT 9
US-09-373-962-27
Sequence 27, Application US/09373962
Patent No. 6177407
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
APPLICANT: dizerega, Gere
TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
FILE REFERENCE: 98364A
CURRENT APPLICATION NUMBER: US/09/373,962
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: All analogue 9
US-09-373-962-27

Query Match 33.3%; Score 29; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YIRPF 12
DB 4 YIRPF 8

RESULT 10
US-09-245-680-27
Sequence 27, Application US/09245680B
Patent No. 6239109
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
APPLICANT: dizerega, Gere
TITLE OF INVENTION: Method of Promoting Erythropoiesis
FILE REFERENCE: 98009B
CURRENT APPLICATION NUMBER: US/09/245,680B
CURRENT FILING DATE: 1999-02-08
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: All analogue 9
US-09-245-680-27

Query Match 33.3%; Score 29; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YIRPF 12
|||||
DB 4 YIRPF 8

RESULT 11

US-09-198-806C-27
; Sequence 27, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dzizega, Gere
; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem
; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation
; FILE REFERENCE: 97,017-F1
; CURRENT APPLICATION NUMBER: US/09/198,806C
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue 9
US-09-198-806C-27

Query Match

33.3%; Score 29; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YIRPF 12
|||||
DB 4 YIRPF 8

RESULT 12

US-09-352-191-27
; Sequence 27, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dzizega, Gere
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
; FILE REFERENCE: 98365B
; CURRENT APPLICATION NUMBER: US/09/352,191
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue 9
US-09-352-191-27

Query Match 33.3%; Score 29; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YIRPF 12
|||||
DB 4 YIRPF 8

RESULT 13
US-09-012-400-27
; Sequence 27, Application US/09012400D
; Patent No. 6335195
; GENERAL INFORMATION:

; APPLICANT: Rodgers, Kathleen
; APPLICANT: dzizega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell
; TITLE OF INVENTION: Proliferation and Differentiation
; FILE REFERENCE: 97,017-G
; CURRENT APPLICATION NUMBER: US/09/012,400D
; CURRENT FILING DATE: 1998-01-23
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue 9
US-09-012-400-27

Query Match

33.3%; Score 29; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YIRPF 12
|||||
DB 4 YIRPF 8

RESULT 14

US-09-264-563-27
; Sequence 27, Application US/09264563A
; Patent No. 6455500
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dzizega, Gere
; TITLE OF INVENTION: Radiation Therapy Methods
; FILE REFERENCE: 97017K1
; CURRENT APPLICATION NUMBER: US/09/264,563A
; CURRENT FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue 9
US-09-264-563-27

Query Match 33.3%; Score 29; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YIRPF 12
|||||
DB 4 YIRPF 8

RESULT 15

PCT-US93-07964-8
; Sequence 8, Application 93/07964
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 93/07964
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated.
PCR-US93-07964-8

Query Match 33.3%; Score 29; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 4 YYSSY 8
 |||||
Db 3 YYSSY 7

Search completed: February 25, 2003, 11:52:52
Job time : 31 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:41:07 ; Search time 84 Seconds
(without alignments)
22.208 Million cell updates/sec

Title: US-09-743-482a-12

Perfect score: 87

Sequence: 1 DMHYSSYRPFAY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 228063

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	14	21	AAV78324
2	40	46.0	12	21	AAV88111
3	35	40.2	12	20	AAV24391
4	34	39.1	12	21	AAV88163
5	33	37.9	6	21	AAV56545
6	33	37.9	6	21	AAV50763
7	33	37.9	9	20	AAV46860
8	33	37.9	13	23	ABR83043
9	31	35.6	14	23	ABG65981
10	30	34.5	10	18	AAW32760

11	30	34.5	10	20	AAW95251	Anti-progesterone
12	29	33.3	7	19	AAW65639	Angiotensin III an
13	29	33.3	7	23	ABG60368	Selective targetin
14	29	33.3	8	15	AAW50020	Leukocyte adhesion
15	29	33.3	8	15	AAW50023	Leukocyte adhesion
16	29	33.3	8	19	AAW65623	Angiotensin II an
17	29	33.3	8	19	AAW64753	Angiotensin II an
18	29	33.3	8	19	AAW71136	Angiotensin II pep
19	29	33.3	8	19	AAW49609	Angiotensin II an
20	29	33.3	8	20	AAW42362	Angiotensin analog
21	29	33.3	8	20	AAW30563	Angiotensin II an
22	29	33.3	8	20	AAW30667	Amino acid sequenc
23	29	33.3	8	20	AAW32738	Angiotensin II an
24	29	33.3	8	20	AAW33792	Angiotensin II an
25	29	33.3	8	20	AAW15368	Angiotensin II (AI
26	29	33.3	8	20	AAW15328	Angiotensin II (AI
27	29	33.3	8	20	AAW25028	Angiotensin II (AI
28	29	33.3	8	20	AAW25031	Leukocyte adhesion
29	29	33.3	8	21	AAW27427	Leukocyte adhesion
30	29	33.3	8	21	AAW28125	Angiotensin II an
31	29	33.3	8	21	AAW84149	Angiotensin II an
32	29	33.3	8	21	AAW77062	Amino acid sequenc
33	29	33.3	8	21	AAW57424	Angiotensin II (AI
34	29	33.3	8	22	AAW08895	Angiotensin peptid
35	29	33.3	8	22	AAW03012	Angiotensin II (AI
36	29	33.3	8	22	AAW03175	Human angiotensin
37	29	33.3	8	23	AAW19211	Angiotensin II pep
38	29	33.3	9	15	AAW85791	Angiotensin AII pe
39	29	33.3	9	20	AAW50019	Leukocyte adhesion
40	29	33.3	9	20	AAW50027	Leukocyte adhesion
41	29	33.3	9	22	AAW98543	Human TADG-15 pept
42	29	33.3	10	2	AAW10183	Sequence of new go
43	29	33.3	10	6	AAW50787	Sequence of new go
44	29	33.3	10	6	AAW50224	Gonadotropin rele
45	29	33.3	10	6	AAW50175	Gonadotropin rele

ALIGNMENTS

RESULT 1
ID AAV78324 standard; Protein; 14 AA.
AC AAV78324;
XX
XX
DT 04-MAY-2000 (first entry)
XX
XX
DE Anti-zeta-chain antibody 2-B-5 VH-region CDR3 protein sequence.
KW Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
KW complementary determining region; CDR; autoimmune disease; cytotoxic;
KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.
XX
XX
OS Rattus norvegicus.
XX
XX
PN WO200003016-A1.
XX
XX
PD 20-JAN-2000.
XX
XX
PF 09-JUL-1999; 99WO-EP04838.
XX
XX
PR 10-JUL-1998; 98EP-0112867.
XX
XX
PA (CONN-) CONNEX GMBH.
XX
XX
PI Refter C;
XX
XX
DR WPI; 2000-160926/14.
XX
XX
DR N-PSDB; AA288322.
XX
XX
PT New oligonucleotide, polypeptide, antibody useful for treating

CC regulating expression of the gene to produce the biomolecule in the
CC cell; and (2) monitoring the cell in the animal for a phenotypic effect;
CC where a cell that manifests a phenotypic effect indicates that the
CC biomolecule produced in the cell is a biomolecule that produces a
CC phenotypic effect on the cell. The methods couple the validation of a
CC target for drug discovery with the development of an assay to identify
CC compounds that cause a phenotypic effect on the target cell. The methods
CC can be used to identify compounds that bind to and modulate the function
CC of target components of a cell whose function is known or unknown. The
CC methods can be used to identify pathogen growth inhibitors, and
CC compounds that prevent/inhibit infection of a mammal by a pathogen.
CC The present sequence represents a peptide used in an example
CC from the present invention.

XX
XX
SQ Sequence 12 AA;
QY
Db
Query Match 40.2%; Score 35; DB 20; Length 12;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DMHYSSY 8
:|:|:|:
Db 5 NMYYTASM 12

RESULT 4
AA588163
ID AAY88163 standard; peptide; 12 AA.
XX
XX AAY88163;
AC
XX
DT 17-OCT-2000 (first entry)
XX
DE Fluorescein binding peptide fluorett from phage clone Flu413.
XX
KM Fluorett; fluorophore dye; fluorescent; detection; diagnostic.
XX
OS Synthetic.
XX
PN WO200023463-A2.
XX
PD 27-APR-2000.
XX
PF 15-OCT-1999; 99WO-US24266.
XX
PR 16-OCT-1998; 98US-0104465.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Nolan GP, Rozinov MN;
XX
DR WPI; 2000-339647/29.
XX
PT Novel fluorett peptides which bind with high specificity to
PT fluorophore dyes, useful for detecting biological materials, molecules,
PT target analytes, and intra- and inter-molecular interactions -
XX
XX
PS Disclosure: Page 36; 64pp; English.

CC This invention describes a novel peptide (I) termed a fluorett which
CC comprises a sequence of at least 8 amino acids and which binds to a
CC fluorophore dye. The fluorett may be used in detecting biological
CC materials, molecules or target analytes, intracellular events, and intra-
CC and inter-molecular interactions, as well as discovering effective
CC inhibitors. They may also be used for in vitro assays using a large set
CC of fluorophore dyes, e.g. in detection of viral and delivery systems,
CC diagnostics and high throughput assays. The new peptides, due to their
CC small size, are not intrusive to the systems being studied hence, permit
CC detection and analysis of a target moiety or molecule while minimizing
CC target modification. Unlike conventional techniques such as the
CC light-emitting technique, the use of fluorett minimizes or avoid
CC substantial genetic manipulations which may disrupt, interfere, or alter
CC the process being measured. This sequence represents a peptide fluorett

CC capable of binding to Fluorescein which is described in the method
CC of the invention.

XX
XX
SQ Sequence 12 AA;
QY
Db
Query Match 39.1%; Score 34; DB 21; Length 12;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 WHYVS 6
:|:|:|:
Db 6 WHYVA 10

RESULT 5
AA56545
ID AAY56545 standard; peptide; 6 AA.
XX
XX AAY56545;
AC
XX
DT 21-FEB-2000 (first entry)
XX
DE Factor VIII binding substrate peptide SEQ ID NO:1.
XX
KM Human; Factor VIII; Factor VIII binding substrate; purification.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN US5998589-A.
XX
PD 07-DEC-1999.
XX
PF 09-JUL-1999; 99US-0350605.
XX
PR 03-SEP-1998; 98US-0146402.
XX
PA (FARB) BAYER CORP.
XX
PI Davis JP, Buettner JA;
XX
DR WPI; 2000-052560/04.
XX
PT Purification process for human Factor VIII -
XX
PS Claim 1; Column 3; 13pp; English.

CC A method has been developed of purifying Factor VIII. The method
CC comprises contacting a solution containing Factor VIII with a
CC Factor VIII-binding substrate and then eluting the bound Factor VIII.
CC The Factor VIII-binding substrate comprises one or more peptides bound
CC to the substrate, the peptides comprising: Trp-His-Tyr-His-Gly;
CC His-Ile-Gln-His-Tyr-His; and His-Gln-Tyr-Gly-Tyr-His. The method is
CC useful for the purification of human Factor VIII. Prior art methods
CC left monoclonal antibodies in the Factor VIII effluent because of
CC leaching from the support matrix raising the possibility of
CC antigenicity when the final preparation is introduced into animal
CC systems.

XX
XX
SQ Sequence 6 AA;
QY
Db
Query Match 37.9%; Score 33; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WHY 5
:|:|:|:
Db 1 WHY 4

RESULT 6
AA50763
ID AAY50763 standard; peptide; 6 AA.

XX AAY50763;
AC 11-FEB-2000 (first entry)
XX
DT
XX
DE Factor VIII binding domain peptide 1.
XX
XX Factor VIII; affinity purification; plasma.
XX
XX Synthetic.
XX
XX US5994310-A.
XX
XX 30-NOV-1999.
XX
XX 03-SEP-1998; 98US-0146402.
XX
XX 03-SEP-1998; 98US-0146402.
XX
XX (FARB) BAYER CORP.
XX
XX Buettner JA, Davis JP;
XX WPI; 2000-038271/03.
XX
XX A composition for binding Factor VIII comprising a peptide -
XX
XX Claim 1; Column 7-8; 14pp; English.
XX
XX This invention describes a novel composition for binding Factor VIII
XX which comprises a peptide consisting of an available Factor VIII binding
XX domain. The composition is useful for the affinity purification of
XX Factor VIII from plasma. The composition comprises affinity peptides
XX which are more specific than those of the prior art. AAY50763-Y50765
XX represent peptides described in the method of the invention.
XX
SQ Sequence 6 AA:
Query Match 37.9%; Score 33; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 WHY 5
DB 1 WHY 4
RESULT 7
AAY46860
ID AAY46860 standard; Peptide; 9 AA.
XX
AC AAY46860;
XX
XX
DT 01-DEC-1999 (first entry)
XX
XX Immunogenic peptide having a human leukocyte antigen binding motif #1471.
XX
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; Immunisation.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO9945954-A1.
XX
XX 16-SEP-1999.
XX
XX 13-MAR-1998; 98WO-US05039.
XX
XX 13-MAR-1998; 98WO-US05039.

XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Kubo RT, Sidney J, Cells E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -
XX
XX Claim 1; Page 87; 150pp; English.
XX
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.
XX Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)
XX e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically and can be used to induce a cytotoxic T cell
XX response, by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polypeptides encoding the immunogenic peptides are also useful
XX therapeutically and for immunisation as above.
XX
SQ Sequence 9 AA:
Query Match 37.9%; Score 33; DB 20; Length 9;
Best Local Similarity 44.4%; Pred. No. 7.8e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 1; Gaps 0;
QY 2 WHYSSYIR 10
DB 1 WTYFDITYMR 9
RESULT 8
ABB83043
ID ABB83043 standard; peptide; 13 AA.
XX
XX ABB83043;
XX
XX
DT 27-AUG-2002 (first entry)
XX
XX Transferrin receptor gene mapped peptide #29.
XX
XX Peptide database; peptide characterisation; computer-mediated;
XX exon identification; mutation; polymorphic; exon-intron boundary;
XX post-translational modification; clinical diagnosis;
XX transferrin receptor gene.
XX
XX Unidentified.
XX
XX WO200221139-A2.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-GB04034.
XX
XX 08-SEP-2000; 2000GB-0022136.
XX
XX 13-SEP-2000; 2000US-232273P.
XX
XX 28-NOV-2000; 2000US-0724405.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

CC within the human platelet glycoprotein (gp) Ib/IX complex. More
 CC specifically the Mab is 52-2. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through
 CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
 CC the ristocetin induced aggregation of platelets.

CC Sequence 10 AA:

Query Match 34.5%; Score 30; DB 18; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

OY 2 WHYSSYIRP 11
 11 1111
 Db 5 WH---YIRP 10

RESULT 11

AAW95251
 ID AAW95251 standard; peptide: 10 AA.

AC AAW95251;

DT 11-MAR-1999 (first entry)

DE Anti-progesterone antibody Vh region (clone 1578/p6) CDR H3 sequence.

XX ARR: protein selection; display: cell free system; genetic information;

KW reverse transcription; single-chain antibody; RT-PCR; primer; drug;

KM antibody-ribosome-mRNA complex; antibody engineering; progesterone;

KW testosterone; human

OS Homo sapiens.

PN WO954312-A1.

PD 03-DEC-1998.

PF 28-MAY-1998; 98WO-GB01564.

PR 28-FEB-1998; 98GB-0004195.

PR 28-MAY-1997; 97GB-0010829.

PR 26-NOV-1997; 97GB-0024850.

PA (BABR-) BABRAHAM INST.

PI He M, Taussig MJ;

DR WPI: 1999-059832/05.

PT In vitro display and evolution of proteins - by transcription and

PT translation of DNA in a cell free system, selection and recovery of

PT complexes and RT-PCR on RNA bound to ribosomes

PS Example 13; Fig 19; 62pp; English.

XX The invention relates to methods for the display and selection of
 CC proteins or peptides; and for recovery of the genetic material encoding
 CC them. One method comprises (a) transcription and translation of DNA in a
 CC cell free system such that complexed particles are formed, each
 CC comprising at least one individual nascent protein or peptide or other
 CC DNA expression product associated with one or more ribosomes and the
 CC specific mRNA encoding the protein or peptide; (b) contacting the
 CC complexed particles with a ligand, antigen, antibody or other agent in
 CC order to select particles through binding to the protein or peptide
 CC product; and (c) recovering the genetic information encoding the protein
 CC or peptide as DNA by RT-PCR carried out on the mRNA while the latter
 CC remains bound to the complexed particle. The steps of display, selection
 CC and recovery can be repeated in consecutive cycles. The method is

CC exemplified using single-chain antibody constructs as antibody-ribosome-
 CC mRNA complexes (ARMs). Methods in which the DNA is produced by RT-PCR,
 CC methods for making antibodies of human, mouse or rat are also provided.
 CC The methods can be used for the display and selection of single chain
 CC antibody fragments from libraries, antibody engineering, selection of
 CC human antibodies and selection of proteins from mRNA libraries. They can
 CC also be used to select ligands for combining sites or receptors, such
 CC as ligands having potential uses as drugs or therapeutics. By carrying out the
 CC RT-PCR recovery step directly on the intact ribosome complex without
 CC prior dissociation to release the mRNA maximal efficiency and
 CC sensitivity can be obtained. Peptides AAW95247 to AAW95271 represent
 CC sequences of human anti-progesterone and anti-testosterone antibodies
 CC isolated from an immunised transgenic mouse by ARM display.

CC Sequence 10 AA:

Query Match 34.5%; Score 30; DB 20; Length 10;
 Best Local Similarity 42.9%; Pred. No. 1.7e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

OY 1 DMHYSSYIRPFAY 14
 11:1 111
 Db 3 DMNY-----PFDY 10

RESULT 12

AAW65639
 ID AAW65639 standard; peptide: 7 AA.

AC AAW65639;

DT 09-NOV-1998 (first entry)

DE Angiotensin III analogue #6.

XX angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;

KW wound healing.

OS Synthetic.

OS Homo sapiens.

PN WO9826795-A1.

PD 25-JUN-1998.

PF 16-DEC-1997; 97WO-US23461.

PR 15-DEC-1997; 97US-0990664.

PR 16-DEC-1996; 96US-0028310.

PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

PI Dizerega GS, Rodgers KE;

DR WPI: 1998-362518/31.

PT Promoting incorporation of skin graft onto underlying tissue -

PT comprises pre-treating graft with angiotensin II, or analogue or

PT peptide fragment

PS Example 4; Page 17; 82pp; English.

XX The invention relates to the use of angiotensin II (AII), AII analogues,
 CC AII fragments and AII fragment analogues for promoting incorporation of a
 CC skin graft into underlying tissue of a mammal. The peptides are effective
 CC in accelerating the growth or healing of skin grafts and in accelerating
 CC re-epithelialisation and tissue repair, even at very low concentrations
 CC They can significantly accelerate the rate of healing at nanomolar levels
 CC in vivo. AII accelerates wound repair by increased neovascularisation,
 CC growth factor release, re-epithelialisation, extracellular matrix production
 CC and increased flow of blood and nutrients to the injured tissue. Use of
 CC the above peptides other than AII itself (an extremely potent vaso-
 CC constrictor) may avoid the side-effects of AII, such as increase in blood

CC pressure and thirst. The present sequence represents an angiotensin
 CC III analogue which was also shown to be effective in promoting the
 CC healing of full thickness dermal wounds.
 XX
 SQ Sequence 7 AA;

Query Match 33.3%; Score 29; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 YIRPF 12
 DB 3 YIRPF 7

RESULT 13
 ABG60368
 ID ABG60368 standard; Peptide: 7 AA.
 AC ABG60368;

DT 30-JUL-2002 (first entry)
 DE Selective targeting peptide #43.

XX Targeting peptide: cancer; arthritis; diabetes; inflammatory disease;
 KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;
 KW viral infection; cardiovascular disease; degenerative disease; ischemia;
 KW inflammation; macular degeneration; antiinflammatory; antidiabetic;
 KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
 KW gene therapy.

OS Synthetic.

PN WO200220769-A1.

PD 14-MAR-2002.

PE 07-SEP-2001; 2001WO-US27692.

PR 08-SEP-2000; 2000US-231266P.

XX 17-JAN-2001; 2001US-0765101.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Arap W, Pasqualini R;

DR WPI; 2002-415731/44.

XX Targeting peptides identified by phage display, useful for targeting
 PT delivery to an organ or tissue, particularly for treating a disease,
 PT e.g. cancer, inflammatory or autoimmune diseases, infections or
 PT cardiovascular disease -

PS Claim 22; Page 62; 317pp; English.

XX The invention relates to an isolated peptide of 100 amino acids or less
 CC in size useful for targeting delivery to an organ or tissue, particularly
 CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory
 CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral
 CC infection, cardiovascular disease or degenerative disease. The peptide is
 CC also useful for inducing apoptosis, particularly to a subject with
 CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,
 CC inflammation or macular degeneration. Furthermore, the peptide is useful
 CC for diagnosing the diseases cited above. Targeting peptides of the
 CC invention can also be used to deliver an agent to a foetus, by attaching
 CC a peptide to the agent and administering the peptide to a pregnant
 CC subject. Sequences ABG60336-ABG60574 represent selective targeting
 CC peptides of the invention.

SQ Sequence 7 AA;

Query Match 33.3%; Score 29; DB 23; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 YIRPF 12
 DB 1 YIRPF 5

RESULT 14
 AAR50020
 ID AAR50020 standard; peptide; 8 AA.
 AC AAR50020;

DT 22-SEP-1994 (first entry)

DE Leukocyte adhesion inhibiting peptide #8.

XX Inhibition; leukocyte; adhesion; P-selectin; cellular adherence;
 KW platelet; endothelium; inflammation; coagulation; ischemia;
 KW reperfusion injury; bacterial sepsis; atherosclerosis;
 KW disseminated intravenous coagulation; rheumatoid arthritis;
 KW adult respiratory distress syndrome; tumour metastasis.

OS Synthetic.

PN WO9405314-A.

PD 17-MAR-1994.

PE 24-AUG-1993; 93WO-US07964.

PR 08-SEP-1992; 92US-0941652.

PA (CENZ) CENTOCOR INC.

PI Epps LA, Heavner GA;

DR WPI; 1994-100852/12.

XX New peptide(s) which inhibit binding of selectins - esp. to
 PT prevent leucocyte adhesion, useful for treating inflammation,
 PT reperfusion injury etc., also for diagnosis of defective
 PT selectin-binding ligands

PS Claim 4; Page 39; 56pp; English.

XX The sequences given in AAR50013-35 are peptides which are capable of
 CC inhibiting leukocyte adhesion. These sequences represent portions
 CC of the P-selectin sequence. They inhibit binding of P, E and L
 CC selectins, so inhibit cellular adherence, particularly of leukocytes
 CC to platelets and endothelium. They can be used to treat
 CC inflammation, coagulation, ischemia, reperfusion injury, bacterial
 CC sepsis, disseminated intravenous coagulation, adult respiratory
 CC distress syndrome, tumour metastasis, rheumatoid arthritis and
 CC atherosclerosis.

SQ Sequence 8 AA;

Query Match 33.3%; Score 29; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSSY 8
 DB 3 YSSY 7

RESULT 15
 AAR50023
 ID AAR50023 standard; peptide; 8 AA.
 AC AAR50023;

XX 22-SEP-1994 (first entry)

DT XX Leukocyte adhesion inhibiting peptide #11.

DE XX Inhibitor: leukocyte; adhesion; P-selectin; cellular adherence;
 KW platelet; endothelium; inflammation; coagulation; ischemia;
 KW reperfusion injury; bacterial sepsis; atherosclerosis;
 KW disseminated intravenous coagulation; rheumatoid arthritis;
 KW adult respiratory distress syndrome; tumour metastasis.

XX Synthetic.

OS WO9405314-A.

PN 17-MAR-1994.

PD 24-AUG-1993: 93WO-US07964.

XX 08-SEP-1992: 92US-0941652.

PR (CENT) CENTOCOR INC.

XX Epps LA, Heavner GA;

PI WPI; 1994-100852/12.

XX New peptide(s) which inhibit binding of selectins - esp. to
 PT prevent leukocyte adhesion, useful for treating inflammation,
 PT reperfusion injury etc., also for diagnosis of defective
 PT selectin-binding ligands

XX Claim 4; Page 39; 56pp; English.

PS The sequences given in AAR50013-35 are peptides which are capable of
 XX inhibiting leukocyte adhesion. These sequences represent portions
 CC of the P-selectin sequence. They inhibit binding of P, E and L
 CC selectins, so inhibit cellular adherence, particularly of leukocytes
 CC to platelets and endothelium. They can be used to treat
 CC inflammation, coagulation, ischemia, reperfusion injury, bacterial
 CC sepsis, disseminated intravenous coagulation, adult respiratory
 CC distress syndrome, tumour metastasis, rheumatoid arthritis and
 CC atherosclerosis.

XX Sequence 8 AA:

Query Match 33.3%; Score 29; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Gaps 0;

OY 4 YSSSY 8

DB 4 YSSSY 8

Search completed: February 25, 2003, 11:50:30
 Job time : 85 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:51:27 ; Search time 12 Seconds
(without alignments)
36.248 Million cell updates/sec

Title: US-09-743-482A-12

Perfect score: 87

Sequence: 1 DMHYSSYRPFAY 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 31954

Minimum DB seq length: 0

Maximum DB seq length: 14

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	37.9	13	10	US-09-950-313-51
2	29	33.3	8	9	US-09-900-936-27
3	29	33.3	8	10	US-09-771-192-27
4	29	33.3	8	10	US-09-837-697A-27
5	28	33.3	13	9	US-09-309-196-108
6	28	32.2	9	9	US-09-900-936-35
7	28	32.2	9	10	US-09-771-192-35
8	27	31.0	9	10	US-09-748-451-19
9	27	31.0	10	9	US-09-810-601-35
10	27	31.0	10	9	US-09-810-601-36
11	27	31.0	10	9	US-09-810-601-37
12	27	31.0	13	9	US-10-016-634A-101
13	27	31.0	14	10	US-09-155-076-1
14	26	29.9	8	9	US-09-185-908-92
15	26	29.9	9	9	US-09-185-908-93
16	26	29.9	10	9	US-09-185-908-94
17	26	29.9	14	10	US-09-056-1608-3
18	25.5	29.3	13	9	US-09-971-980-52
19	25	28.7	7	9	US-09-782-397-21

20	25	28.7	8	9	US-09-900-936-24	Sequence 24, Appl
21	25	28.7	8	10	US-09-771-192-24	Sequence 24, Appl
22	25	28.7	8	10	US-09-828-708-50	Sequence 50, Appl
23	25	28.7	8	10	US-09-828-708-53	Sequence 53, Appl
24	25	28.7	8	10	US-09-837-697A-24	Sequence 24, Appl
25	25	28.7	9	10	US-09-935-682-21	Sequence 21, Appl
26	25	28.7	11	10	US-09-780-070-21	Sequence 21, Appl
27	25	28.7	11	10	US-09-813-653-22	Sequence 22, Appl
28	24.5	28.2	9	9	US-09-185-908-145	Sequence 145, App
29	24	27.6	5	9	US-09-900-936-15	Sequence 15, Appl
30	24	27.6	5	10	US-09-771-192-15	Sequence 15, Appl
31	24	27.6	5	10	US-09-837-697A-15	Sequence 15, Appl
32	24	27.6	6	9	US-09-900-936-3	Sequence 3, Appl1
33	24	27.6	6	10	US-09-771-192-3	Sequence 3, Appl1
34	24	27.6	6	10	US-09-837-697A-3	Sequence 3, Appl1
35	24	27.6	6	10	US-09-147-450-10	Sequence 10, Appl
36	24	27.6	7	9	US-09-900-936-2	Sequence 2, Appl1
37	24	27.6	7	9	US-09-900-936-12	Sequence 12, Appl
38	24	27.6	7	10	US-09-771-192-2	Sequence 2, Appl1
39	24	27.6	7	10	US-09-837-697A-2	Sequence 2, Appl1
40	24	27.6	7	10	US-09-837-697A-12	Sequence 12, Appl
41	24	27.6	7	10	US-09-837-697A-12	Sequence 12, Appl
42	24	27.6	8	9	US-09-900-936-1	Sequence 1, Appl1
43	24	27.6	8	9	US-09-900-936-22	Sequence 22, Appl
44	24	27.6	8	9	US-09-900-936-23	Sequence 23, Appl
45	24	27.6	9	9	US-09-900-936-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-09-950-313-51

Sequence 51, Application US/09950313

Patent No. US20020102610A1

GENERAL INFORMATION:

APPLICANT: TOWNSEND, ROBERT

APPLICANT: ROBINSON, ANDREW

TITLE OF INVENTION: AUTOMATED IDENTIFICATION OF PEPTIDES

FILE REFERENCE: 9195-064

CURRENT APPLICATION NUMBER: US/09/950,313

CURRENT FILING DATE: 2001-09-10

PRIOR APPLICATION NUMBER: UK 0022,136.6

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/232,273

PRIOR FILING DATE: 2000-09-13

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PatentIn version 3.1

SEQ ID NO 51

LENGTH: 13

TYPE: PRT

ORGANISM: Homo sapiens

US-09-950-313-51

Query Match

Best Local Similarity 37.9%; Score 33; DB 10; Length 13;

Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DMHYSSYRPF 11

DB 2 EYHFLSPVSP 12

RESULT 2

US-09-900-936-27

Sequence 27, Application US/09900936

Patent No. US20020105141A1

GENERAL INFORMATION:

APPLICANT: Rodgers, Kathleen

APPLICANT: dizerega, Gere

TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation

TITLE OF INVENTION: or Differentiation

FILE REFERENCE: 00-506-A

CURRENT APPLICATION NUMBER: US/09/900,936
CURRENT FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 27
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: All analogue 9
US-09-900-936-27

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 YIRPF 12
DB 4 YIRPF 8

RESULT 3
US-09-771-192-27
Sequence 27, Application US/09771192
Patent No. US2002049162A1
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
FILE REFERENCE: 99-1043-A
CURRENT APPLICATION NUMBER: US/09/771,192
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 27
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: All analogue 9
US-09-771-192-27

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 YIRPF 12
DB 4 YIRPF 8

RESULT 4
US-09-837-697A-27
Sequence 27, Application US/09837697A
Patent No. US20020146823A1
GENERAL INFORMATION:
APPLICANT: University of Southern California
APPLICANT: Rogers, Kathleen E.
APPLICANT: diZerega, Gere
TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Proliferation
FILE REFERENCE: 97,017-F1A
CURRENT APPLICATION NUMBER: US/09/837,697A
CURRENT FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentln version 3.1
SEQ ID NO 27
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: All analogue 9
US-09-837-697A-27

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 YIRPF 12
DB 4 YIRPF 8

RESULT 5
US-09-309-196-108
Sequence 108, Application US/09309196
Publication No. US20030008380A1
GENERAL INFORMATION:
APPLICANT: FOWLES, Dana M.
APPLICANT: BROACH, Jim
APPLICANT: MANFREDI, John
APPLICANT: KLEIN, Christine
APPLICANT: MORPHY, Andrew J.
APPLICANT: PAUL, Jeremy
APPLICANT: TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/309,196
CLASSIFICATION:
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/322,137
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOLWES-2C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-309-196-108

Query Match
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 WHYYSSY 8
DB 1 WHWLSLY 7

RESULT 6

US-09-900-936-35
; Sequence 35, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dzizega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; TITLE OF INVENTION: or Differentiation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue 17
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: homo Ser
US-09-900-936-35

Query Match 32.2%; Score 28; DB 9; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.3e+05;

Matches 5; Conservative 0; Mismatches 1; Indels 0;

OY 7 SYIRPF 12
||| ||

Db 4 SYIRPF 9

RESULT 7

US-09-771-192-35
; Sequence 35, Application US/09771192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dzizega, Gere
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A
; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue 17
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: homo Ser
US-09-771-192-35

Query Match 32.2%; Score 28; DB 10; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.3e+05;

Matches 5; Conservative 0; Mismatches 1; Indels 0;

OY 7 SYIRPF 12
||| ||

Db 4 SYIRPF 9

RESULT 8

US-09-748-451-19
; Sequence 19, Application US/09748451
; Patent No. US20010011078A1

; GENERAL INFORMATION:

; APPLICANT: WANG, XIAODONG
; APPLICANT: LIU, XUESONG
; TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN APOPTOSIS
; FILE REFERENCE: US200107545A1
; CURRENT APPLICATION NUMBER: US/09/748,451
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/061,702
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-748-451-19

Query Match 31.0%; Score 27; DB 10; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.3e+05;

OY 1 DMHYT 5
||| ||

Db 3 DMHYT 7

RESULT 9

US-09-810-601-35
; Sequence 35, Application US/09810601
; Patent No. US2002017545A1
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Compositions and Methods for Treating Gonadotrophin
; TITLE OF INVENTION: Related Illnesses
; FILE REFERENCE: 2947
; CURRENT APPLICATION NUMBER: US/09/810,601
; CURRENT FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gonadotrophin
; OTHER INFORMATION: Release Hormone Analogue
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa at position 1 is Pyroglu; PYRROLIDONE
; OTHER INFORMATION: CARBOXYLIC ACID;
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: Xaa at position 10 is Gly-NH2; AMIDATION
; PUBLICATION INFORMATION:
; PATENT DOCUMENT NUMBER: 5631226
; PATENT FILING DATE: 1993-07-07
; PUBLICATION DATE: 1997-05-20
; PUBLICATION INFORMATION:
; AUTHORS: Rouselle, Christophe
; JOURNAL: Mol. Pharmacol.
; VOLUME: 57
; PAGES: 679-686
; DATE: 2000
US-09-810-601-35

Query Match 31.0%; Score 27; DB 9; Length 10;

Best Local Similarity 50.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 YYSYIRP 11
::| |::|

Db 2 HWSYIRP 9

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RESULT 10
US-09-810-601-36
; Sequence 36, Application US/09810601
; Patent No. US20020177545A1
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Compositions and Methods for Treating Gonadotrophin
; FILE REFERENCE: 2947
; CURRENT APPLICATION NUMBER: US/09/810,601
; CURRENT FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gonadotrophin
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa at position 1 is Pyroglu; PYRROLIDONE
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: Xaa at position 10 is ethylamide
; PUBLICATION INFORMATION:
; PATENT DOCUMENT NUMBER: 5631226
; PATENT FILING DATE: 1993-07-07
; PUBLICATION DATE: 1997-05-20
; AUTHORS: Roussette, Christophe
; JOURNAL: Mol. Pharmacol.
; VOLUME: 57
; PAGES: 679-686
; DATE: 2000
; US-09-810-601-36

Query Match
Best Local Similarity 31.0%; Score 27; DB 9; Length 10;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 YVSSYLRP 11
Db 2 HWSYLRLP 9

RESULT 11
US-09-810-601-37
; Sequence 37, Application US/09810601
; Patent No. US20020177545A1
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Compositions and Methods for Treating Gonadotrophin
; FILE REFERENCE: 2947
; CURRENT APPLICATION NUMBER: US/09/810,601
; CURRENT FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 10
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gonadotrophin
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa at position 1 is Pyroglu; PYRROLIDONE
; OTHER INFORMATION: CARBOXYLIC ACID;
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NAME/KEY: MOD_RES
LOCATION: (10)
OTHER INFORMATION: Xaa at position 10 is Aza-gly-NH2
PUBLICATION INFORMATION:
PATENT DOCUMENT NUMBER: 5631226
PATENT FILING DATE: 1993-07-07
PUBLICATION DATE: 1997-05-20
AUTHORS: Roussette, Christophe
JOURNAL: Mol. Pharmacol.
VOLUME: 57
PAGES: 679-686
DATE: 2000
US-09-810-601-37

Query Match
Best Local Similarity 31.0%; Score 27; DB 9; Length 10;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 YVSSYLRP 11
Db 2 HWSYLRLP 9

RESULT 12
US-10-016-634A-101
; Sequence 101, Application US/10016634A
; Patent No. US20020192666A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Hervé
; APPLICANT: Ghosh, Malavika
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and
; FILE REFERENCE: DEX-0255
; CURRENT APPLICATION NUMBER: US/10/016,634A
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,258
; PUBLICATION DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 13
; TYPE: PRP
; ORGANISM: Homo sapiens
; US-10-016-634A-101

Query Match
Best Local Similarity 31.0%; Score 27; DB 9; Length 13;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DMHYS 6
Db 7 DMHLS 12

RESULT 13
US-09-155-076-1
; Sequence 1, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
; APPLICANT: Greenfield et al., Susan A.
; TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCOLINESTERASE,
; FILE REFERENCE: 98-0967*/WMC/00263
; CURRENT APPLICATION NUMBER: US/09/155,076A
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: PRP
; ORGANISM: Artificial Sequence
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
US-09-155-076-1

Query Match

Best Local Similarity 31.0%; Score 27; DB 10; Length 14;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 DMHYSSYI 9

DB 2 EFHWMSSYM 10

RESULT 14

US-09-185-908-92
Sequence 92, Application US/09185908A
Publication No. US20020193294A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
FILE REFERENCE: 100086.409
CURRENT APPLICATION NUMBER: US/09/185,908A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 92
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Product of
FEATURE:
OTHER INFORMATION: synthesis based on mouse claudin-1 sequence
US-09-185-908-92

Query Match

Best Local Similarity 29.9%; Score 26; DB 9; Length 8;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 DMHYYS 6

DB 1 DMKIYS 6

RESULT 15

US-09-185-908-93
Sequence 93, Application US/09185908A
Publication No. US20020193294A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
FILE REFERENCE: 100086.409
CURRENT APPLICATION NUMBER: US/09/185,908A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 93
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Product of
FEATURE:
OTHER INFORMATION: synthesis based on mouse claudin-1 sequence
US-09-185-908-93

Query Match

29.9%; Score 26; DB 9; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 DMHYYS 6

DB 1 DMKIYS 6

Search completed: February 25, 2003, 11:55:59
Job time : 13 secs

4. 5.

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:47:22 : Search time 27 Seconds
(without alignments)
106.839 Million cell updates/sec

Title: US-09-743-482A-12
Perfect score: 87
Sequence: 1 DMHYSSYRPFAY 14

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 2683

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	32.2	8	13	P79940 xenopus lae
2	28	32.2	14	2	P82996 pseudomonas
3	27	31.0	10	13	O9PS07 O9PS07 alligator m
4	24	27.6	10	13	O9PRY8 triakis scy
5	24	27.6	14	5	O10757 thermomyzom
6	22	25.3	9	4	O9UC36 homo sapien
7	21	24.1	12	2	O53183 rhodococcus
8	20	23.0	11	4	O60842 homo sapien
9	20	23.0	13	13	O9PVC5 galaxias ma
10	20	23.0	13	13	O9PVB7 fundulus he
11	20	23.0	13	13	O9PVB6 poecilia la
12	20	23.0	13	13	O9PVB5 sargocentrio
13	20	23.0	13	13	O9PVB4 zeus faber
14	20	23.0	13	13	O9PVB3 hippocampus
15	20	23.0	13	13	O9PVB2 mastacembel
16	20	23.0	13	13	O9PVB1 dendrochiru

17	20	23.0	13	13	O9PVB0 dicentrarch
18	20	23.0	13	13	O9PVA9 epinephelus
19	20	23.0	13	13	O9PVA7 diplosiphichu
20	20	23.0	13	13	O9PVA6 salarias sp
21	20	23.0	13	13	O9PVA5 cryptocentri
22	20	23.0	13	13	O9PVA4 siganus sp.
23	20	23.0	13	13	O9PVA3 acanthurus
24	20	23.0	13	13	O9PVA2 thunnus sp.
25	20	23.0	13	13	O9PVA1 stromateus
26	20	23.0	13	13	O9PVA0 colisa laii
27	20	23.0	13	13	O9PV99 channa sp.
28	20	23.0	13	13	O9PV98 psittodes s
29	20	23.0	13	13	O9PV97 balistes sp
30	20	23.0	13	13	O9PV96 ostracion s
31	20	23.0	13	13	O9PV95 mola mola (
32	20	23.0	14	8	O98696 hordeum vul
33	20	23.0	14	12	O98692 human cytom
34	19	21.8	9	8	O8W8X4 diadema mex
35	19	21.8	10	12	O90349 hepatitis g
36	19	21.8	10	13	O9PRU9 sparus aura
37	19	21.8	13	4	O9UC27 homo sapien
38	19	21.8	13	12	O91BN1 influenza a
39	19	21.8	14	2	O9R506 burkholderi
40	19	21.8	14	8	O9MT61 allium cepa
41	19	21.8	14	8	O9MRV1 allium satl
42	19	21.8	14	8	O9MRV4 allium por
43	19	21.8	14	8	O9MRT8 aloce vera (
44	18	20.7	7	8	O98866 spinacia ol
45	18	20.7	10	8	P82136 spinacia ol

ALIGNMENTS

RESULT 1

ID P79940 PRELIMINARY: PRT: 8 AA.
AC P79940;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE XMeis1-4 protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=6335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97202105; PubMed-9049632;
RA Steelman S., Moskow J.J., Muzynski K., North C., Druck T.,
RA Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.,
RT "Identification of a conserved family of Meis1-related homeobox
RT genes.";
RL Genome Res. 7:142-156(1997).
DR EMBL; U68389; AAB19199.1; -.
DR TRANSFAC; T03410; -.
FT NON_TER
SQ SEQUENCE 8 AA: 1187 MW: 278B51F37B11F40B CRC64:

Query Match 32.2%; Score 28; DB 13; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DMHY 4
DB 4 EWHY 7
RESULT 2
ID P82996 PRELIMINARY: PRT: 14 AA.
AC P82996;

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DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Glutathione S-transferase (EC 2.5.1.18) (Fragment).
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, SUBUNIT, AND SUBCELLULAR
  LOCATION.
RX STRAIN=PAW85;
RX PubMed=11900268;
RA Santos P.M., Mignogna G., Heipleper H.J., Zennaro E.;
RT "Occurrence and properties of glutathione S-transferases in phenol-
  degrading Pseudomonas strains";
RL Res. Microbiol. 153:89-98(2002).
CC -1- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER OF
  EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
CC -1- CATALYTIC ACTIVITY: RX + GLUTATHIONE = HX + R-S-GLUTATHIONE.
CC -1- SUBUNIT: MONOMER AND HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY.
KM Transferase.
FT NON_TER
SQ SEQUENCE 14 AA; 1741 MW; 22CB292210EE3B7 CRC64;

Query Match
Best Local Similarity 32.2%; Score 28; DB 2; Length 14;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 WHYYS 6
   :|||
   2 WHYYS 6

RESULT 3
ID Q9PS07 PRELIMINARY; PRT; 10 AA.
AC Q9PS07;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE Angiotensin I, ANG I.
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RX MEDLINE=93307610; PubMed=8319878;
RA Takel Y., Silldorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,
RT Stephens G.A., Sakakibara S.;
RT "New angiotensin I isolated from a reptile, Alligator
  mississippiensis";
RL Gen. Comp. Endocrinol. 90:214-219(1993).
FT NON_TER
SQ SEQUENCE 10 AA; 1216 MW; CEE3BD761F2DB42 CRC64;

Query Match
Best Local Similarity 31.0%; Score 27; DB 13; Length 10;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 YIRPFA 13
   :|||
   4 YIRPFA 9

RESULT 4
ID Q9PRY8 PRELIMINARY; PRT; 10 AA.
AC Q9PRY8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

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DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE Angiotensin I.
OS Triakis scyllium (Leopard shark) (Triakis scyllia).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes; Triakidae;
OC Triakis.
OX NCBI_TaxID=30494;
RN [1]
RP SEQUENCE.
RX MEDLINE=94141412; PubMed=8308464;
RA Takel Y., Hasegawa Y., Watanabe T.X., Nakajima K., Hazon N.;
RT "A novel angiotensin I isolated from an elasmobranch fish.";
RL J. Endocrinol. 139:281-285(1993).
SQ SEQUENCE 10 AA; 1284 MW; 20F02FD761E04B47 CRC64;

Query Match
Best Local Similarity 27.6%; Score 24; DB 13; Length 10;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 YIRPF 12
   :|||
   4 YIRPF 8

RESULT 5
ID Q10757 PRELIMINARY; PRT; 14 AA.
AC Q10757;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE Angiotensinogen (Fragment).
OS Thromyzon tessulatum (leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudindae; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Thromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RX MEDLINE=95365039; PubMed=7637887;
RA Laurent V., Bulet P., Salzert M.A.;
RT "A comparison of the leech Thromyzon tessulatum angiotensin I-like
  molecule with forms of vertebrate angiotensinogens: a hormonal system
  conserved in the course of evolution.";
RL Neurosci. Lett. 190:175-178(1995).
RN [2]
RP SEQUENCE OF 1-10.
RC TISSUE=BRAIN;
RX MEDLINE=96201949; PubMed=8612806;
RA Laurent V., Salzert M.;
RT "Metabolism of angiotensins by head membranes of the leech Thromyzon
  tessulatum.";
RL FEBS Lett. 384:123-127(1996).
CC -1- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.
KM Glycoprotein; Serpin.
FT NON_TER
SQ SEQUENCE 14 AA; 1763 MW; 335109D8EEFBD7 CRC64;

Query Match
Best Local Similarity 27.6%; Score 24; DB 5; Length 14;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 YIRPF 12
   :|||
   4 YIRPF 8

RESULT 6
ID Q9UC36 PRELIMINARY; PRT; 9 AA.
AC Q9UC36;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

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```

DE 28 kDa heat shock protein homolog fragment 1 (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92218434; PubMed=1560006;
RA Kato K., Shinozaki H., Goto S., Inaguma Y., Morishita R., Asano T.;
RT "Copurification of small heat shock protein with alpha B crystallin
RT from human skeletal muscle."
RL J. Biol. Chem. 267:7718-7725(1992).
FT NON_TER
SQ SEQUENCE 9 AA; 1220 MW; 26933415B1F77B43 CRC64;

Query Match
Best Local Similarity 25.3%; Score 22; DB 4; Length 9;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DMHYIS 6
DB 1 DMVPHS 6

RESULT 7
053183 PRELIMINARY; PRT; 12 AA.
ID 053183;
AC 053183;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Beta-subunit of nitrile hydratase (Fragment).
OS Rhodococcus sp.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=1831;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N-774;
RX MEDLINE=95072315; PubMed=7765511;
RA Hashimoto Y., Nishiyama M., Horinouchi S., Beppu T.;
RT "The nitrile hydratase gene from Rhodococcus sp. N-774 requires its
RT downstream region for efficient expression."
RL Biosci. Biotechnol. Biochem. 58:1859-1865(1994).
DR EMBL: D30033; BAA06273.1;
DR InterPro: IPR003168; Nhasse_beta.
DR Pfam: PF02211; Nhasse_beta; 1.
FT NON_TER
SQ SEQUENCE 12 AA; 1323 MW; 7A5DEF7D993B587B CRC64;

Query Match
Best Local Similarity 24.1%; Score 21; DB 2; Length 12;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 YSYIRPEA 13
DB 4 EGYLEPAA 12

RESULT 8
060842 PRELIMINARY; PRT; 11 AA.
ID 060842;
AC 060842;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Carbonic anhydrase (Fragment).
GN CA3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RA Sowden J., Smith H., Morrison K., Edwards Y.;
RT "Sequence comparisons and functional studies of the proximal promoter
RT of the carbonic anhydrase 3 (CA3) gene."
RL Gene 214:157-165(1999).
DR EMBL: AJ006473; CA07056.1;
FT NON_TER
SQ SEQUENCE 11 AA; 1293 MW; 7DB6AF84CB58637B CRC64;

Query Match
Best Local Similarity 23.0%; Score 20; DB 13; Length 11;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DMHYIS 6
DB 4 EWGYAS 9

RESULT 9
09PVC5 PRELIMINARY; PRT; 13 AA.
ID 09PVC5;
AC 09PVC5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Galaxias maculatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proteocephalopterygii; Salmoniformes; Galaxiidae; Galaxias.
OX NCBI_TaxID=61620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GH4AGAL;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL: AF134600; AAD54085.1;
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF00103; hormone; 1.
FT NON_TER
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match
Best Local Similarity 23.0%; Score 20; DB 13; Length 13;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DMHYSSYI 9
DB 5 DMHKEVYL 13

RESULT 10
09PVB7 PRELIMINARY; PRT; 13 AA.
ID 09PVB7;
AC 09PVB7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Fundulus heteroclitus (killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]

```

RP SEQUENCE FROM N.A.
 RC STRAIN-GH4AFUNDULUS;
 RX MEDLINE-99398697; PubMed-10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate evolution."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL: AF134608; AAD54093.1;
 DR InterPro: IPR001400; Somatotropin.
 DR Pfam: PF00103; hormone; 1.
 FT NON_TER 1 13
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 23.0%; Score 20; DB 13; Length 13;
 Best Local Similarity 33.3%; Pred. No. 8.2e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 DMHYSSYI 9
 DB 5 DMHKVETYL 13

RESULT 11
 O9PVB6 PRELIMINARY; PRT; 13 AA.
 ID O9PVB6;
 AC O9PVB6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Growth hormone (Fragment).
 GN GH.
 OS Poecilia latipinna.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
 OC Cyprinodontiformes; Poeciliidae; Poecilia.
 OX NCBI_TaxID=48699;
 RN (1)
 RN SEQUENCE FROM N.A.
 RC STRAIN-GH4AMOLLY;
 RX MEDLINE-99398697; PubMed-10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate evolution."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL: AF134609; AAD54094.1;
 DR InterPro: IPR001400; Somatotropin.
 DR Pfam: PF00103; hormone; 1.
 FT NON_TER 1 13
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 23.0%; Score 20; DB 13; Length 13;
 Best Local Similarity 33.3%; Pred. No. 8.2e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 DMHYSSYI 9
 DB 5 DMHKVETYL 13

RESULT 12
 O9PVB5 PRELIMINARY; PRT; 13 AA.
 ID O9PVB5;
 AC O9PVB5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Growth hormone (Fragment).
 GN GH.
 OS Sargocentron sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Beryciformes; Holocentridae;
 OC Sargocentron.
 OX NCBI_TaxID=94226;
 RN (1)
 RN SEQUENCE FROM N.A.
 RC STRAIN-GH4ASQUIR;
 RX MEDLINE-99398697; PubMed-10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate evolution."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL: AF134610; AAD54095.1;
 DR InterPro: IPR001400; Somatotropin.
 DR Pfam: PF00103; hormone; 1.
 FT NON_TER 1 13
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 23.0%; Score 20; DB 13; Length 13;
 Best Local Similarity 33.3%; Pred. No. 8.2e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 DMHYSSYI 9
 DB 5 DMHKVETYL 13

RESULT 13
 O9PVB4 PRELIMINARY; PRT; 13 AA.
 ID O9PVB4;
 AC O9PVB4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Growth hormone (Fragment).
 GN GH.
 OS Zeus faber (John Dory).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Zelformes; Zelfidae; Zeus.
 OX NCBI_TaxID=64108;
 RN (1)
 RN SEQUENCE FROM N.A.
 RC STRAIN-GH4ADIRIES;
 RX MEDLINE-99398697; PubMed-10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate evolution."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL: AF134611; AAD54096.1;
 DR InterPro: IPR001400; Somatotropin.
 DR Pfam: PF00103; hormone; 1.
 FT NON_TER 1 13
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 23.0%; Score 20; DB 13; Length 13;
 Best Local Similarity 33.3%; Pred. No. 8.2e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 DMHYSSYI 9
 DB 5 DMHKVETYL 13

RESULT 14
 O9PVB3 PRELIMINARY; PRT; 13 AA.
 ID O9PVB3;
 AC O9PVB3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE Growth hormone (Fragment).
 GN GH.
 OS Hippocampus sp.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percomorpha; Gastroleiiformes;
 CC Synbranchiidae; Hippocampus.
 OX NCBI_TaxID=72047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GH4SEAHOUSE;
 RX MEDLINE=99398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate
 evolution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL: AF134613; AAD54097.1;
 DR InterPro: IPR001400; Somatotropin.
 FT Non_TER 1
 FT NON_TER 13
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 23.0%; Score 20; DB 13; Length 13;
 Best Local Similarity 33.3%; Pred. No. 8.2e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

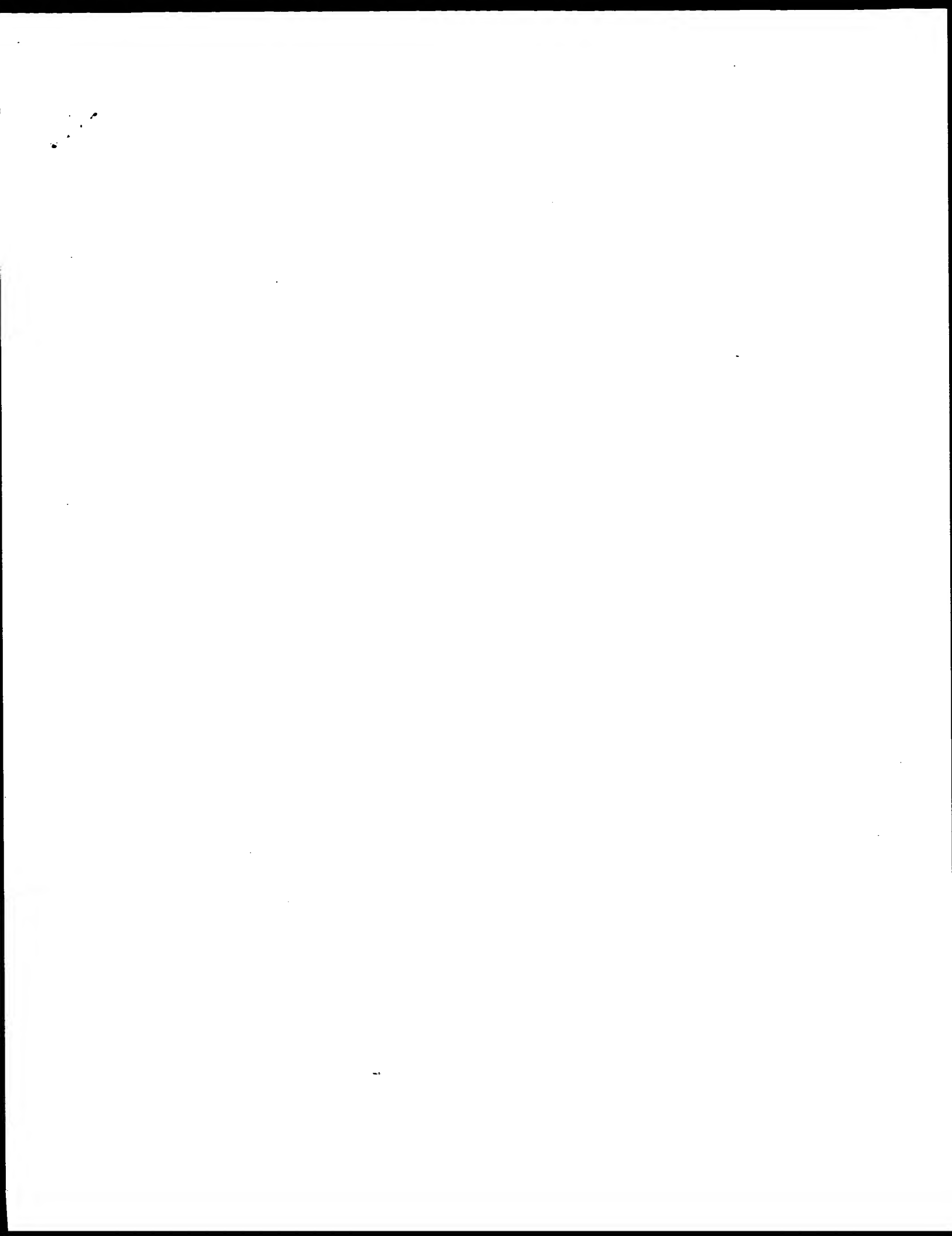
QY 1 DMHYSSYI 9
 | | : | :
 Db 5 DMHKVETYL 13

RESULT 15

Q9PVB2 PRELIMINARY; PRT; 13 AA.
 AC Q9PVB2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Growth hormone (Fragment).
 GN GH.
 OS Mastacembelus sp.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percomorpha; Synbranchiiformes;
 CC Mastacembelidae; Mastacembelus.
 OX NCBI_TaxID=94235;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GH4AMASTA;
 RX MEDLINE=99398697; PubMed=10468597;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate
 evolution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL: AF134613; AAD54098.1;
 DR InterPro: IPR001400; Somatotropin.
 DR Pfam: PF00103; hormone; 1.
 FT Non_TER 1
 FT NON_TER 13
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 23.0%; Score 20; DB 13; Length 13;
 Best Local Similarity 33.3%; Pred. No. 8.2e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DMHYSSYI 9
 | | : | :
 Db 5 DMHKVETYL 13



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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:41:27 : Search time 11 seconds

(without alignments)
52.788 Million cell updates/sec

Title: US-09-743-482a-12

Sequence: 87
1 DMHYSSYIRPFAY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 633

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	27.6	8	1	ANG2_BOTJA
2	24	27.6	10	1	ANGT_CHICK
3	24	27.6	10	1	GONI_CHEPR
4	24	27.6	14	1	ANGT_HORSE
5	24	27.6	14	1	HY14_PIG
6	23	26.4	10	1	ANG1_BOTJA
7	23	26.4	10	1	ANGT_BOVIN
8	23	26.4	11	1	ANGT_CRIGE
9	19	21.8	8	1	ALL3_CYPDO
10	19	21.8	8	1	ALL4_CALVO
11	19	21.8	8	1	ALL4_CALVO
12	19	21.8	14	1	MAST_POLJA
13	18	20.7	7	1	FAR3_HABCO
14	18	20.7	7	1	FAR3_PANRE
15	18	20.7	8	1	ALL6_CARMA
16	18	20.7	9	1	ALL6_CARMA
17	18	20.7	9	1	FARP_CALSI
18	18	20.7	11	1	CS15_BACSU
19	18	20.7	14	1	CXAL_CONCN
20	18	20.7	14	1	MARI_ALTSP
21	17	19.5	7	1	ALL3_CARMA
22	17	19.5	7	1	ALL4_CARMA
23	17	19.5	7	1	ALL5_CARMA
24	17	19.5	7	1	HY7_PIG
25	17	19.5	8	1	AKH_MEIHL
26	17	19.5	8	1	ALL7_CARMA
27	17	19.5	8	1	ALL8_CARMA
28	17	19.5	8	1	ALL9_CARMA
29	17	19.5	8	1	PKR2_PERAM
30	17	19.5	10	1	AKHX_LOCM1
31	17	19.5	10	1	GONI_ALIMI
32	17	19.5	10	1	GONI_ONCKE
33	17	19.5	10	1	GONI_PETMA

34	17	19.5	10	1	Q2OB_COMTE
35	17	19.5	12	1	UR2A_CARCO
36	17	19.5	12	1	UR2B_CARCO
37	17	19.5	12	1	UR2B_CYPRA
38	17	19.5	12	1	UR2_GILMT
39	17	19.5	12	1	UR2_POLSP
40	17	19.5	12	1	UR2_SCYCA
41	17	19.5	13	1	YPE2_LACIC
42	17	19.5	14	1	ECDC_LYMDI
43	16	18.4	5	1	HTF_ARPTR
44	16	18.4	10	1	HTF_TABAT
45	16	18.4	10	1	TKNB_ONCMY

ALIGNMENTS

RESULT 1					
ANG2_BOTJA	STANDARD:	PRT:	8 AA.		
AC 010582:					
DT 01-OCT-1996 (Rel. 34, Created)					
DT 01-OCT-1996 (Rel. 34, Last sequence update)					
DT 15-DEC-1998 (Rel. 37, Last annotation update)					
DE Angiotensin-like peptide II (Fragment).					
OS Bothrops jararaca (Jararaca).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;					
OC Viperidae; Crotalinae; Bothrops.					
OX NCBI_TaxID=8724;					
RN [1]					
RP SEQUENCE.					
RC TISSUE=Plasma;					
RX MEDLINE=96208932; PubMed=8829801;					
RA Borgehesi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;					
RT "Isolation and identification of angiotensin-like peptides from the					
RT Plasma of the snake Bothrops jararaca."					
RL Comp. Biochem. Physiol. 113B:467-473(1996).					
CC -I- SIMILARITY: BELONGS TO THE SERPIN FAMILY.					
DR Interpro: IPR000215; Serpin.					
DR PROSITE: PS00284; SERPIN; PARTIAL.					
KW Vasoconstrictor; Plasma; Serpin.					
FT NON_TER					
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;					
Query Match 27.6%; Score 24; DB 1; Length 8;					
Best Local Similarity 80.0%; Pred. No. 1; 1e-05;					
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY 8 YRPF 12					
DB 4 YHPF 8					
RESULT 2					
ANGT_CHICK	STANDARD:	PRT:	10 AA.		
AC P01018:					
DT 21-JUL-1986 (Rel. 01, Created)					
DT 21-JUL-1986 (Rel. 01, Last sequence update)					
DT 15-JUN-2002 (Rel. 41, Last annotation update)					
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang					
DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]					
DE (Fragment).					
GN AGT OR SERPINB8.					
OS Gallus gallus (Chicken), and					
OS Coturnix coturnix japonica (Japanese quail).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;					
OC Gallus.					
OX NCBI_TaxID=9031, 93934;					
RN [1]					
RP SEQUENCE.					

RC SPECIES-Chicken;
 RA MEDLINE=74127845; PubMed=4361802;
 RA Nakayama T., Nakajima T., Sotabe H.;
 RT "Comparative studies on angiotensins. 3. Structure of fowl
 RT angiotensin and its identification by DNS-method.";
 RL Chem. Pharm. Bull. 21:2085-2087(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-C.C. Japonica;
 RX MEDLINE=90284684; PubMed=2191893;
 RA Takel Y., Hasegawa Y.;
 RT "Vasopressor and depressor effects of native angiotensins and
 RT inhibition of these effects in the Japanese quail.";
 RL Gen. Comp. Endocrinol. 79:12-22(1990).
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN, ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR: A01250; A01250.
 DR PIR: A90917; A90917.
 DR PIR: A60624; A60624.
 DR InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1232 MW; CEFEBDD761F2DB42 CRC64;
 Query Match 27.6%; Score 24; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 4.5e+02;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 8 YIRPFA 13
 ID 1 11
 Db 4 YIHFFS 9
 AC P80677;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Gonadolibetin I (Gonadotropin-releasing hormone I) (GNRH-I)
 DE (Lulibetin I).
 OS Chelysoma productum.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 OC Phlebobranchia; Corellidae; Chelysoma.
 OX NCBI_Taxid=71177;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96413669; PubMed=8816823;
 RA Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
 RA Park M., Rivlier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;
 RT "Two new forms of gonadotropin-releasing hormone in a protochordate
 RT and the evolutionary implications.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).
 CC -1- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND
 CC FOLLICLE-STIMULATING HORMONES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: GNRH NEURONS LIE WITHIN BLOOD SINUSUS CLOSE TO
 CC THE GONADUCTS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING
 CC THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.
 CC -1- MASS SPECTROMETRY: MW=1246.56; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
 DR InterPro: IPR002012; GNRH.

DR Pfam: PF00446; GNRH. 1.
 DR PROSITE: PS00473; GNRH. 1.
 KW Hormone; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 10 AA; 1264 MW; 284B3639DB5AB5A3 CRC64;
 Query Match 27.6%; Score 24; DB 1; Length 10;
 Best Local Similarity 37.5%; Pred. No. 4.5e+02;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 4 YYSYTRP 11
 ID 1 11
 Db 2 HNSDYFKP 9
 AC P01016;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
 DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
 DE (Fragment).
 GN AGT OR SERPIN8.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_Taxid=9796;
 RN [1]
 RP SEQUENCE.
 RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
 RT "The preparation, purification, and amino acid sequence of a
 RT polypeptide renin substrate.";
 RL J. Exp. Med. 106:439-453(1957).
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN, ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
 CC plasma.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR: A01250; A01250.
 DR InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFBD7 CRC64;
 Query Match 27.6%; Score 24; DB 1; Length 14;
 Best Local Similarity 80.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 YIRPFA 12
 ID 1 11
 Db 4 YIHFF 8
 AC P01155;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 RESULT 5
 ID HY14_PIG STANDARD; PRT; 14 AA.
 AC P01155;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)

DE Hypothalamic tetradecapeptide.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RA Schlesinger D.H., Niall H.D., Lanthicum G.L., Dupont A.,
RL Submitted (NOV-1976) to the PIR data bank.
DR PIR: A01419; MYPG14.
KW Amidation.
FT MOD_RES
SQ SEQUENCE 14 AA; 1648 MW; 3DD87E2419D3E47 CRC64;
Query Match 27.6%; Score 24; DB 1; Length 14;
Best Local Similarity 44.4%; Pred. No. 6.3e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY 6 SSYRPFAY 14
DB 6 SPYLPPLCY 14
RESULT 6
ANGT_BOVJA STANDARD; PRT; 10 AA.
ID ANGT_BOVJA
AC G10581;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide I (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucce J., Carmona E., Piccarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca."
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER
SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2D842 CRC64;
Query Match 26.4%; Score 23; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 6.3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 8 YIRPF 12
DB 4 YVHPF 8
RESULT 7
ANGT_BOVIN STANDARD; PRT; 10 AA.
ID ANGT_BOVIN
AC P01017;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
DE II); Angiotensin III (Ang III) (Des-Asp1]-angiotensin II)]
DE (Fragment).
GN AGT OR SERPINAB.
OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Elliott D.F., Peart W.S.;
RT "The amino acid sequence in a hypertensin."
RL Biochem. J. 65:246-254(1957).
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
CC plasma.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR PIR: A01250; A01250.
DR PIR: A90345; A90345.
DR InterPro: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 2 8 ANGIOTENSIN II.
FT NON_TER
SQ SEQUENCE 10 AA; 1282 MW; CEFEBDD761F2D842 CRC64;
Query Match 26.4%; Score 23; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 6.3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 8 YIRPF 12
DB 4 YVHPF 8
RESULT 8
ANGT_CRIGE STANDARD; PRT; 11 AA.
ID ANGT_CRIGE
AC P09037;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Crinia angiotensin II.
OS Crinia georgiana (Quacking frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Crinia.
OX NCBI_TaxID=8374;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=80024575; PubMed=488254;
RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
RT "Amino acid composition and sequence of crinia-angiotensin, an
RT angiotensin II-like endecapeptide from the skin of the Australian
RT frog Crinia georgiana."
RL Experientia 35:1132-1133(1979).
DR PIR: S07207; S07207.
KW Vasoconstrictor.
SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;
Query Match 26.4%; Score 23; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.9e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 8 YIRPF 12
DB 7 YVHPF 11

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RESULT 9
ALL3_CYPDPO STANDARD: PRT: 8 AA.
AC P82154:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Cydiastatin 3.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Ditrysia; Tortricidae; Tortricidae; Olethreutinae; Cydia.
NX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Davey H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD.RES 8 AA: 926 MW; C82879D5AB477415 CRC64;
SQ SEQUENCE 8 AA: 926 MW; C82879D5AB477415 CRC64;

Query Match 21.8%; Score 19; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1,1e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 RPEAY 14
DB 2 RPYSF 6

RESULT 10
ALL4_CALVO STANDARD: PRT: 8 AA.
ID ALL4_CALVO
AC P41840;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Callistostatin 4 (Leu-callistostatin 4).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Oestroidea; Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=93211980; PubMed=8460157;
RA Duvé H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callistostatin: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=94291167; PubMed=8020069;
RA Duvé H., Thorpe A.;
RT "Distribution and functional significance of Leu-callistostatins in
RT the blowfly Calliphora vomitoria.";
RL Cell Tissue Res. 276:367-379(1994).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -1- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCEBERAL
CC COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY
CC SYSTEM AND INTESTINE.

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CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR: D47393; D47393.
KW Neuropeptide; Amidation.
FT MOD.RES 8 AA: 954 MW; D32879D5AB47740A CRC64;
SQ SEQUENCE 8 AA: 954 MW; D32879D5AB47740A CRC64;

Query Match 21.8%; Score 19; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1,1e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 RPEAY 14
DB 2 RPYSF 6

RESULT 11
ALL4_CYPDPO STANDARD: PRT: 8 AA.
ID ALL4_CYPDPO
AC P82154;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 4.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Ditrysia; Tortricidae; Tortricidae; Olethreutinae; Cydia.
NX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Davey H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD.RES 8 AA: 910 MW; 922879D5AB47740D CRC64;
SQ SEQUENCE 8 AA: 910 MW; 922879D5AB47740D CRC64;

Query Match 21.8%; Score 19; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1,1e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 RPEAY 14
DB 2 RPYSF 6

RESULT 12
MAST_POLJA STANDARD: PRT: 14 AA.
ID MAST_POLJA
AC P01517;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Polistes mastoparan.
OS Polistes jadvigae (Paper wasp).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespidae; Vespidae; Polistinae; Polistes.
OX NCBI_TaxID=7457;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Hirai Y., Ueno Y., Yasuhara T., Yoshida H., Nakajima T.;
RA "A new mast cell degranulating peptide, polistes mastoparan, in the
RT venom of Polistes jadvigae.";
RL Biomed. Res. 1:185-187(1980).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
CC THAT COUPLE TO PHOSPHOLIPASE C.

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DR PIR: A01780; OMWAPP.
 KW Mast cell degradation; Venom; Amidation.
 FT MOD_RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA: 1636 MW: 26472A53BF477808 CRC64;
 Query Match 21.8%; Score 19; DB 1; Length 14;
 Best Local Similarity 33.3%; Pred. No. 3.3e+03;
 Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 DMHYSSYL 9
 11
 Db 2 DMKKGQHI 10

RESULT 13
 FAR3_HAECCO STANDARD; PRT; 7 AA.
 AC P81258;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide PF3 (KSAYMR-amide).
 OS Haemonchus contortus (Barber pole worm).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdiltida; Strongylida;
 OC Trichostrongylidae; Haemonchidae; Haemonchinae; Haemonchus.
 OX NCBI_TaxID=6289;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Neuron;
 RX MEDLINE=99318264; PubMed=10391380;
 RA Marks N.J., Sangster N.C., Maule A.G., Halton D.W., Thompson D.P.,
 RA Geary T.G., Shaw C.;
 RT "Structural characterisation and pharmacology of KHEYLRFamide (AF2)
 and KSAYMRamide (PF3/AF8) from Haemonchus contortus.";
 RL Mol. Biochem. Parasitol. 100:185-194(1999).
 CC -1- FUNCTION: ACTIVE ON NEUROMUSCULATURE.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA: 902 MW: 69D4068B5DC5B350 CRC64;
 Query Match 20.7%; Score 18; DB 1; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 SSYLR 10
 11
 Db 2 SAYMR 6

RESULT 14
 FAR3_PANRE STANDARD; PRT; 7 AA.
 AC P41874;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRamide-like neuropeptide PF3 (KSAYMR-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdiltida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=94235053; PubMed=8179635;
 RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
 RA Geary T.G., Thim L.;
 RT "KSAYMRamide: a novel FMRamide-related heptapeptide from the free-
 living nematode, Panagrellus redivivus, which is myoactive in the
 parasitic nematode, Ascaris suum".
 RL Biochem. Biophys. Res. Commun. 200:973-980(1994).
 CC -1- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT

CC MUSCLE TENSION INCREASE.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR: PC2132; PC2132.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7 7
 SQ SEQUENCE 7 AA: 902 MW: 69D4068B5DC5B350 CRC64;
 Query Match 20.7%; Score 18; DB 1; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

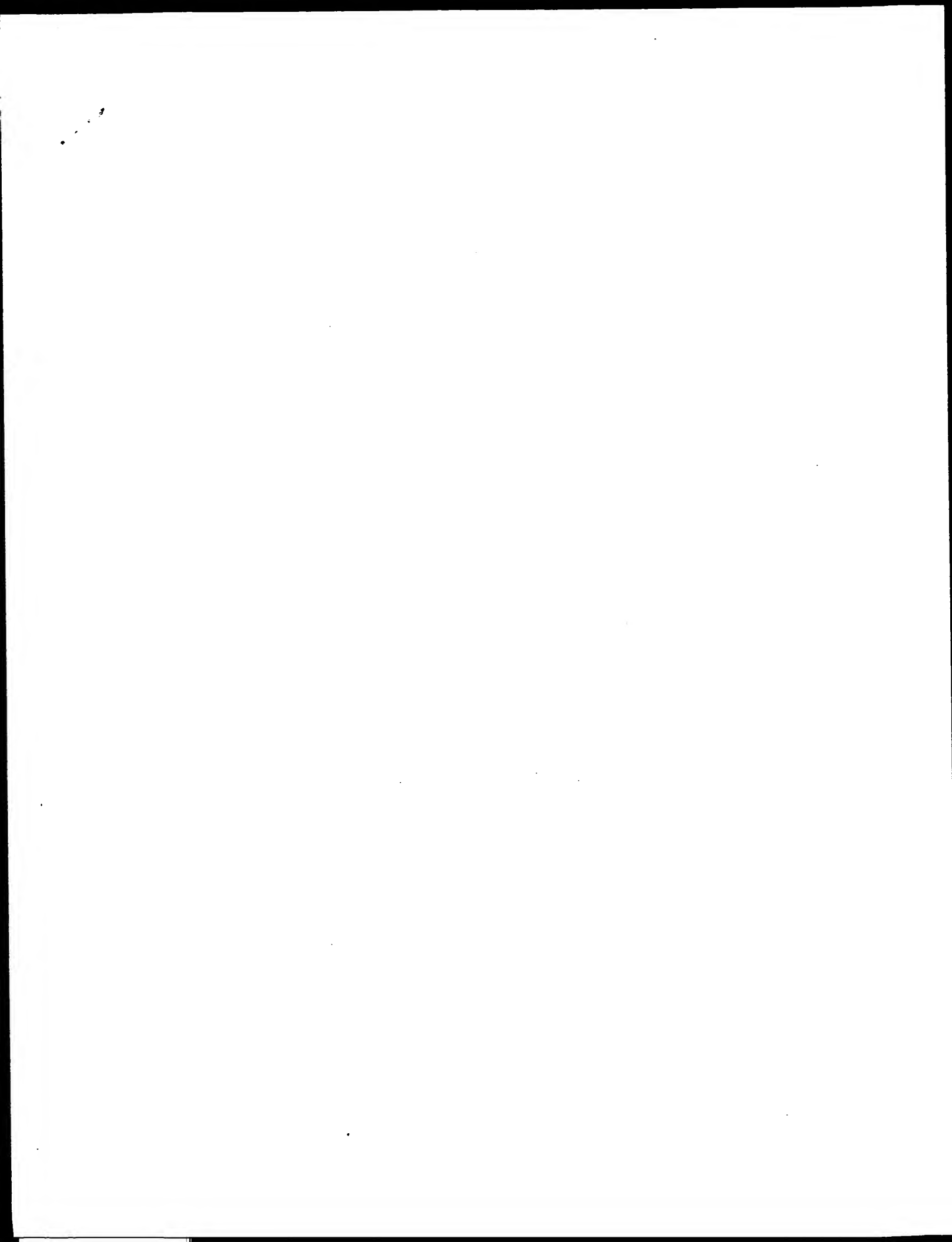
OY 6 SSYLR 10
 11
 Db 2 SAYMR 6

RESULT 15
 AL16_CARMA STANDARD; PRT; 8 AA.
 AC P81819;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinus statin 16.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Dove H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997)
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 813 MW: 7C286B45AB476878 CRC64;

Query Match 20.7%; Score 18; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 11 PFAY 14
 11
 Db 3 PYSY 6

Search completed: February 25, 2003, 11:50:47
 Job time : 12 secs



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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:48:27 : Search time 45 seconds

(without alignments)
29,908 Million cell updates/sec

Title: US-09-743-482A-12

Perfect score: 87

Sequence: 1 DMHYSSYIRPAY 14

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 2093

Minimum DB seq length: 0

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	32.2	14	2	PH1628
2	26	29.9	14	2	PT0254
3	24	27.6	10	2	A60624
4	24	27.6	10	2	S65432
5	24	27.6	10	2	A50917
6	24	27.6	14	1	NYPG14
7	24	27.6	14	2	A01250
8	23	26.4	10	2	A80345
9	23	26.4	11	2	S07207
10	23	26.4	11	2	B41946
11	23	26.4	12	2	S25056
12	23	26.4	13	2	PH1593
13	22	25.3	10	2	B38887
14	22	25.3	11	2	S68392
15	22	25.3	11	2	PT0250
16	22	25.3	11	2	S68649
17	22	25.3	12	2	PH1675
18	22	25.3	12	2	PH1324
19	22	25.3	12	2	S25039
20	22	25.3	13	2	PH1676
21	22	25.3	14	2	PH1677
22	22	25.3	14	2	PH1705
23	22	25.3	14	2	S38307
24	21	24.1	13	2	PC4391
25	20	23.0	10	2	PT0291
26	20	23.0	13	2	A54326
27	20	23.0	14	2	S60353
28	20	23.0	14	2	PT0232
29	20	23.0	14	2	PT0252

30	19	21.8	8	2	D47393	neuropeptide calla
31	19	21.8	9	2	PT0270	Ig heavy chain CRD
32	19	21.8	9	2	G41946	T-cell receptor ga
33	19	21.8	10	2	A60410	beta-neodorphin
34	19	21.8	12	2	G64003	hypothetical prote
35	19	21.8	12	2	PH1308	Ig heavy chain DJ
36	19	21.8	13	2	S47358	T-cell antigen rec
37	19	21.8	13	2	PH0928	T-cell receptor be
38	19	21.8	14	1	OMWAPP	polistes mastopara
39	19	21.8	14	2	M44920	2-halobenzoate 1,2
40	19	21.8	14	2	PH1322	Ig heavy chain DJ
41	19	21.8	14	2	PH1601	Ig H chain V-D-J r
42	18	20.7	7	2	PC2132	FMRFamide-related
43	18	20.7	7	2	E33932	Ig mu chain D regi
44	18	20.7	8	2	S68325	blood cell protein
45	18	20.7	9	2	S36850	Ig heavy chain V r.

ALIGNMENTS

RESULT 1

PH1628
Ig H chain V-D-J region (clone B-less 151) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1628

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

U:Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less

A:Reference number: PH1580; MUID:93301609; PMID:8315387

A:Accession: PH1628

A:Molecule type: DNA

A:Residues: 1-14 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: Immunoglobulin

Query Match

Best Local Similarity 32.2%; Score 28; DB 2; Length 14;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HYYSSYI 9

DB 4 HYYSNLL 10

RESULT 2

PT0254
Ig heavy chain CRD3 region (clone 2-115A) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0254

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity a

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0254

A:Molecule type: DNA

A:Residues: 1-14 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 29.9%; Score 26; DB 2; Length 14;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HYYSS 7

DB 5 HYYDS 9

RESULT 3

A60624

angiotensin I - Japanese quail
C:Species: Coturnix coturnix japonica (Japanese quail)
C>Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
C:Accession: A60624
R:Takei, Y.; Hasegawa, Y.
Gen. Comp. Endocrinol. 79, 12-22, 1990
A:Title: Vasopressor and depressor effects of native angiotensins and inhibition of the
A:Reference number: A60624; PMID:90284684; PMID:2191893
A:Molecule type: protein
A:Residues: 1-10 <NAK>
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 27.6%; Score 24; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.9e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 8 YIRPFA 13
I: I:
Db 4 YIHFFS 9

RESULT 4
S65432
angiotensin I - horn fly (fragment)
C:Species: Haematobia irritans (horn fly)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65432
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Ridding, G.; Elvin, C.; Kemp, D.; Willadsen, F.
Eur. J. Biochem. 237, 414-423, 1996
A:Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran
A:Reference number: S65431; PMID:96215437; PMID:8647080
A:Accession: S65432
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <WU>
A:Note: The source is designated as Haematobia irritans exigua

Query Match 27.6%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 YIRPF 12
I: I:
Db 4 YIHFF 8

RESULT 5
A90917
angiotensin precursor - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C:Accession: A90917; A01250
R:Nakayama, T.; Nakajima, T.; Sokabe, H.
Chem. Pharm. Bull. 21, 2095-2087, 1973
A:Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its
A:Reference number: A90917; PMID:74127845; PMID:4361802
A:Accession: A90917
A:Molecule type: protein
A:Residues: 1-10 <NAK>
C:Keywords: blood pressure control; hormone; vasoconstrictor
F:1-10/Product: angiotensin I #status experimental <AN1>
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 27.6%; Score 24; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.9e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 YIRPFA 13
I: I:
Db 4 YIHFFS 9

RESULT 6
NIPG14
hypothalamic tetradecapeptide - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 23-Aug-1996
C:Accession: A01419
R:Schlesinger, D.H.; Miall, H.D.; Linthicum, G.L.; Dupont, A.; Schally, A.V.
submitted to the Atlas, November 1976
A:Reference number: A01419
A:Accession: A01419
A:Molecule type: protein
A:Residues: 1-14 <SCH>
C:Superfamily: hypothalamic tetradecapeptide
C:Keywords: amidated carboxyl end; hypothalamus
F:14/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 27.6%; Score 24; DB 1; Length 14;
Best Local Similarity 44.4%; Pred. No. 9.7e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 6 SYIRPFAY 14
I: I: I:
Db 6 SEPLYPLGY 14

RESULT 7
A01250
angiotensin precursor - horse (fragment)
C:Species: Equus caballus (domestic horse)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Mar-1998
C:Accession: A92775; A01250
R:Skedgs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A:Reference number: A92775
A:Accession: A92775
A:Molecule type: protein
A:Residues: 1-14 <SKE>
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; hormone; vasoconstrictor
F:1-10/Product: angiotensin I #status experimental <AN1>
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 27.6%; Score 24; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 YIRPF 12
I: I:
Db 4 YIHFF 8

RESULT 8
A90345
angiotensin precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C:Accession: A90345; A01250
R:Elliot, D.F.; Peart, W.S.
Biochem. J. 65, 246-254, 1957
A:Title: The amino acid sequence in a hypertensin.
A:Reference number: A90345
A:Accession: A90345
A:Molecule type: protein
A:Residues: 1-10 <ELL>
C:Keywords: blood pressure control; hormone; vasoconstrictor
F:1-10/Product: angiotensin I #status experimental <AN1>
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 26.4%; Score 23; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 9.9e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 YIRPF 12
1: 11
Db 4 YVHPF 8

RESULT 9
S07207

Crinia-angiotensin, skin - frog (Crinia georgiana)
C:Species: Crinia georgiana
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Aug-2000
C:Accession: S07207
R:Espamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.
Expertella 35, 1132-1133, 1979
A:Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II-11
A:Reference number: S07207; MUID:80024575; PMID:488254
A:Accession: S07207
A:Molecule type: protein
A:Residues: 1-11 <ERS>
C:Superfamily: unassigned animal peptides

Query Match 26.4%; Score 23; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 YIRPF 12
1: 11
Db 7 YVHPF 11

RESULT 10
B41946

T-cell receptor gamma chain (1L.57) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: B41946
R:Whetzel, M.; Mosley, R.L.; Whetzel, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A:Reference number: A41946; MUID:92049316; PMID:1658619
A:Accession: B41946
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-11 <WHE>
C:Keywords: T-cell receptor

Query Match 26.4%; Score 23; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 1.1e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 WHYSSY 8
1: 11
Db 5 WYSSGF 11

RESULT 11
S25056

Ig heavy chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C:Accession: S25056
R:Jacob, J.; Kelsoe, G.
Submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny
A:Reference number: S25024
A:Accession: S25056
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-12 <JAC>
A:Cross-references: EMBL:X67386; NID:950927; PIDN:CA447798.1; PID:q1333920
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 26.4%; Score 23; DB 2; Length 12;

Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 WHYSSY 8
1: 11
Db 5 YYYSSY 11

RESULT 12
PH1593

Ig H chain V-D-J region (wild-type clone 144) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1593
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-1ess
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1593
A:Molecule type: DNA
A:Residues: 1-13 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 26.4%; Score 23; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 HYYS 6
1: 11
Db 7 HYXA 10

RESULT 13
B38887

T-cell receptor gamma chain (5t.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: B38887
R:Whetzel, M.; Mosley, R.L.; Whetzel, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma
A:Reference number: A41946; MUID:92049316; PMID:1658619
A:Accession: B38887
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-10 <WHE>
C:Keywords: T-cell receptor

Query Match 25.3%; Score 22; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 WHYSS 7
1: 11
Db 3 WARYSS 8

RESULT 14
S68392

H+-transporting two-sector ATPase (EC 3.6.3.14) chain I - Chlamydomonas reinhardtii
N:Alternate names: ATP synthase chain I
C:Species: chloroplast Chlamydomonas reinhardtii
C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 03-Jun-2002
C:Accession: S68392
R:Fiedler, H.R.; Schmid, R.; Ieu, S.; Shavit, N.; Strötman, H.
FEBS Lett. 377, 163-166, 1995
A:Title: Isolation of CF(O)CF(1) from Chlamydomonas reinhardtii cw15 and the N-termi
A:Reference number: S68388; MUID:96128220; PMID:8543042
A:Accession: S68392
A:Molecule type: protein
A:Residues: 1-11 <FIE>
A:Experimental source: strain CW15

C:Genetics:

A:Genome: chloroplast

C:Superfamily: H⁺-transporting ATP synthase protein 6

C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; thyl

Query Match

25.3%; Score 22; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 3 HXY 5

DB 7 HXY 9

RESULT 15

PT0250

Ig heavy chain CRD3 region (clone 2-109B) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0250

R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0250

A:Molecule type: DNA

A:Residues: 1-11 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match

25.3%; Score 22; DB 2; Length 11;

Best Local Similarity 33.3%; Pred. No. 1.6e+03;

Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 YSXYRPEA 13

DB 3 YGDFGRPYS 11

Search completed: February 25, 2003, 11:52:14
Job time : 46 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:37:51 : Search time 14 Seconds
(without alignments)
35.728 Million cell updates/sec

Title: US-09-743-482a-10
Perfect score: 104
Sequence: 1 WIRPGNGNTKYNQKFNQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 120122

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	68.3	17	4	US-08-479-089A-8
2	65	62.5	17	1	US-08-318-970B-7
3	64	61.5	17	2	US-08-116-778E-7
4	64	61.5	17	2	US-08-438-562-7
5	64	61.5	17	2	US-08-483-528B-95
6	64	61.5	17	4	US-09-393-385B-106
7	62	59.6	17	2	US-08-482-228-40
8	62	59.6	17	3	US-08-482-528-40
9	60	57.7	17	2	US-08-672-345C-65
10	60	57.7	17	4	US-09-214-095D-65
11	59	56.7	17	1	US-08-137-117D-144
12	59	56.7	17	2	US-08-436-717-144
13	59	56.7	17	2	US-08-232-081B-2
14	58	55.8	17	4	US-07-987-264-2
15	57	54.8	17	2	US-08-182-067-14
16	57	54.8	17	2	US-08-465-313-14
17	57	54.8	17	2	US-09-171-945-31
18	55	52.9	17	4	US-08-646-265A-116
19	53	51.0	17	2	US-08-672-345C-59
20	53	51.0	17	4	US-09-214-095D-59
21	52	50.0	17	3	US-08-836-561-41
22	51	49.0	17	1	US-08-264-093-16
23	51	49.0	17	2	US-08-672-345C-62
24	51	49.0	17	2	US-08-672-345C-77
25	51	49.0	17	4	US-09-214-095D-62
26	51	49.0	17	4	US-09-214-095D-77
27	50	48.1	17	1	US-07-946-421-5

28	50	48.1	17	3	US-08-974-899-11	Sequence 11, Appl
29	49	47.1	17	1	US-08-318-970B-4	Sequence 4, Appl
30	47	45.2	17	2	US-08-672-345C-68	Sequence 68, Appl
31	47	45.2	17	3	US-08-974-899-23	Sequence 23, Appl
32	47	45.2	17	4	US-09-214-095D-68	Sequence 68, Appl
33	45	43.3	17	3	US-08-836-561-47	Sequence 47, Appl
34	45	43.3	17	2	US-08-476-176B-51	Sequence 51, Appl
35	43	41.3	17	2	US-08-814-806-9	Sequence 9, Appl
36	43	41.3	17	3	US-08-127-721A-51	Sequence 51, Appl
37	43	41.3	17	3	US-08-485-246A-51	Sequence 51, Appl
38	41	39.4	17	4	US-09-425-638A-78	Sequence 78, Appl
39	41	39.4	17	4	US-09-543-004-78	Sequence 78, Appl
40	41	39.4	17	4	US-09-406-532-6	Sequence 6, Appl
41	40	38.5	17	1	US-08-353-400-28	Sequence 28, Appl
42	40	38.5	17	4	US-09-425-638A-76	Sequence 76, Appl
43	40	38.5	17	4	US-09-543-004-76	Sequence 76, Appl
44	38	36.5	17	3	US-08-513-968-78	Sequence 78, Appl
45	38	36.5	17	4	US-09-406-532-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-479-089A-8
Sequence 8, Application US/08479089A
Patent No. 6383487
GENERAL INFORMATION:
APPLICANT: Amloc, Peter L.
APPLICANT: Akbar, Arne N.
APPLICANT: Heinlich, Gunther
APPLICANT: Camisuli, Salvatore
TITLE OF INVENTION: CD25 Binding Molecules
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 6383487artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: NJ
COUNTRY: USA
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,089A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/669,545
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9019323
FILING DATE: 05-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Furman, Diane E.
REGISTRATION NUMBER: 31,104
REFERENCE/DOCKET NUMBER: 100-7617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6924
TELEFAX: (908) 522-6955
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-479-089A-8

Query Match 68.3%; Score 71; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.00035;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IYPGNGTKYNOKFNG 17
| | | | | : | | | | |
DB 2 IYPGNSDTSYNOKFEG 17

RESULT 2

US-08-318-970B-7
; Sequence 7, Application US/08318970B
; Patent No. 5389573
; GENERAL INFORMATION:
; APPLICANT: HIDEAKI HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIDROPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steiberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDR2-4
; OTHER INFORMATION: hypervariable region
US-08-318-970B-7

Query Match 62.5%; Score 65; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 0.0026;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 IYPGNGTKYNOKFNG 17
| | | | | : | | | | |
DB 2 IYPGDSDTRYTEKFG 17

RESULT 3
US-08-116-778E-7
; Sequence 7, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUMANA, YOSHIHISA

APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-778E-7

Query Match 61.5%; Score 64; DB 2; Length 17;
Best Local Similarity 73.3%; Pred. No. 0.0036;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 WIYPNGTKYNOKF 15
| | | | | : | | | | |
DB 1 WIYPNGTKYNOKF 15

RESULT 4

US-08-438-562-7
; Sequence 7, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUMANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-438-562-7

Query Match 61.5% Score 64; DB 2; Length 17;
Best Local Similarity 73.3%; Pred. No. 0.0036;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIYPNGNTKYNQKF 15
:|||||
DB 1 YIYPNGGTGYNQKF 15

RESULT 5

US-08-483-528B-95
Sequence 95, Application US/08483528B
Patent No. 5939532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUMANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-528B-95

Query Match 61.5% Score 64; DB 2; Length 17;
Best Local Similarity 73.3%; Pred. No. 0.0036;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 WIYPNGNTKYNQKF 15
:|||||

DB 1 YIYPNGGTGYNQKF 15

RESULT 6

US-09-393-385B-106
Sequence 106, Application US/09393385B
Patent No. 6423511
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUMANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,385B
FILING DATE: 27-JUN-96
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-393-385B-106

Query Match 61.5% Score 64; DB 4; Length 17;
Best Local Similarity 73.3%; Pred. No. 0.0036;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIYPNGNTKYNQKF 15
:|||||
DB 1 YIYPNGGTGYNQKF 15

RESULT 7

US-08-482-228-40
Sequence 40, Application US/08482228
Patent No. 5968753
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillemo, Roy
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA

ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,228
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gutthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-228-40

Query Match 59.6%; Score 62; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 0.0069;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IYPGNGNTKYNQKE 15
DB 2 IYPGSDGDTRYTQKE 15

RESULT 8
US-08-482-528-40
Sequence 40, Application US/08482528
Patent No. 6017719
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Gutthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,528
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gutthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-528-40

Query Match 59.6%; Score 62; DB 3; Length 17;
Best Local Similarity 71.4%; Pred. No. 0.0069;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IYPGNGNTKYNQKE 15
DB 2 IYPGSDGDTRYTQKE 15

RESULT 9
US-08-672-345C-65
Sequence 65, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry, Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-65

Query Match 57.7%; Score 60; DB 2; Length 17;
Best Local Similarity 64.7%; Pred. No. 0.013;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIYPGNGNTKYNQKENG 17
DB 1 YIDPSNGDTFYNQKEQG 17

RESULT 10
US-09-214-095D-65
Sequence 65, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214, 095D

;; CURRENT FILING DATE: 1999-07-19
;; NUMBER OF SEQ ID NOS: 121
;; SOFTWARE: Patent version 3.0
;; SEQ ID NO 65
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Murinae gen. sp.
US-09-214-095D-65

Query Match 57.7%; Score 60; DB 4; Length 17;
Best Local Similarity 64.7%; Pred. No. 0.013;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIYPGNGTKYNOKFNG 17
Db 1 YIDPSNGDTFYNOKFQ 17

RESULT 11

US-08-137-117D-144
Sequence 144, Application US/08137117D

Patent No. 5795965
GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

APPLICANT: SATO, Koh

APPLICANT: BENDIG, Mary

APPLICANT: JONES, Steven

APPLICANT: SALDANHA, Jose

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/137,117D

FILING DATE: 20-DEC-1993

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/JP92/00544

FILING DATE: 24-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476

FILING DATE: 25-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.

REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/126/AAOK

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 144:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-137-117D-144

Query Match 56.7%; Score 59; DB 1; Length 17;

Best Local Similarity 64.7%; Pred. No. 0.019;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIYPGNGTKYNOKFNG 17
Db 1 YIDPFNGTSTYNOKFKG 17

RESULT 12

US-08-436-717-144

Sequence 144, Application US/08436717

Patent No. 5817790

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

APPLICANT: SATO, Koh

APPLICANT: BENDIG, Mary

APPLICANT: JONES, Steven

APPLICANT: SALDANHA, Jose

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,717

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/137,117

FILING DATE: 20-DEC-1993

APPLICATION NUMBER: WO PCT/JP92/00544

FILING DATE: 24-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476

FILING DATE: 25-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.

REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/126/AAOK

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 144:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-436-717-144

Query Match 56.7%; Score 59; DB 2; Length 17;

Best Local Similarity 64.7%; Pred. No. 0.019;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIYPGNGTKYNOKFNG 17
Db 1 YIDPFNGTSTYNOKFKG 17

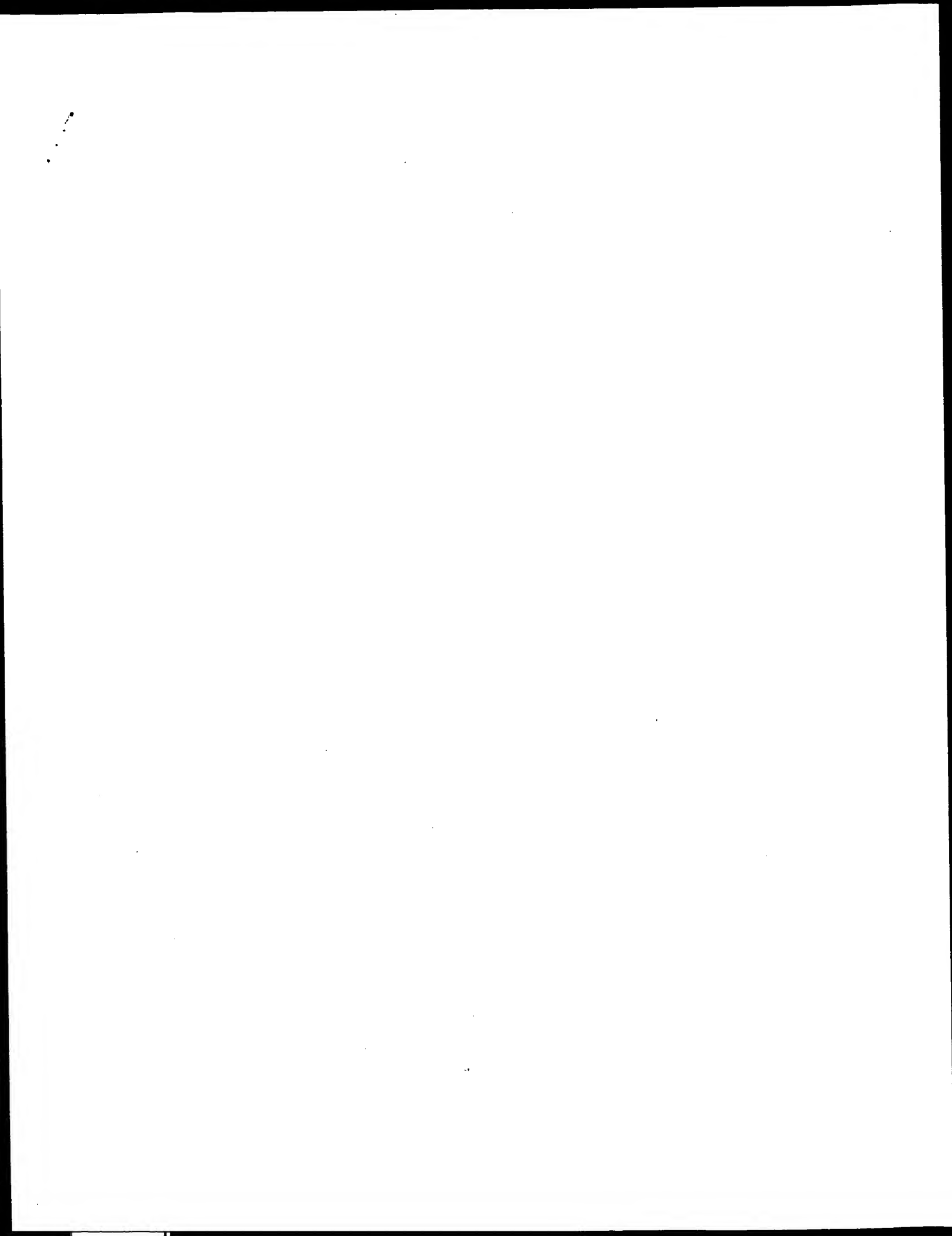
RESULT 13
US-08-232-081B-2
Sequence 2, Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WILDENES, JOHN
APPLICANT: MOCUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-232-081B-2
Query Match 56.7%; Score 59; DB 2; Length 17;
Best Local Similarity 56.8%; Pred. No. 0.019;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 TYPGNGNTKRYNKGKENG 17
DB 2 INPTNGNTKRYDKPKFG 17
RESULT 14
US-07-987-264-2
Sequence 2, Application US/07987264
Patent No. 6204366
GENERAL INFORMATION:
APPLICANT: VERHOEVEN, MARTINE ELISA
TITLE OF INVENTION: SPECIFIC BINDING AGENTS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/987,264
FILING DATE: 08-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9019553.8
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB PCT/GB91/01511
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 200232/P30950USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-987-264-2
Query Match 55.8%; Score 58; DB 4; Length 17;
Best Local Similarity 56.2%; Pred. No. 0.026;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 2 TYPGNGNTKRYNKGKENG 17
DB 2 ILPGSNNSRYNKEKFG 17
RESULT 15
US-08-182-067-14
Sequence 14, Application US/08182067
Patent No. 5985279
GENERAL INFORMATION:
APPLICANT: WALDMANN, HERMAN
APPLICANT: SIMS, MARTIN
APPLICANT: CROWE, SCOTT
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,067
FILING DATE: 23-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01289
FILING DATE: 15-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9115364.3
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1786-118A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040

TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-182-067-14

Query Match 54.8%; Score 57; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 0.036;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 WIPGNGNTKYNQKF 15
| | | | | | | | | |
Db 1 WIDPEDGETTKYGQKF 15

Search completed: February 25, 2003, 11:41:22
Job time : 15 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:40:47 : Search time 31 Seconds
(without alignments)
17.038 Million cell updates/sec

Title: US-09-743-482a-10

Perfect score: 104

Sequence: 1 WIYPCNGNTKYNOKFNG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 36430

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB pep:*
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14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	71	68.3	17	10	US-09-770-002-2
3	66	63.5	17	9	US-10-032-482-15
4	59	54.8	17	9	US-10-146-305-13
5	57	54.8	17	9	US-10-032-482-18
6	57	54.8	17	10	US-09-809-739-7
7	57	54.8	17	10	US-09-910-059-31
8	55	52.9	17	9	US-09-749-873-116
9	54	51.9	17	10	US-09-748-960-13
10	52	50.0	17	10	US-09-924-099-7
11	51	49.0	16	9	US-09-423-800-63
12	51	49.0	17	10	US-09-976-787-22
13	51	49.0	17	10	US-09-865-198-21
14	50	48.1	17	10	US-09-976-787-2
15	50	48.1	17	10	US-09-865-198-2
16	49	47.1	17	9	US-10-032-482-12
17	49	47.1	17	10	US-09-861-294-33
18	47	45.2	17	9	US-10-153-159-33
19	47	45.2	17	9	US-10-153-176-33

20	46	44.2	17	9	US-09-249-011A-12	Sequence 12, Appl
21	46	44.2	17	9	US-10-153-159-32	Sequence 32, Appl
22	46	44.2	17	9	US-10-153-176-32	Sequence 32, Appl
23	43	41.3	17	9	US-09-293-854-9	Sequence 9, Appl1
24	43	41.3	17	9	US-10-153-159-34	Sequence 34, Appl
25	43	41.3	17	9	US-10-153-176-34	Sequence 34, Appl
26	38	36.5	16	9	US-10-153-159-35	Sequence 35, Appl
27	38	36.5	16	9	US-10-153-176-35	Sequence 35, Appl
28	38	36.5	17	9	US-10-153-159-31	Sequence 31, Appl
29	38	36.5	17	9	US-10-153-176-31	Sequence 31, Appl
30	37.5	36.1	16	9	US-09-968-561A-254	Sequence 254, App
31	37.5	36.1	16	10	US-09-192-854-143	Sequence 143, App
32	37	35.6	17	10	US-09-217-268B-33	Sequence 33, Appl
33	37	35.6	17	10	US-09-965-099-9	Sequence 9, Appl1
34	37	35.6	17	12	US-10-051-852-9	Sequence 9, Appl1
35	36	34.6	15	10	US-09-953-510-77	Sequence 77, Appl
36	36	34.6	15	10	US-09-953-510-78	Sequence 78, Appl
37	36	34.6	17	9	US-10-032-482-9	Sequence 9, Appl1
38	36	34.6	17	10	US-09-828-708-28	Sequence 28, Appl
39	35.5	34.1	16	10	US-09-828-708-27	Sequence 27, Appl
40	33.5	32.2	16	10	US-09-865-483-13	Sequence 13, Appl
41	33	31.7	17	9	US-09-968-561A-110	Sequence 110, App
42	33	31.7	17	10	US-09-192-854-68	Sequence 68, Appl
43	32	30.8	17	10	US-09-286-240-21	Sequence 21, Appl
44	31	29.8	17	10	US-09-832-312-50	Sequence 50, Appl
45	30	28.8	16	10	US-09-947-925A-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-861-294-15
Sequence 15, Application US/09861294
Patent No. US20020098190A1
GENERAL INFORMATION:
APPLICANT: Malaya CHATTERJEE
APPLICANT: Kenneth A. POON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TUMORS BEARING HMG AND CEA ANTIGENS
FILE REFERENCE: 30414200620
CURRENT APPLICATION NUMBER: US/09/861,294
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/049,540
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 09/096,244
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 17
TYPE: PRT
ORGANISM: Mus musculus
US-09-861-294-15
Query Match 68.3%, Score 71; DB 10; Length 17;
Best Local Similarity 75.0%; Pred. No. 8.8e-05;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 IYPCNGNTKYNOKFNG 17
DB 2 IFPGNGDYVYNOKFNG 17
RESULT 2
US-09-770-002-2
Sequence 2, Application US/09770002
Patent No. US20020110558A1
GENERAL INFORMATION:
APPLICANT: Peter Lloyd Amlot
APPLICANT: Max H. Schreier
APPLICANT: Karin Schreier
TITLE OF INVENTION: Use of CD25 binding molecules in the

```

; TITLE OF INVENTION: treatment of rheumatoid arthritis or skin diseases.
; FILE REFERENCE: 4-30583A/30967C1
; CURRENT APPLICATION NUMBER: US/09/770,002
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/EP99/05316
; PRIOR FILING DATE: 1999-07-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-770-002-2

Query Match
Best Local Similarity 75.0%; Score 61; DB 10; Length 17;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGNGTKYKNGKNG 17
DB 2 IYPGNSDTYKNGKFG 17

RESULT 3
; US-10-032-482-15
; Sequence 15, Application US/10032482
; Publication No. US20020197270A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTHER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: Ruiz, Pedro
; APPLICANT: EREZ-ALON, Neta
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/10/032,482
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US/09/445,602
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-032-482-15

Query Match
Best Local Similarity 63.5%; Score 66; DB 9; Length 17;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNGTKYKNGKNG 17
DB 2 IYPNGGTTYKNGKFG 17

RESULT 4
; US-10-146-305-13
; Sequence 13, Application US/10146305
; Patent No. US20020173035A1
; GENERAL INFORMATION:
; APPLICANT: YUHAN CORPORATION
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
; FILE REFERENCE: OVI17440
; CURRENT APPLICATION NUMBER: US/10/146,305
; CURRENT FILING DATE: 2002-05-15
```

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; PRIOR APPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-10-146-305-13

Query Match
Best Local Similarity 56.7%; Score 59; DB 9; Length 17;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGNGTKYKNGKNG 17
DB 2 INPGSGGTNYKNGKFG 17

RESULT 5
; US-10-032-482-18
; Sequence 18, Application US/10032482
; Publication No. US20020197270A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTHER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: Ruiz, Pedro
; APPLICANT: EREZ-ALON, Neta
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/10/032,482
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US/09/445,602
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-032-482-18

Query Match
Best Local Similarity 54.8%; Score 57; DB 9; Length 17;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIYPGNGTKYKNGKNG 17
DB 1 WIDPENGDTYKNGKFG 17

RESULT 6
; US-09-809-739-7
; Sequence 7, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
```

```
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(17)
; OTHER INFORMATION: CDR2 of yfc51.1 heavy chain
; OTHER INFORMATION: Rat
US-09-809-739-7

Query Match
Best Local Similarity 54.8%; Score 57; DB 10; Length 17;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 1 WIDPEDEGKTKGOKF 15
| | | | | | | | | | | | | | | | | | |

RESULT 7
US-09-910-059-31
; Sequence 31, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-910-059-31

Query Match
Best Local Similarity 54.8%; Score 57; DB 10; Length 17;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 1 WIDPEDEGKTKGOKF 17
| | | | | | | | | | | | | | | | | | |

RESULT 8
US-09-749-873-116
; Sequence 116, Application US/09749873
; Publication No. US20030023045A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; MEDULOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
```

```
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/749,873
FILING DATE: 29-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 116:

US-09-749-873-116

Query Match
Best Local Similarity 52.9%; Score 55; DB 9; Length 17;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 2 IYDNGNTKYNKFKNG 17
| | | | | | | | | | | | | | | | | | |

RESULT 9
US-09-748-960-13
; Sequence 13, Application US/09748960
; Patent No. US20010046496A1
; GENERAL INFORMATION:
; APPLICANT: Bretman, Lee R.
; APPLICANT: Fox, Judith A.
; APPLICANT: Allison, David Edward
; TITLE OF INVENTION: Method of Administering an Antibody
; FILE REFERENCE: 1855.2007-001
; CURRENT APPLICATION NUMBER: US/09/748,960
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: US 09/550,082
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(17)
; OTHER INFORMATION: CDR2 of the heavy chain of antibodies Act-1 and
; OTHER INFORMATION: LDP-02
US-09-748-960-13

Query Match
Best Local Similarity 51.9%; Score 54; DB 10; Length 17;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 IYPCNGNTKYNOKEG 17
| | | | | | | | | |
Db 2 IDPESNTNMYNOKEFG 17

RESULT 10
US-09-924-099-7
; Sequence 7, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takahori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924, 099
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: 09/365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 7
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-7

Query Match 50.0%; Score 52; DB 10; Length 17;
Best Local Similarity 71.4%; Pred. No. 0.064;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IYPCNGNTKYNOKEG 15
| | | | | | | | | |
Db 2 IDPYNCDTSYNOKF 15

RESULT 11
US-09-423-800-63
; Sequence 63, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIAKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentia Ver. 2.1
; SEQ ID NO 63
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-63

Query Match 49.0%; Score 51; DB 9; Length 16;
Best Local Similarity 61.5%; Pred. No. 0.085;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 5 GNCNTKYNOKEFG 17

Db 4 GGDTRYSQKFKG 16
| | | | | | | | | |

RESULT 12
US-09-976-787-22
; Sequence 22, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: WILTE, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; PRIOR FILING DATE: 2001-10-12
; CURRENT APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-22

Query Match 49.0%; Score 51; DB 10; Length 17;
Best Local Similarity 52.9%; Pred. No. 0.091;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 WIYPCNGNTKYNOKEG 17
| | | | | | | | | |
Db 1 WIDPENGSDYAPKFOG 17

RESULT 13
US-09-865-198-21
; Sequence 21, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-21

Query Match 49.0%; Score 51; DB 10; Length 17;
Best Local Similarity 52.9%; Pred. No. 0.091;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 WIYPCNGNTKYNOKEG 17
| | | | | | | | | |
Db 1 WIDPENGSDYAPKFOG 17

RESULT 14
US-09-976-787-2
; Sequence 2, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: WILTE, Larry

```

; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-2

```

```

Query Match          48.1%; Score 50; DB 10; Length 17;
Best Local Similarity 52.9%; Pred. No. 0.13;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```

```

Oy 1 WYPGNGTKYKQKFG 17
    |||::| ||
Db 1 WIDPENGDSGYAPKFG 17

```

```

RESULT 15
US-09-865-198-2
; Sequence 2, Application US/09865198
; Patent No. US2002010345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-2

```

```

Query Match          48.1%; Score 50; DB 10; Length 17;
Best Local Similarity 52.9%; Pred. No. 0.13;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```

```

Oy 1 WYPGNGTKYKQKFG 17
    |||::| ||
Db 1 WIDPENGDSGYAPKFG 17

```

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Search completed: February 25, 2003, 11:48:58
Job time : 31 secs

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6.

PT autoimmune disease, immune deficiencies, T-cell malignancies and
 XX infectious diseases -
 PS Claim 10; Fig 6; 79pp; English.
 XX
 CC The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is
 CC encoded by (I), is obtained by immunising a rat with jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,
 CC infectious diseases, and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC or viral infections. The antibody, and fragments of it, can be useful for
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC treatment of NK-cell derived malignancies. It can also be useful for the
 CC determination of zeta-chain or eta-chain expression on NK-cells,
 CC T-lymphocytes or their precursors. The present sequence represents the
 CC CDR2 of the VH-region of the anti-zeta-chain antibody 2-B-5, produced
 CC by rats from the present invention.
 CC
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 104; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WIYPGNGNTKYKNGKENG 17
 DB 1 WIYPGNGNTKYKNGKENG 17
 RESULT 2
 AAU99850
 ID AAU99850 standard; Peptide: 17 AA.
 AC AAU99850;
 XX
 DT 07-OCT-2002 (first entry)
 DE Mouse AC10 antibody heavy chain CDR2 (H2).
 XX
 KW Gene therapy: vaccine; CD30 binding; cytostatic; cytotoxic;
 KW Hodgkin's Disease; mouse; AC10 antibody; heavy chain CDR;
 KW complementarity determining region.
 XX
 OS Mus musculus.
 XX
 PN WO200243661-A2.
 XX
 PD 06-JUN-2002.
 XX
 PF 28-NOV-2001; 2001WO-US44811.
 XX
 PR 28-NOV-2000; 2000US-0724406.
 XX
 PA (SEAT-) SEATTLE GENETICS INC.
 XX
 PI Francisco JA, Risdon G, Wahl AF, Siegall CB;
 XX
 DR WPI; 2002-557522/59.
 DR N-PSDB; ABK88122.
 XX
 PT Novel antibody that immunospecifically binds to CD30, useful for
 PT treating Hodgkin's disease, exerts a cytostatic or cytotoxic effect on
 PT Hodgkin's Disease cell line, and is not monoclonal antibody AC10 or
 PT HeFl-1 -
 PS Claim 9; Page 97; 103pp; English.
 XX

CC The invention describes an antibody (I) that immunospecifically binds to
 CC CD30, exerts a cytostatic or cytotoxic effect on Hodgkin's Disease cell
 CC line, and is not monoclonal antibody AC10 or HeFl-1 and does not result
 CC from cleavage of AC10 or HeFl-1 with pepsin. (I), a protein
 CC (II) that competes for CD30 binding with the monoclonal antibodies AC10
 CC or HeFl, or exerts a cytotoxic or cytostatic effect on a Hodgkins
 CC disease cell line and the nucleic acid encoding the protein (II) are
 CC useful for the treatment or prevention of Hodgkin's Disease in a subject,
 CC by administering (I) to the subject, in the absence of conjugation to a
 CC cytostatic or cytotoxic agent, respectively and a pharmaceutically
 CC acceptable carrier. This is the amino acid sequence of the mouse AC10
 CC antibody heavy chain complementarity determining region 2 (CDR2), a
 CC polypeptide that competes with AC10 for CD30 binding.
 CC
 XX
 SQ Sequence 17 AA;
 Query Match 86.5%; Score 90; DB 23; Length 17;
 Best Local Similarity 82.4%; Pred No. 2.2e-07;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WIYPGNGNTKYKNGKENG 17
 DB 1 WIYPGNGNTKYKNGKENG 17
 RESULT 3
 AAAY95240
 ID AAAY95240 standard; Peptide: 17 AA.
 XX
 AC AAAY95240;
 XX
 DT 29-AUG-2000 (first entry)
 DE Human monoclonal antibody 21/28/CL VH CDR2.
 XX
 KW Human: monoclonal antibody; 21/28/CL; humanised antibody; CC49;
 KW HUC49; CDR; complementarity determining region; carcinoma;
 KW colon cancer; tumor associated glycoprotein-72; TAG-72;
 KW tumour marker; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..9 /note="specificity determining region"
 PN WO200026394-A1.
 XX
 PD 11-MAY-2000.
 XX
 PF 29-OCT-1999; 99WO-US25552.
 XX
 PR 31-OCT-1998; 98US-0106534.
 PR 02-NOV-1998; 98US-0106757.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Kashmiri SVS, Padlan EA, Schlom J;
 XX
 DR WPI; 2000-365637/31.
 XX
 PT Chimeric variants of CC49 monoclonal antibodies useful for detecting
 PT and treating cancers associated with the expression of the pancreaticoma
 PT tumor-associated antigen TAG-72 -
 PS Disclosure; Fig 2; 76pp; English.
 XX
 CC The present sequence is that of complementarity determining region
 CC 2 (L-CDR2) of the heavy chain variable region (VH) of human
 CC monoclonal antibody 21/28/CL. The invention is directed toward
 CC mouse-human chimeric variants of CC49 MAb's with minimal murine
 CC content, to methods of making such variants, and to their
 CC therapeutic application. Variants are provided of hucc49, a

CC humanised MAb formed by grafting hypervariable regions from murine
CC CC49 into VL and VH frameworks of human MAb's LEN and 21/28' CL,
CC respectively, while retaining murine framework residues required
CC for integrity of the antigen combining site structure. HuCC49
CC binds to the human pancreatic tumor associated glycoprotein-72
CC (TAG-72), which is found on the surface of certain human tumours.
CC Novel variants of huCC49 of the invention have fewer than all 6
CC CDRs of CC49 present. Also provided are specificity determining
CC region (SDR) variants of huCC49 in which only SDRs of at least 1
CC CDR from CC49 are present. Particular variants of HuCC9 have
CC either L-CDR1 and/or L-CDR2 from human MAb LEN. These variants
CC have the same or 2-fold lower affinity constant than HuCC49. They
CC are used in claimed methods of treating cancer and for detecting
CC cancer cells that express TAG-72.

SO Sequence 17 AA;

Query Match 73.1%; Score 76; DB 21; Length 17;
Best Local Similarity 76.5%; Pred. No. 3.4e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIPGNGNTRKYNOKFG 17
DB 1 WINAGNGNTRKYNOKFG 17

RESULT 4
AAY40700
ID AAY40700 standard; peptide; 15 AA.
XX
AC AAY40700;
XX
DT 01-DEC-1999 (first entry)
XX
DE A3 derivative #21, beta strand of scaffold protein structure.
XX
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
XX tumour; chemotherapeutic agent.
XX
OS Synthetic.
XX
PN EP947582-A1.
PD 06-OCT-1999.
XX
PF 31-MAR-1998; 98EP-0870065.
XX
PR 31-MAR-1998; 98EP-0870065.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX
DR WPI; 1999-542958/46.
XX
PT New scaffold protein, useful for stabilizing antigens used as vaccines
XX
PS Disclosure; Page 6; 105pp; English.

CC Sequences AAY40680-Y40703 are functionally equivalent derivatives of the
CC A3 peptide (AAY40605) which forms part of a scaffold protein. A3 is a
CC beta strand peptide which forms part of a beta sheet. Peptides
CC (AAY40601-Y40609) together form a single-chain scaffold protein which
CC contains at least 1 disulfide bond, contains less than 10% alpha helix
CC and contains at least 6 beta-strands. The scaffold protein is constructed
CC of beta strands S1-S6, and may also include beta strands A1-A3, or any
CC functionally equivalent derivative of these sequences. The beta strands
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets, with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each

CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines.

SO Sequence 15 AA;

Query Match 72.1%; Score 75; DB 20; Length 15;
Best Local Similarity 80.0%; Pred. No. 4.3e-05;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YPGNGNTRKYNOKFG 17
DB 1 YPGSGNTRKYNEKFG 15

RESULT 5
AAB30039
ID AAB30039 standard; Peptide; 15 AA.
XX
AC AAB30039;
XX
DT 09-FEB-2001 (first entry)
XX
DE Scaffold protein SCA A3 peptide SEQ ID NO: 100.
XX
KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
XX SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
XX diabetic retinopathy; atherosclerosis.
XX
OS Synthetic.
XX
PN WO200060070-A1.
PD 12-OCT-2000.
XX
PF 01-APR-1999; 99WO-EP02283.
XX
PR 01-APR-1999; 99WO-EP02283.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX
DR WPI; 2000-665002/64.
XX
PT Scaffold composed of single-chain polypeptide having beta sandwich
XX architecture carrying new and randomized peptide sequences useful as
XX supporting framework and carrying antigen- or receptor binding
XX fragments -
XX
PS Disclosure; Page 14; 68pp; English.

CC The present invention is concerned with producing scaffold proteins
CC based upon the human CTLA-4 SCA domain. These scaffold proteins can be
CC used as a scaffold to bind antigen- or receptor-binding fragments. These
CC can be used in the treatment of diseases such as cancer,
CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and
CC diabetic retinopathy. Sequences AAB29930-B29939 were used in the
CC production of the proteins of the invention.

SO Sequence 15 AA;

Query Match 72.1%; Score 75; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 4.3e-05;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YPGNGNTKYNOKFNG 17
 |||:|||||:|
 Db 1 YPGSGNTKYNKFKG 15

RESULT 6
 AAW27348
 ID AAW27348 standard; peptide; 17 AA.

AC AAW27348;

DT 12-DEC-1997 (first entry)

DE CDR2 from murine anti-human IgE receptor antibody light chain.

KM Complementarity determining region; CDR2; murine; mouse; human;
 KM high affinity; immunoglobulin E; receptor; monoclonal antibody;
 KM IgE; MAb; light chain; variable region; humanised; semi-chimeric;
 KM chimeric; treatment; prevention; disease; allergy.

OS Mus spp.

PN JP09191886-A.

PD 29-JUL-1997.

PF 19-JAN-1996; 96JP-0024816.

PR 19-JAN-1996; 96JP-0024816.

PA (ASAK) ASAKI BREWERIES LTD.

PA (NIKK-) NIKKA WHISKEY KK.

PA (TORI) TORII YAKUHIIN KK.

PA (TSUR/) TSURA T.

DR WPI: 1997-429186/40.

XX Humanised, semi-chimeric and chimeric antibodies against human

PT high-affinity IgE receptor - useful medically and have low

PS antigenicity in humans

XX Claim 1; Page 13; 26pp; Japanese.

CC The present complementarity determining region 2 (CDR2), which is
 CC from a murine, anti-human high affinity immunoglobulin E (IgE)
 CC receptor, monoclonal antibody (MAb) light chain variable region,
 CC can be used in the preparation of humanised or semi-chimeric
 CC anti-human high affinity IgE receptor MAb. The MAb can be used to
 CC treat or prevent diseases, specifically allergies, associated with
 CC the receptor. The humanised, semi-chimeric or chimeric MAb have
 CC very low antigenicity in humans.

SQ Sequence 17 AA;

Query Match 72.1%; Score 75; DB 18; Length 17;

Best Local Similarity 70.6%; Pred. No. 4.9e-05;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIYPGNGNTKYNOKFNG 17
 |||:|||||:|
 Db 1 WIYPKVNNTKYNKFKG 17

RESULT 7
 AAU08360
 ID AAU08360 standard; peptide; 17 AA.

AC AAU08360;

DT 17-DEC-2001 (first entry)

DE Antibody heavy chain variable region CDR2 #1.

XX Antibody; heavy chain; CDR2; complementarity determining region; OPGp;
 KW osteopathic; osteoprotegrin binding protein; osteoclast formation;
 KW bone resorption; loss of bone mass; bone tumour; osteoporosis;
 KW bone cancer; rheumatoid arthritis; hypercalcaemia of malignancy;
 KW steroid-induced osteoporosis.

OS Synthetic.

PN WO200162932-A1.

PD 30-AUG-2001.

PF 23-FEB-2001; 2001WO-US05973.

PR 23-FEB-2000; 2000US-051139.

PR 22-FEB-2001; 2001US-0791153.

PA (AMGE-) AMGEN INC.

PI Deshpande RV, Hiltz A, Boyle WJ, Sullivan JK;

DR WPI: 2001-557706/62.

XX Antibodies that bind antagonistically to osteoprotegrin binding
 PT protein, useful for treating osteoporosis, metastasis of cancer to
 PT bone, rheumatoid arthritis, hypercalcaemia of malignancy and
 PT steroid-induced osteoporosis -

PS Claim 14; Page 129; 239pp; English.

XX The invention relates to an antibody or antigen binding domain (or
 CC fragment, variant or derivative), which binds to an osteoprotegrin
 CC binding protein (OPGp) and which is an antagonistic antibody.
 CC The antibody or antigen binding domain may be administered to inhibit
 CC osteoclast formation or activation, inhibit bone resorption in a mammal,
 CC prevent or treat loss of bone mass in a mammal and to prevent or treat
 CC tumour cell growth in bone. The loss of bone mass results from
 CC osteoporosis, metastasis of cancer to bone, rheumatoid arthritis,
 CC hypercalcaemia of malignancy and steroid-induced osteoporosis. The
 CC present sequence is an antibody heavy chain variable region
 CC complementarity determining region, CDR2, which can be incorporated into
 CC an antibody/antigen binding domain of the invention.

SQ Sequence 17 AA;

Query Match 69.2%; Score 72; DB 22; Length 17;

Best Local Similarity 70.6%; Pred. No. 0.00015;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIYPGNGNTKYNOKFNG 17
 |||:|||||:|
 Db 1 WINAGNGNTKFSQKFG 17

RESULT 8
 AAB12175
 ID AAB12175 standard; peptide; 17 AA.

AC AAB12175;

DT 10-NOV-2000 (first entry)

DE Human CDR2 for IL-2R monoclonal antibody.

KM Human; CDR; humanised antibody; complementarity determining region;

KW IL-2alpha; interleukin-2 receptor; transplant rejection; CD25;

OS Immunosuppression.

OS Homo sapiens.

PN WO200030679-A1.

PD 02-JUN-2000.
 XX
 PF 22-NOV-1999; 99WO-EP08988.
 PR 23-NOV-1998; 98GB-0025632.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PI Feutren G, Howell RK, Marbach P, Roberts A, Schreier MH, Schulz M;
 XX MPI: 2000-399934/34.
 XX
 PT Preventing or treating transplant rejection in a recipient comprises
 PT administering a monoclonal antibody specific for interleukin-2 receptor
 PT beyond the very early phase following transplantation -
 XX
 PS Disclosure; Page 2; 17pp; English.
 CC
 CC The present sequence is a human complementarily determining region (CDR).
 CC This sequence was used to generate a humanised antibody specific for the
 CC alpha subunit of Interleukin-2 receptor (IL-2Ralpha). The humanised
 CC IL-2Ralpha antibody would be useful for preventing or treating transplant
 CC rejection in a recipient of organ, tissue or modified or unmodified cell
 CC transplant. The use of a monoclonal antibody specific for IL-2R decreases
 CC transplant rejection in an immunosuppression-intolerant or non-compliant
 CC recipient compared with available therapies. Also, undesirable side
 CC effects associated with current treatments e.g. renal dysfunction,
 CC hirsutism, gingival hyperplasia and hypertension are avoided.
 CC
 SQ Sequence 17 AA:

Query Match 68.3%; Score 71; DB 21; Length 17;
 Best Local Similarity 75.0%; Pred. No. 0.00021;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IYPGNGNTKYNQKFG 17
 |||||:|||||I
 Db 2 IYPGNSDTSYNQKFG 17

RESULT 9
 ID AAY80140 standard; peptide; 17 AA.
 AC AAY80140;
 XX
 DT 19-MAY-2000 (first entry)
 DE Chimeric anti-CD25 antibody Ig heavy chain hypervariable region CDR2.
 XX
 KW Chimeric anti-CD25 antibody; CD25 binding molecule; immunoglobulin;
 KW hypervariable region; complementary determining region; CDR1; CDR2; CDR3;
 XX inflammation; rheumatoid arthritis; hyperproliferative skin disease.
 OS Homo sapiens.
 XX
 PN WO200006604-A2.
 PD 10-FEB-2000.
 XX
 PF 26-JUL-1999; 99WO-EP05316.
 PR 27-JUL-1998; 98GB-0016281.
 PR 27-MAY-1999; 99GB-0012460.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PA (UNLO) UNIV COLLEGE LONDON.
 PI Amiot PL, Schreier MH;
 XX
 DR MPI: 2000-183090/16.

XX
 PT Use of CD25 binding molecules in the treatment of rheumatoid arthritis
 PT and inflammatory or hyperproliferative skin diseases -
 XX
 PS Claim 1; Page 11; 14pp; English.
 XX

The present invention describes CD25 binding molecules, which are used
 to treat rheumatoid arthritis and inflammatory or hyperproliferative
 skin diseases. The CD25 binding molecule comprises at least one
 antigen binding site comprising at least one domain in which comprises
 sequence, the hypervariable regions CDR1 (having the sequence RYWMH),
 CDR2 (having the sequence AIVPGNSDTSYNQKFG) and CDR3 (having the
 sequence DYGVFPF), or their direct equivalents. The CD25 binding
 molecules are used in the treatment of rheumatoid arthritis and
 inflammatory or hyperproliferative skin diseases, such as psoriasis,
 atypical dermatitis, contact dermatitis and further eczematous
 dermatitises, seborrheic dermatitis and further eczematous
 bullous pemphigoid, Epidermolysis bullosa, urticaria, angiodemas,
 vasculitides, erythemas, cutaneous eosinophilias, lupus erythematosus
 and acne. A more preferred CD25 binding molecule for use in accordance
 with the present invention is selected from a chimeric anti-CD25 antibody
 which comprises at least: (1) one immunoglobulin heavy chain, or
 fragment, which comprises (1) a variable domain comprising in sequence
 the hypervariable regions CDR1, CDR2 and CDR3 (as above) and (11) the
 constant part, or fragment, of a human heavy chain; and (2) one
 immunoglobulin light chain, or fragment, which comprises (1) a variable
 domain comprising in sequence the hypervariable regions CDR1, CDR2,
 and CDR3 (ASSSISWQ, DTSKLAS and HORSSTY, respectively) and (11) the
 constant part, or fragment, of a human light chain.
 XX

SQ Sequence 17 AA:
 Query Match 68.3%; Score 71; DB 21; Length 17;
 Best Local Similarity 75.0%; Pred. No. 0.00021;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IYPGNGNTKYNQKFG 17
 |||||:|||||I
 Db 2 IYPGNSDTSYNQKFG 17

RESULT 10
 ID AAO14423 standard; peptide; 17 AA.
 AC AAO14423;
 XX
 DT 03-MAY-2002 (first entry)
 DE CD25 binding protein domain 1 hypervariable region CDR2.
 XX
 KW CD25 binding protein; hypervariable region; CDR2; gastrointestinal tract;
 KW inflammatory disease; irritable bowel syndrome; IBS; Crohn's disease;
 KW ulcerative colitis; inflammatory intestinal disease; medication.
 XX
 OS unidentified.
 XX
 PN WO200172845-A1.
 PD 04-OCT-2001.
 XX
 PF 28-MAR-2001; 2001WO-EP03541.
 PR 30-MAR-2000; 2000GB-0007911.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PI Adam H, Faerber L;
 XX
 DR MPI: 2001-626258/72.
 XX
 PT CD25 binding molecule which comprises antigen binding site comprising

2

DD 2 LF PGNGL J21 NYNFK NO 27

RESULT 13
AAU70377
ID AAU70377 standard; Peptide: 17 AA.
XX
AC AAU70377;
XX
DT 14-FEB-2002 (first entry)
XX
DE Mouse heavy chain II CDR 2.
XX
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW Complementarily determining region; framework region; IgBP;
KW Transgenic plant; immunoglobulin binding protein array;
XX IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX
OS Mus musculus.
XX
FN WO200183806-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14349.
XX
PR 02-MAY-2000; 2000US-0563222.
XX
FA (EPIC-) EPICYTE PHARM INC.
XX
PI Hlatt AC, Hein MB;
XX
DR WPI: 2002-055482/07.
XX
PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array -
XX
PS Disclosure: Page 15; 12pp; English.
XX
CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that
CC binds to a ligand, and transformed plant cells are selected, and
CC preparing an IgBP array in plant cells. At least one peptide sequence has
CC at least 75% sequence identity to a framework region (FR) of a native
CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.
CC The method is useful for preparing an immunoglobulin binding protein
CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)
CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The
CC CHBP is useful for discovery of e.g. screening assays of IgBPs having
CC desired characteristics. The present sequence is a mammalian
CC immunoglobulin derived peptide that may be incorporated into an IgBP of
CC the invention.
XX
SQ Sequence 17 AA:
XX
Query Match 64.4%; Score 67; DB 23; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.00088;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 2 IYPNGNTRYNOKFNG 17
DB 1 | | | | | | | | | | | | | | | |
2 IYPNGNTRYNOKFNG 17

RESULT 14
AAW89159
ID AAW89159 standard; peptide: 17 AA.
XX

AC AAW89159;
XX
DT 25-MAR-1999 (first entry)
XX
DE Anti-p53 monoclonal antibody 248 CDR2 heavy chain based peptide.
XX
KW Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
KW immune response; tumour associated antigen; metastatic cancer.
XX
OS Mus sp.
OS Synthetic.
XX
FN WO9856416-A1.
XX
PD 17-DEC-1998.
XX
PF 09-JUN-1998; 98WO-IL00266.
XX
PR 09-JUN-1997; 97IL-0121041.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;
PI Wolkowicz R;
XX
DR WPI: 1999-070296/06.
XX
PT Use of a monoclonal antibody to a tumour-associated antigen - to
PT induce anti-tumour immunity or elicit an increased immune response
PT to the antigen
XX
PS Claim 7; Page 29; 47pp; English.
XX
CC The present invention describes the use of an immunogen (A) to induce
CC anti-tumour immunity; to elicit an increased immune response to tumour
CC associated antigen (TAA) and/or to induce an immune response to mutant
CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
CC (MAB) to TAA, or its fragment; (ii) a peptide based on a CDR
CC (complementarily determining region) on the heavy or light chain of MAB
CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
CC variable (V) region of MAB. In a gene delivery vehicle. The present
CC sequence represents a peptide based on CDR2 of the heavy chain of
CC anti-p53 MAB 248. Also described is a method for generating sequence-
CC specific, anti-DNA antibodies (Ab) by immunising a mammal with a MAB
CC directed to a domain containing a DNA-binding site of a DNA-binding
CC protein. (A) is used to treat a wide variety of primary and metastatic
CC cancers, particularly those where p53 is involved. Ab are used for
CC diagnosis (e.g. to determine critical sequences in animal or plant
CC breeding); to identify bacteria and other parasites; to determine
CC parentage; in forensic science; to isolate specific genes for DNA
CC vaccination; in gene sequencing and cloning; also possibly for activation
CC of selected therapeutic genes in plants, animals and humans. (A) induce
CC an effective anti-tumour response without causing harm to the patient.
CC The method uses (A) to generate anti-TAA by exploiting the anti-idiotype
CC network.
XX
SQ Sequence 17 AA:
XX
Query Match 63.5%; Score 66; DB 20; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 2 IYPNGNTRYNOKFNG 17
DB 1 | | | | | | | | | | | | | | | |
2 IYPNGNTRYNOKFNG 17

RESULT 15
AAB10011
ID AAB10011 standard; protein: 17 AA.
XX
AC AAB10011;
XX

DT 01-NOV-2000 (first entry)
 XX
 DE H. pylori beta-urease-binding antibody heavy chain CDR2 protein #2.
 XX
 KW Acid-resistant microorganism; detection; faecal; intestine; infection;
 KW monoclonal antibody; heavy chain; complementarity determining region;
 KW CDR; beta-urease.
 XX
 OS Unidentified.
 XX
 PN WO200026671-A1.
 PD 11-MAY-2000.
 XX
 PF 29-OCT-1999; 99WO-EF08212.
 XX
 PR 29-OCT-1998; 98EP-0120517.
 PR 06-NOV-1998; 98EP-0120687.
 XX
 PA (CONN-) CONNEX GMBH.
 XX
 PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
 PI Ringels A;
 XX
 DR WPI: 2000-365747/31.
 DR N-PSDB: AAA40167.
 XX
 PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
 PT pylori, comprises reacting a faecal sample with two binding reagents for
 PT antigens that survive intestinal passage.
 XX
 PS Claim 26; Page 22; 84pp; German.
 XX
 CC This invention describes a novel method for the detection of a mammalian
 CC infection by an acid-resistant microorganism (A) by treating a faecal
 CC sample with at least two different monoclonal antibodies (Mab) (or their
 CC fragments or derivatives) or aptamers (collectively (I)) and detecting
 CC formation of a complex (C) between (I) and the corresponding antigen of
 CC (A). The first and second (I) bind to epitopes of different antigens
 CC (Ag). These epitopes are present, after passage through the intestines,
 CC in at least some mammals, and have either: (i) their native structure;
 CC or (ii) a structure against which an antibody is produced by an animal
 CC infected or immunized with (A), or its extract, lysate, derived protein
 CC or fragment, or with a synthetic peptide. Practically all mammals display
 CC at least one of the specified epitopes. The method is used to detect
 CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
 CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus,
 CC M. tuberculosis, C. jejuni and C. pylori. (I) may also be used
 CC therapeutically. The method is direct and non-invasive, and provides an
 CC inexpensive and easily standardizable diagnosis, despite possible
 CC degradation of antigens during passage through the intestines. This
 CC sequence represents a fragment of a H. pylori beta-urease-binding
 CC antibody heavy chain complementarity determining region CDR2 which is
 CC used to illustrate the method of the invention.
 XX
 SQ Sequence 17 AA:
 Query Match 62.5%; Score 65; DB 21; Length 17;
 Best Local Similarity 68.8%; Pred. No. 0.0018;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IYPGNGNTKYNGKFNK 17
 ||||:|:| | | | |
 DB 2 IYPGDGTNYNGKFKG 17

Search completed: February 25, 2003, 11:38:25
 Job time : 35 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:34:41 ; Search time 29 Seconds
(without alignments)
24.314 Million cell updates/sec

Title: US-09-743-482A-10

Perfect score: 104

Sequence: 1 WIPGNGNTRKYNQKENG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 883

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	24.0	12	1	TA10_TREME
2	23	22.1	15	1	UC14_MAIZE
3	22	21.2	14	1	RS19_PMBP
4	22	21.2	14	1	TKN1_SCHGR
5	21	20.2	15	1	OBPA_MAMBR
6	21	20.2	17	1	RANK_RANRU
7	20.5	19.7	10	1	GON2_CHICK
8	20	19.2	8	1	UPAA_HUMAN
9	20	19.2	9	1	FARP_CALSI
10	20	19.2	10	1	SP34_DICMU
11	20	19.2	10	1	UH05_RAT
12	20	19.2	11	1	PKC1_CARMO
13	20	19.2	15	1	GLN2_PINPS
14	20	19.2	16	1	RIPK_TRIKI
15	20	19.2	17	1	PH4_PBRAM
16	19	18.3	10	1	UXA6_CHLTR
17	19	18.3	12	1	UR2B_CYPCA
18	19	18.3	13	1	BPL1_BOTJA
19	19	18.3	14	1	RS19_CLOPP
20	19	18.3	14	1	RS19_LOMBP
21	19	18.3	15	1	CBPB_PROAT
22	19	18.3	15	1	FGFL_CANFA
23	19	18.3	16	1	OD02_BOVIN
24	18	17.3	9	1	FAR4_CALVO
25	18	17.3	9	1	HUTU_KLEAV
26	18	17.3	12	1	UH03_RAT
27	18	17.3	13	1	LIGA_TRAVE
28	18	17.3	13	1	SAZA_ONCMY
29	18	17.3	13	1	SAZB_ONCMY
30	18	17.3	13	1	TA13_TREME
31	18	17.3	13	1	TP13_PHYRO
32	18	17.3	14	1	HY14_PIG
33	18	17.3	14	1	NEJ2_FASHE

ALIGNMENTS

34	18	17.3	14	1	UN07_CLOPA	P81352 clostridium
35	18	17.3	14	1	UN46_CLOPA	P81362 clostridium
36	18	17.3	15	1	FKB7_PINPS	P81104 pinus pinus
37	18	17.3	15	1	LEC1_POSC	P22582 psophocarpus
38	18	17.3	16	1	FOR2_MYRGU	P81437 myrmecia gu
39	18	17.3	17	1	PK5_PBRAM	P82617 petriplaneta
40	17.5	16.8	10	1	GON1_ALMT	P37041 alligator m
41	17.5	16.8	10	1	GON3_ONCKE	P20367 oncorhynchus
42	17	16.3	10	1	BPP2_BOTIN	P30422 bothrops in
43	17	16.3	10	1	RL16_ACHLA	P29221 acholeplasm
44	17	16.3	11	1	TRC2_CALVO	P41518 calliphora
45	17	16.3	12	1	RS19_CUYEP	Q46490 clover yell

RESULT 1
ID TA10_TREME STANDARD; PRT; 12 AA.

AC P01371;
DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-NOV-1991 (Rel. 20, Last annotation update)

DE Tremetogen A-10.

OS Tremella mesenterica (Jelly fungus).

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;

OC Tremellomycetidae; Tremellales; Tremellaceae; Tremella.

ON NCBI_TaxID=5217;

RN (1)

RP SEQUENCE.

RA Sakagami Y., Yoshida M., Isogai A., Suzuki A.;

RT "Peptide sex hormones inducing conjugation tube formation in

compatible mating-type cells of Tremella mesenterica.";

RL Science 212:1525-1527(1981).

CC -!- FUNCTION: TREMERGEN A-10 IS PRODUCED BY THE A MATING-TYPE CELLS

AND INDUCES FORMATION OF CONJUGATION TUBES IN A MATING-TYPE CELLS.

DR PIR; A01642; JTG0.

KW Lipoprotein; Prenylation; Pheromone.

FT LIPID

SQ SEQUENCE 12 AA; 1246 MW; 84EF574959676DC5 CRC64;

Query Match 24.0%; Score 25; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 PCNG 7

7 PCNG 10

RESULT 2

ID UC14_MAIZE STANDARD; PRT; 15 AA.

AC P80620;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Unknown protein from 2D-page of etiolated coleoptile (Spot 258)

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

OC Panicoidae; Andropogoneae; Zea.

ON NCBI_TaxID=4577;

RN (1)

RP SEQUENCE.

RA TISSUE-Coleoptile;

RA Touzet P., Ricciardi F., Morin C., Damerval C., Huot J.-C.,

RA Peronnet J.-C., Zivy M., de Vienne D.;

RT "The maize two dimensional gel protein database: towards an integrated

genome analysis program.";

RT Theor. Appl. Genet. 93:997-1005(1996).

-1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 5.9, ITS MW IS: 34.6 kDa.

DR MALZE-2DPAGE; P80620; COLEOPTILE.

DR MALZEDB: 123944; "

FT NON-TER 1 1

FT NON-TER 15 15

SO SEQUENCE 15 AA; 1564 MW; CF0BBA0B7DE658 CRC64;

Query Match 22.1%; Score 23; DB 1; Length 15;

Best Local Similarity 44.4%; Pred. No. 9.7e+02;

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 YPGNGTKY 11

Db 2 YGDDGAVY 10

RESULT 3

RS19_PPMBP STANDARD; PRT; 14 AA.

AC 052093; 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE 30S ribosomal protein S19 (Fragment).

GN RPS19 OR RPS19.

OS Pigeon pea witches'-broom phytoplasma.

OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;

OC Acholeplasmataceae; Phycoplasma.

NCBI_TaxID=37700;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94350802; PubMed=8071198;

RA Gunderson D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;

RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for

their classification."

RT J. Bacteriol. 176:5244-5254(1994).

-1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY

TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE S19 FAMILY OF RIBOSOMAL PROTEINS.

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CC EMBL: L27036; AAA83946.1; "

DR InterPro: IPR002222; RIBOSOMAL_S19.

DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.

KW Ribosomal protein; rRNA-binding.

FT NON-TER 1 1

FT SEQUENCE 14 AA; 1668 MW; 8FD46F6B830DFBBA CRC64;

Query Match 21.2%; Score 22; DB 1; Length 14;

Best Local Similarity 44.4%; Pred. No. 1.3e+03;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 6 NGNTKYNOK 14

Db 2 HGHTKDSKK 10

RESULT 4

TKN1_SCHGR STANDARD; PRT; 14 AA.

AC P82470; 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Tachykinin-1 (Scg-mldgut-TK).

OS Schistocerca gregaria (Desert locust).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Orthoptera; Orthoptera; Caelifera;

OC Acridomorpha; Acridoidea; Acrididae; Cyrtacanthacridinae;

OC Schistocerca.

NCBI_TaxID=7010;

RP SEQUENCE, AND MASS SPECTROMETRY.

PC TISSUE=Midgut;

RX MEDLINE=20050081; PubMed=10581195;

RA Veldert D., Baggettman G., Deria R., Maelkens E., Meusen T.,

RT "Identification of a new tachykinin from the midgut of the desert

locust, Schistocerca gregaria, by ESI-Qq-TOF mass spectrometry."

RT Biochem. Biophys. Res. Commun. 266:237-242(1999).

CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY

OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.

CC -1- TISSUE SPECIFICITY: MIDGUT.

CC -1- MASS SPECTROMETRY: MW=1493.79; METHOD=Electrospray

CC -1- SIMILARITY: SIMILAR TO THE COCKROACH LEMTRP 3, A TACHYKININ-

RELATED PEPTIDE ALSO CONFINED TO THE MIDGUT.

KW Tachykinin; Neuropeptide; Amidation.

FT MOD_RES 14 14

FT SEQUENCE 14 AA; 1496 MW; CAAC578C0169FC72 CRC64;

Query Match 21.2%; Score 22; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GNTK 10

Db 1 GNTK 4

RESULT 5

OBPA_MAMBR STANDARD; PRT; 15 AA.

AC P81285; 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 38, Last annotation update)

DE Antennal odorant-binding protein (AOBP) (Fragment).

OS Manestra brassicae.

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;

OC Diptera; Noctuidae; Noctuidae; Hadeninae; Mamestra.

NCBI_TaxID=55057;

RN [1]

RP SEQUENCE.

RX TISSUE=Antenna;

RX MEDLINE=99097262; PubMed=9878563;

RA Bobot J., Sobrio F., Lucas P., Nagnan-Le Meunier P.;

RT "Functional characterization of a new class of odorant-binding

proteins in the moth Mamestra brassicae."

RT Biochem. Biophys. Res. Commun. 253:489-494(1998).

CC -1- TISSUE SPECIFICITY: ANTENNA.

DR InterPro: IPR005055; A10_OS-D.

DR Pfam: PF03392; OS-D; 1.

KW Olfaction; Transport.

FT NON-TER 15 15

FT SEQUENCE 15 AA; 1875 MW; 1EE9B36E5A74BAA CRC64;

Query Match 20.2%; Score 21; DB 1; Length 15;

Best Local Similarity 42.9%; Pred. No. 2e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 10 KYNOKFN 16

Db 3 KYTDKID 9

RESULT 6

RANR_RANRU

ID RANR_RANRU STANDARD; PRT; 17 AA.
AC P08952;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ranatensis-R.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranolidae; Ranidae; Rana.
NCBI_TaxID=8410;
RN [1]
RP SEQUENCE
RX MEDLINE=84131098; PubMed=6141890;
RA Nakajima T.;
RL Unpublished results, cited by:
RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
RL Comp. Biochem. Physiol. 77C:99-108(1984).
CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR Interpro: IPR000874; Bombesin.
DR Pfam: PF02044; Bombesin; 1.
DR PROSITE: PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 17
FT MOD_RES 17
SO SEQUENCE 17 AA; 2053 MW; 3A876535581863E CRC64;
Query Match 20.2%; Score 21; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 10 KYNOKENG 17
DB 7 KYNOMATG 14
RESULT 7
GON2_CHICK
ID GON2_CHICK STANDARD; PRT; 10 AA.
AC P37043; P20408; P81750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadoliberin II (Gonadotropin-releasing hormone II) (GNRH-II)
DE (LH-RH II) (Lutiberin II).
OS Gallus gallus (Chicken).
OS Alligator mississippiensis (American alligator),
OS Squallus acanthias (Spiny dogfish),
OS Hydrolyagus colliei (Spotted ratfish) (Pacific ratfish), and
OS Clupea pallasii (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031, 8496, 7797, 7873, 30724;
RN [1]
RP SEQUENCE
RX SPECIES=Chicken; TISSUE=Hypothalamus;
RX MEDLINE=84222059; PubMed=6427779;
RA Miyamoto K., Hasegawa Y., Nomura M., Igarashi M., Kangawa K.,
RA Matsuo H.;
RT "Identification of the second gonadotropin-releasing hormone in
RT chicken hypothalamus: evidence that gonadotropin secretion is
RT probably controlled by two distinct gonadotropin-releasing hormones
RT in avian species.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3874-3878(1984).
RN [2]
RP SEQUENCE
RC SPECIES=A. mississippiensis; TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McKory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";

RL Regul. Pept. 33:105-116(1991).
RN [3]
RP SEQUENCE
RC SPECIES=S. acanthias; TISSUE=Brain;
RX MEDLINE=92335300; PubMed=1631133;
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
RA Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in
RT dogfish brain provides insight into GNRH evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
RN [4]
RP SEQUENCE
RC SPECIES=H. colliei; TISSUE=Brain;
RX MEDLINE=91340067; PubMed=1678723;
RA Lovejoy D.A., Sherwood N.M., Fischer W.H., Jackson B.C., Rivier J.E.,
RA Lee T.;
RT "Primary structure of gonadotropin-releasing hormone from the brain
RT of a holoccephalan (ratfish: Hydrolyagus colliei).";
RL gen. Comp. Endocrinol. 82:152-161(1991).
RN [5]
RP SEQUENCE, AND FUNCTION
RC SPECIES=C. pallasii; TISSUE=Brain, and Pituitary;
RX MEDLINE=20114351; PubMed=10650929;
RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring.";
RL Endocrinology 141:505-512(2000).
CC -1- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
DR PIR: B60066; RHA02.
DR PIR: A61126; A61126.
DR PIR: B46030; B46030.
DR Interpro: IPR02012; GNRH.
DR Pfam: PF00446; GNRH; 1.
DR PROSITE: PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus.
FT MOD_RES 1
FT MOD_RES 1
FT MOD_RES 10
FT MOD_RES 10
SO SEQUENCE 10 AA; 1254 MW; 284B2E437871F5A3 CRC64;
Query Match 19.7%; Score 20.5; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
OY 1 WYFG 5
DB 7 W-YFG 10
RESULT 8
UPAA_HUMAN
ID UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Rivier F., Pasquall C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RT Electrophoresis 13:707-714(1992)
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 7, ITS MW IS: 12 kDa.
 DR SWISS-2DPAGE: P30096; HUMAN.
 FT NON_TER 1 1 F->P.
 FT VARIANT 5 5 /FTID=VAR_000004.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match 19.2%; Score 20; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 YPG 5
 111
 DB 6 YPG 8

RESULT 9
 FARP_CALSI STANDARD; PRT; 9 AA.
 AC P38495;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide.
 OS Callinectes sapidus (Blue crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Callinectes.
 NCBI_TaxID=6763;
 OX NCBI
 RN 11
 RP SEQUENCE.
 RX MEDLINE=92270479; PubMed=1815216;
 RA Kraljick K.G.;
 RT "The identification and structure-activity relations of a
 RT cardioactive FMRFamide-related peptide from the blue crab Callinectes
 RT sapidus.";
 RL Peptides 12:1295-1302(1991).
 CC -1- FUNCTION: CARDIOACTIVE PEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD.RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1159 MW; 134F0729D5A4045B CRC64;

Query Match 19.2%; Score 20; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 YNORF 15
 111
 DB 2 YNRSF 6

RESULT 10
 SP34_DICMU STANDARD; PRT; 10 AA.
 ID SP34_DICMU
 AC P81545;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Surface protein p34 (fragment).
 GN P34.
 OS Dictyostelium mucoroides (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
 OX NCBI_TaxID=31287;
 RN 11
 RP SEQUENCE.
 RC STRAIN=DM-7;
 RA Schreiner S.J.;
 RT "Characterization of a surface protein in macrocysts of Dictyostelium
 RT mucoroides.";
 RL Submitted (NOV-1998) to the SWISS-PROT data bank.

CC -1- FUNCTION: THIS PROTEIN IS PRESENT IN THE MACROCYST PRIMARY WALL
 CC WHICH IS PRODUCED BY AMOEBAE DURING THE ONSET OF SEXUAL
 CC REPRODUCTION.
 CC -1- SUBCELLULAR LOCATION: MACROCYST PRIMARY WALL.
 CC Cell wall.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1190 MW; 1B6A707AA345B50 CRC64;

Query Match 19.2%; Score 20; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 1.8e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 IYPGNGN 8
 111
 DB 3 IYNKDN 9

RESULT 11
 UH05_RAT STANDARD; PRT; 10 AA.
 ID UH05_RAT
 AC P56573;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Unknown protein from 2D-page of heart tissue (Spot P5) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 OX NCBI
 RN 11
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Heart;
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
 RA Jungblut P.R.;
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 8.3, ITS MW IS: 30 kDa.
 FT UNSURE 9 9 OR P.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1269 MW; 00CBA4BB46C5BAB CRC64;

Query Match 19.2%; Score 20; DB 1; Length 10;
 Best Local Similarity 25.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 10 KYNORF 17
 111
 DB 2 QYDSQYDG 9

RESULT 12
 PKC1_CARMO STANDARD; PRT; 11 AA.
 ID PKC1_CARMO
 AC P82684;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-1 (Cam-PK-1) (FAPRL-Amide).
 OS Carausius morosus (Indian stick insect).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Phasmatoidea;
 OC Heteronemidae; Carausius.
 OX NCBI_TaxID=7022;
 RN 11
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RA Pregel R., Kellner R., Gaede G.;
 RT "Myotropic neuropeptides from the retrocerebral complex of the stick
 RT insect, Carausius morosus (Phasmatoidea: Lonchodidae).";
 RL Eur. J. Entomol. 96:275-278(1999).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.

CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro: IPR001484; PYROKININ.
 DR PROSITE: PS00539; PYROKININ; FALSE_NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 11
 SO SEQUENCE 11 AA; 1235 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 19.2%; Score 20; DB 1; Length 11;
 Best Local Similarity 37.5%; Pred. No. 2e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 GNTYTNOK 14
 DB 3 GGTGYTPR 10

RESULT 13
 GLN2_PINPS STANDARD; PRT; 15 AA.
 AC P81107;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Probable glutamine synthetase leaf isozyme (EC 6.3.1.2) (Glutamate--
 ammonia ligase) (S2205/S2287) (M47/M48) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN 11
 RP SEQUENCE.
 RA TISSUE=Needle;
 RA Plomion C., Costa P., Bahman N., Frigerio J.-M.;
 RT Genetic analysis of needle proteins in maritime pine. 1. Mapping
 dominant and codominant protein markers assayed on diploid tissue, in
 a haploid-based genetic map.";
 RL Silvae Genetica 46:161-165(1997).
 RN 12

RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=9274088; PubMed=10344291;
 RA Costa P., Plomion C., Bauw G., Dubos C., Bahman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 proteins.";
 RT Electrophoresis 20:1098-1106(1999).
 RL
 CC -1- FUNCTION: THE LIGHT-MODULATED CHLOROPLAST ENZYME, ENCODED BY A
 CC NUCLEAR GENE AND EXPRESSED PRIMARILY IN LEAVES, IS RESPONSIBLE FOR
 CC THE REASSIMILATION OF THE AMMONIA GENERATED BY PHOTORESPIRATION
 CC (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
 CC L-glutamine.
 CC -1- SUBUNIT: HOMOOCTAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Chloroplast (By similarity).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
 CC 5.7, ITS MW IS: 42 kDa.
 CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
 DR InterPro: IPR001691; GLN_synth.
 DR PROSITE: PS00180; GLNA_1; PARTIAL.
 DR PROSITE: PS00181; GLNA_ATP; PARTIAL.
 KW Ligase; Chloroplast.
 FT NON_TER 1
 FT NON_TER 15
 SO SEQUENCE 15 AA; 1614 MW; 2AA2420BEFD60D27 CRC64;

Query Match 19.2%; Score 20; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 YPG 5
 DB 13 YPG 15

RESULT 14
 RIPK_TRIKI STANDARD; PRT; 16 AA.
 ID RIPK_TRIKI
 AC P16093;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein trichokirin (rRNA N-glycosidase)
 DE (EC 3.2.2.22) (Fragment).
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_TaxID=3677;
 RN 11
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=89005108; PubMed=3262509;
 RA Casellas P., Dussosoy D., Falasca A.I., Barbieri L.,
 RA Guillemot J.C., Ferrara P., Bolognesi A., Centini P., Stippe F.;
 RT "Trichokirin, a ribosome-inactivating protein from the seeds of
 RT Trichosanthes kirilowii Maximowicz. Purification, partial
 RT characterization and use for preparation of immunotoxins.";
 RL Eur. J. Biochem. 176:581-588(1988).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- PFM: GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC PIR: S01669; S01669.
 DR InterPro: IPR001574; RIP.
 DR PROSITE: PS00275; SHIGA_RICIN; PARTIAL.
 KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
 KW Glycoprotein.
 FT NON_TER 16
 FT NON_TER 16
 SO SEQUENCE 16 AA; 1605 MW; 5E268A7F345935A2 CRC64;

Query Match 19.2%; Score 20; DB 1; Length 16;
 Best Local Similarity 33.3%; Pred. No. 3e+03;
 Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 5 GNCNTRYNO 13
 DB 8 GGGTASYEK 16

RESULT 15
 PH4_PERAM STANDARD; PRT; 17 AA.
 ID PH4_PERAM
 AC P82697;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peptide hormone 4 (Pea-VLS-amide).
 OS Periplaneta americana (American cockroach).
 OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN 11
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Abdominal perisymphathetic organs;
 RX MEDLINE=20140865; PubMed=10676456;
 RA Predel R., Eckert M., Holman G.M.;
 RT "The unique neuropeptide pattern in abdominal perisymphathetic organs
 RT of insects.";
 RL Ann. N.Y. Acad. Sci. 897:282-290(1999).
 CC -1- FUNCTION: UNKNOWN.
 CC -1- MASS SPECTROMETRY: MW=1966.48; METHOD=MALDI.
 CC Neuropeptide; Amidation.
 FT MOD_RES 17
 FT MOD_RES 17
 SO SEQUENCE 17 AA; 1968 MW; CAFB57EC08218A9 CRC64;

Query Match 19.2%; Score 20; DB 1; Length 17;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIRPG 5
1 1 1
Db 5 WOLPG 9

Search completed: February 25, 2003, 11:39:01
Job time : 30 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:37:01 : Search time 92 Seconds
(without alignments)
38.074 Million cell updates/sec

Title: US-09-743-482a-10

Sequence: 104
1 WIPGNGNTKYNQKENG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 4013

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvivirus:*
16: sp_bacteriophage:*
17: sp_archaeophages:

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	30.8	15	10	Q42223 arabidopsis
2	30	28.8	13	10	Q43174 solanum tub
3	28	26.9	16	10	Q94F61 triticum ae
4	27	26.0	11	5	Q99292 drosophila
5	27	26.0	17	15	Q78324 human immun
6	27	26.0	17	15	Q78328 human immun
7	26	25.0	17	15	Q9KJMI staphylococ
8	24	23.1	10	4	Q96QAT homo sapien
9	24	23.1	14	5	P82220 bombyx mori
10	24	23.1	16	12	Q99379 alfa mos
11	23	22.1	13	13	P83010 triakis scy
12	23	22.1	15	2	P83069 bacillus ce
13	23	22.1	15	2	O05463 nltrosospi
14	23	22.1	15	10	Q9S8V6 triticum ae
15	22.5	21.6	14	10	P82433 nicotiana t
16	22	21.2	11	9	Q37925 bacterioph

17	22	21.2	15	4	Q9UCB9	Q9UCB9 homo sapien
18	22	21.2	15	6	Q9TQ05	Q9TQ05 bos taurus
19	22	21.2	15	6	Q9TR45	Q9TR45 bos taurus
20	22	21.2	15	11	Q9GVN0	Q9GVN0 ratius sp.
21	22	21.2	16	2	Q9R5E9	Q9R5E9 haemophilus
22	22	21.2	16	8	Q9XNP6	Q9XNP6 boophilus m
23	22	21.2	16	12	Q64975	Q64975 alfa mos
24	22	21.2	17	15	Q78326	Q78326 human immun
25	22	21.2	17	15	Q78345	Q78345 human immun
26	22	21.2	17	15	Q78378	Q78378 human immun
27	22	21.2	17	15	Q78381	Q78381 human immun
28	21	20.2	10	2	P83161	P83161 anabena sp
29	21	20.2	11	10	Q9S8E8	Q9S8E8 psophocarpa
30	21	20.2	12	2	O54226	O54226 saccharopol
31	21	20.2	12	11	Q61331	Q61331 mus musculu
32	21	20.2	13	2	Q9R5I4	Q9R5I4 streptococ
33	21	20.2	14	2	O45876	O45876 clostridium
34	21	20.2	14	2	O45872	O45872 clostridium
35	21	20.2	15	2	Q9R546	Q9R546 mycobacteri
36	21	20.2	15	11	Q9QVD8	Q9QVD8 ratius sp.
37	21	20.2	16	2	P76922	P76922 escherichia
38	21	20.2	17	2	Q9R4A5	Q9R4A5 oerskovia x
39	21	20.2	17	15	Q78323	Q78323 human immun
40	21	20.2	17	15	Q78327	Q78327 human immun
41	21	20.2	17	15	Q78380	Q78380 human immun
42	20.5	19.7	11	2	P83146	P83146 bacteroides
43	20	19.2	8	7	Q95213	Q95213 oryctolagus
44	20	19.2	8	12	O84156	O84156 orf virus
45	20	19.2	10	2	Q9R5N2	Q9R5N2 clostridium

ALIGNMENTS

RESULT 1

Q42223 PRELIMINARY: PRT: 15 AA.
AC Q42223
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE Auxin-repressed protein homolog (Fragment).
OC Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eufrosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-DRY SEEDS OF A. THALIANA ECOTYPE COLUMBIA;
RA Raynal M., Grelliet F., Laudie M., Meyer Y., Cooke R., Delseny M.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z29842; CA82814.1; -.
FT NON-TER
SQ SEQUENCE 15 AA: 1895 MW: 2990C00FDB0F8526 CRC64:

Query Match 30.8%; Score 32; DB 10; Length 15;
Best Local Similarity 36.4%; Pred. NO. 1.7e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 WIPGNGNTKY 11
Db 4 WYSGDSRIKH 14

RESULT 2

Q43174 PRELIMINARY: PRT: 13 AA.
AC Q43174
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Beta-fructofuranosidase (EC 3.2.1.26) (Fragment).

OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. CARA.
 RA MEDLINE=96279736; PubMed=8710506;
 RX Bouray A.S., Hedley P.E., Maddison A., Maugh R., Machray G.C.:
 RT "Exon skipping induced by cold stress in a potato invertase gene
 transcript";
 RL Nucleic Acids Res. 24:2347-2351(1996).
 DR EMBL: X95821; CA65087.1; -.
 KW Glycosidase; Hydrolase.
 FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA: 1541 MW: 1B3053E7384C6874 CRC64;

Query Match 28.8%; Score 30; DB 10; Length 13;
 Best Local Similarity 50.0%; Pred. No. 3e+02;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 WIVPGNGNTKRYN 12
 Db 1 WINDPNGPMYTN 12

RESULT 3
 ID 094F61 PRELIMINARY; PRT: 16 AA.
 AC 094F61;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Prolamin-box binding factor (Fragment).
 GN PBF.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. CHEYENNE;
 RA Chen Z., Fleming J., Zhi Y., Yi M.;
 RT "Sequence of the prolamin-box binding factor (PBF) promoter sequence
 from wheat";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF385139; AAK64285.1; -.
 FT NON_TER 16 16
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA: 1770 MW: B406423B4FEF76B CRC64;

Query Match 26.9%; Score 28; DB 10; Length 16;
 Best Local Similarity 33.3%; Pred. No. 7.8e+02;
 Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 IYVGNGNTKRYNQ 13
 Db 4 VFPSNSKSKAGQ 15

RESULT 4
 ID 099292 PRELIMINARY; PRT: 11 AA.
 AC 099292;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Bicorn protein (Fragment).
 GN BCB.
 OS Drosophila heteroneura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=32382;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91184004; PubMed=2081457;
 RA MacDonald P.M.;
 RT "bicoid mRNA localization signal: phylogenetic conservation of
 function and RNA secondary structure";
 RL Development 110:161-171(1990).
 CC -I- FUNCTION: BICOID IS SEGMENT-POLARITY PROTEIN THAT PROVIDES
 CC POSITIONAL CUES FOR THE DEVELOPMENT OF HEAD AND THORACIC SEGMENTS.
 CC BCD REGULATES THE EXPRESSION OF ZYGOTIC GENES, POSSIBLY THROUGH
 CC ITS HOMEDOMAIN, AND INHIBITS THE ACTIVITY OF OTHER MATERNAL GENE
 CC PRODUCTS. IT IS POSSIBLE THAT BCD ALSO BINDS RNA.
 DR EMBL: M32125; AAA28386.1; -.
 KW FLYBASE: FBgn0012352; Dmet\bcd.
 KW DNA-binding; Developmental protein; Homeobox; Nuclear protein;
 KW RNA-binding; Segmentation polarity protein; Transcription regulation.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA: 1221 MW: 8CE802305DD9D6C1 CRC64;

Query Match 26.0%; Score 27; DB 5; Length 11;
 Best Local Similarity 50.0%; Pred. No. 7.3e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 GNTKYNCKEN 16
 Db 2 GNTGFAYCFN 11

RESULT 5
 ID 078324 PRELIMINARY; PRT: 17 AA.
 AC 078324;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Viral sample FIPAR5B (Florida patient A), partial env cds, V5 region
 (Fragment).
 GN Human immunodeficiency virus type 1.
 OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Zhang L.Q., Leigh-Brown A.J.;
 RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92271245; PubMed=1589796;
 RA Ou C.-Y., Ciesielski C.A., Myers G., Banda C.I., Luo C.C.,
 RA Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
 RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
 RA Jaffe H.W.;
 RT "Molecular Epidemiology of HIV Transmission in a Dental Practice";
 RL Science 256:1165-1171(1992).
 DR EMBL: M92110; AAA44466.1; -.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA: 1651 MW: 3473A0BB802CA370 CRC64;

Query Match 26.0%; Score 27; DB 15; Length 17;
 Best Local Similarity 45.5%; Pred. No. 1.2e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 GNGNTKYNCKP 15
 Db 1 GGNNTKSETF 11

RESULT 6
 ID 078328 PRELIMINARY; PRT: 17 AA.

078328;
AC 01-NOV-1996 (TremBurel. 01, Created)
DT 01-NOV-1996 (TremBurel. 01, Last sequence update)
DE 01-DEC-2001 (TremBurel. 19, Last annotation update)
DE Viral sample FLPARSE (Florida patient A), partial env cds, v5 region (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L.O., Leigh-Brown A.J.;
RL Submitted (Apr-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=92271245; Pubmed=1589796;
RX Ou C.-Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C., Korber B.T.M., Mullins J.I., Schochetman G., Berelman R.L., Economou A.N., Witte J.J., Furman L.J., Salten G.A., Curran J.W., Jaffe H.W.;
RT "Molecular Epidemiology of HIV Transmission in a Dental Practice."; Science 256:1165-1171(1992).
RL EMBL: M92113; AAA44469.1; -.
DR NON_TER 1 17
FT NON_TER 1 17
SQ SEQUENCE 17 AA; 1750 MW; 346FDD8B802CA370 CRC64;

Query Match 26.0%; Score 27; DB 15; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0;

QY 5 GNGTKYNOKE 15
| | | | |
Db 1 GNGTKGSEPE 11

RESULT 7
ID 09KJMI PRELIMINARY; PRT; 17 AA.
AC 09KJMI;
DT 01-OCT-2000 (TremBurel. 15, Created)
DT 01-OCT-2000 (TremBurel. 15, Last sequence update)
DE Heparin-binding protein (Fragment).
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_Taxid=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RP12;
RA Fallgren C., Ute M., Ljungh A.;
RT "Isolation and characterization of a 17 kDa staphylococcal heparin binding protein with broad specificity."; Submitted (Jul-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF167348; AAF89616.1; -.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1942 MW; 0204BB80DC4C1E18 CRC64;

Query Match 25.0%; Score 26; DB 2; Length 17;
Best Local Similarity 57.1%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0;

QY 11 YNOKENG 17
| | | | |
Db 7 YTKKNG 13

RESULT 8
ID 0960A7 PRELIMINARY; PRT; 10 AA.
AC 0960A7;
DT 01-DEC-2001 (TremBurel. 19, Created)

DT 01-DEC-2001 (TremBurel. 19, Last sequence update)
DT 01-DEC-2001 (TremBurel. 19, Last annotation update)
DE BA151a2.1 (cd42 guanine exchange factor (GEF) 9 (Colllybistin, PEM-2, HPEM-2, KIAA424)) (Fragment).
GN ARRGEP9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Whitehead S.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL451106; CAC88408.1; -.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1122 MW; 39925CB878640043 CRC64;

QY 1 WYPCNG 7
| | | | |
Db 3 WIRGSG 9

RESULT 9
ID P82220 PRELIMINARY; PRT; 14 AA.
AC P82220;
DT 01-OCT-2001 (TremBurel. 18, Created)
DT 01-OCT-2001 (TremBurel. 18, Last sequence update)
DE 01-OCT-2001 (TremBurel. 18, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
OX NCBI_Taxid=7091;
RN [1]
RP SEQUENCE.
RC STRAIN-XIHHANG X KEMING; TISSUE-BODY WALL, AND FAT BODY;
RA MEDLINE=21177481; Pubmed=11280994;
RX Zhong B.X.;
RT "Protein database for several tissues derived from five instar of silkworm.";
FT I Chuan Hsueh Pao 28:217-224(2001).
RL NON_TER 14 14
SQ SEQUENCE 14 AA; 1566 MW; 3F6E8265CA389778 CRC64;

Query Match 23.1%; Score 24; DB 5; Length 14;
Best Local Similarity 57.1%; Pred. No. 2.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0;

QY 7 GNTKYNQ 13
| | | | |
Db 8 GNXXNE 14

RESULT 10
ID 099379 PRELIMINARY; PRT; 16 AA.
AC 099379;
DT 01-NOV-1996 (TremBurel. 01, Created)
DT 01-NOV-1996 (TremBurel. 01, Last sequence update)
DT 01-NOV-1998 (TremBurel. 08, Last annotation update)
DE 35 kDa protein (Fragment).
OS Alfalfa mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae; Alfamovirus.
OX NCBI_Taxid=12321;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=83220821; PubMed=6856476;
 RA Ravelandro M., Godefroy-Colburn T., Plink L.;
 RT "Structure of the 5'-terminal untranslated region of the genomic RNAs
 from two strains of alfalfa mosaic virus.";
 RL Nucleic Acids Res. 11:2815-2826(1983).
 DR EMBL: M36391; AAA46293.1; -.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1679 MW; ABC0F9A7F3D06EB CRC64;
 Query Match 23.1%; Score 24; DB 12; Length 16;
 Best Local Similarity 50.0%; Pred. No. 3.3e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Oy 8 NTRYNOKENG 17
 Db 3 NTRYNOKENG 12
 RESULT 11
 ID P83010 PRELIMINARY; PRT; 13 AA.
 AC P83010;
 DT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Phospholemman (FYXD domain-containing ion transport regulator 1)
 DE (Fragment).
 OS Triakis scyllium (Leopard shark) (Triakis scyllia).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes; Triakidae;
 OC Triakis.
 OX NCBI_TaxID=30494;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=RECTAL GLAND;
 RA Schuurmans Stekhoven F.M.A.H., Plik G., Wendelaar Bonga S.E.;
 RT "Phospholemman in the rectal gland of sharks.";
 RL Submitted (JUN-2001) to the SWISS-PROT data bank.
 CC -1- FUNCTION: INDUCES A HYPERPOLARIZATION-ACTIVATED CHLORIDE CURRENT
 WHEN EXPRESSED IN XENOPUS OOCYTES. MAY HAVE A FUNCTIONAL ROLE IN
 MUSCLE CONTRACTION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. MICROSOMAL
 CC MEMBRANE.
 CC -1- PTM: MAJOR PLASMA MEMBRANE SUBSTRATE FOR CAMP-DEPENDENT PROTEIN
 KINASE (PK-A) AND PROTEIN KINASE C (PK-C) IN SEVERAL DIFFERENT
 CC TISSUES. PHOSPHORYLATED IN RESPONSE TO INSULIN AND ADRENERGIC
 CC STIMULATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FYXD FAMILY.
 DR InterPro: IPR000272; AtP1G1_PLM_MAT8.
 DR PROSITE: PS01310; FYXD; PARTIAL.
 KW Transmembrane; Phosphorylation; Ionic channel; Ion transport;
 KW Microsome.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1497 MW; ID140C92C1AE1444 CRC64;
 Query Match 22.1%; Score 23; DB 13; Length 13;
 Best Local Similarity 33.3%; Pred. No. 3.7e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 4 PGNNGNTKYN 12
 Db 4 PANNEDREN 12
 RESULT 12
 ID P83069 PRELIMINARY; PRT; 15 AA.
 AC P83069;
 DT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
 OS Bacillus cereus.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE, AND INDUCTION.
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (JUL-2003) to the SWISS-PROT data bank.
 CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE - DIHYDROXY-
 CC ACETONE PHOSPHATE.
 CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- INDUCTION: BY SALT STRESS AND HEAT SHOCK.
 CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
 DR InterPro: IPR000652; Triophos_Isomase.
 DR Pfam: PF00121; TIM; 1.
 DR PROSITE: PS00171; TIM; PARTIAL.
 KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
 KW Pentose shunt; Heat shock.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1712 MW; 3AFC432EDBCA2171 CRC64;
 Query Match 22.1%; Score 23; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 4.4e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 7 GNTKYNQ 13
 Db 8 GNXXMK 14
 RESULT 13
 ID 005463 PRELIMINARY; PRT; 15 AA.
 AC 005463;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Ammonia monooxygenase subunit Amoc1 (Fragment).
 GN AMOC1.
 OS Nitrosospira multiformis.
 OC Bacteria; Proteobacteria; beta subdivision;
 OC Ammonia-oxidizing bacteria; Nitrosospira.
 OX NCBI_TaxID=1231;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC25196;
 RA Norton J.M., Alizerrecia J., Klotz M.G.;
 RT "The ammonia monooxygenase operon in Nitrosolobus multiformis.";
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U91603; AAB51758.1; -.
 KW Monooxygenase.
 FT NON_TER 1 1
 SQ SEQUENCE 15 AA; 1774 MW; 030B7989F1284A67 CRC64;
 Query Match 22.1%; Score 23; DB 2; Length 15;
 Best Local Similarity 28.6%; Pred. No. 4.4e+03;
 Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 Oy 2 TYPGNGNTKYNQ 15
 Db 2 VIPNNRIVPYDKAF 15
 RESULT 14
 ID Q9S8V6 PRELIMINARY; PRT; 15 AA.
 AC Q9S8V6;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
 DE High-molecular-weight glutelin subunit (Fragment).
 OS Triticum aestivum (Wheat).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Trilicaceae; Trilicum.
 OX NCBI_TaxID=4565;

RN [1]
 RP SEQUENCE
 RX MEDLINE=93003354; Pubmed=1390908;
 RA Tao H.P.; Adalsteins A.E.; Kasarda D.D.;
 RT "Intermolecular disulfide bonds link specific high-molecular-weight
 RT glutenin subunits in wheat endosperm";
 RL Biochim. Biophys. Acta 1159:13-21(1992).
 SQ SEQUENCE 15 AA; 1649 MW; 29DBF77EB5A51F0D CRC64;

Query Match 22.1%; Score 23; DB 10; Length 15;
 Best Local Similarity 50.0%; Pred. No. 4.4e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 PGNGNTKY 11
 11111
 DB 2 PGCGQGGY 9

RESULT 15

ID P82433 PRELIMINARY; PRT; 14 AA.
 AC P82433;
 DT 01-JUN-2000 (TReMBLrel. 14, Created)
 DT 01-JUN-2000 (TReMBLrel. 14, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE 32 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE
 RC STRAIN=CV, PETIT HAVANA;
 RA Blee K.A.; Bonham V.A.; Mitchell G.P.; Robertson D.; Slabas A.R.;
 RA Wojtaszek P.; Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture";
 RL Planta 0:0-0(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL.
 CC -1- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1446 MW; FE5C7B9C0D5436A CRC64;

Query Match 21.6%; Score 22.5; DB 10; Length 14;
 Best Local Similarity 75.0%; Pred. No. 4.9e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 2 IYPG-NGN 8
 111111
 DB 5 IYXGQNGN 12

Search completed: February 25, 2003, 11:40:41
 Job time : 94 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:30:51 : Search time 30 seconds
(without alignments)
9.808 Million cell updates/sec

Title: US-09-743-482a-8
Perfect score: 59
Sequence: 1 GYFTSYDMH 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 77191

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/CTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	55.9	10	1	US-08-208-886C-87
2	33	55.9	10	1	US-08-704-744-89
3	33	55.9	10	1	US-08-469-557-68
4	33	55.9	10	2	US-08-290-793B-68
5	32	54.2	7	4	US-09-257-069-5
6	32	54.2	10	1	US-08-285-936-51
7	32	54.2	10	1	US-08-487-860-51
8	30	50.8	9	1	US-07-841-997A-39
9	30	50.8	9	1	US-08-290-301-39
10	30	50.8	9	4	US-09-013-598-39
11	29	49.2	10	1	US-08-208-886C-86
12	29	49.2	10	1	US-08-704-744-88
13	29	49.2	10	1	US-08-469-557-67
14	29	49.2	10	2	US-08-290-793B-67
15	29	49.2	10	3	US-08-974-899-10
16	28	47.5	8	1	US-08-487-860-61
17	27	45.8	6	4	US-09-556-605-52
18	27	45.8	7	4	US-09-556-605-51
19	27	45.8	8	4	US-09-556-605-50
20	27	45.8	8	5	PCT-US95-03236-8
21	27	45.8	9	4	US-08-704-170-29
22	27	45.8	9	4	US-09-556-605-49
23	27	45.8	9	5	PCT-US94-02631-29
24	27	45.8	10	1	US-08-208-886C-83
25	27	45.8	10	1	US-08-704-744-85
26	27	45.8	10	1	US-08-469-557-64
27	27	45.8	10	2	US-08-290-793B-64

28	27	45.8	10	4	US-09-556-605-48	Sequence 48, Appl
29	26	44.1	8	2	US-08-902-623-3	Sequence 3, Appl1
30	26	44.1	10	2	US-08-637-759B-417	Sequence 417, App
31	26	44.1	10	3	US-08-871-355A-417	Sequence 417, App
32	26	44.1	10	4	US-09-201-945-417	Sequence 417, App
33	25	42.4	7	5	PCT-US95-03236-54	Sequence 54, Appl
34	25	42.4	8	1	US-08-704-170-69	Sequence 69, Appl
35	25	42.4	8	1	US-08-285-936-50	Sequence 50, Appl
36	25	42.4	8	1	US-08-487-860-50	Sequence 50, Appl
37	25	42.4	8	1	PCT-US94-02631-69	Sequence 69, Appl
38	25	42.4	8	5	PCT-US95-03236-19	Sequence 19, Appl
39	25	42.4	9	4	US-09-644-600-24	Sequence 24, Appl
40	25	42.4	9	4	US-09-644-600-70	Sequence 70, Appl
41	24	40.7	8	1	US-08-310-429A-15	Sequence 15, Appl
42	24	40.7	8	2	US-08-690-734A-14	Sequence 14, Appl
43	24	40.7	8	3	US-08-742-185-14	Sequence 14, Appl
44	24	40.7	9	2	PCT-US95-03236-18	Sequence 18, Appl
45	24	40.7	9	2	US-08-672-345C-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-08-208-886C-87
; Sequence 87, Application US/08208886C
; Patent No. 5597710
; GENERAL INFORMATION:
; APPLICANT: Daille, Barbara
; APPLICANT: Muller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208, 886C
; FILING DATE: March 10, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908 298 2987
; TELEFAX: 908 298 5388
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-208-886C-87
Query Match 55.9% Score 33; DB 1; Length 10;
Best Local Similarity 66.7% Pred. No. 6.1;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYFTSYDM 9


```

:
: APPLICANT: Le, Hung
: APPLICANT: Miller, Kenneth
: APPLICANT: Murgolo, Nicholas
: APPLICANT: Nguyen, Hanh
: APPLICANT: Tindall, Stephen
: APPLICANT: Zavodny, Paul
: TITLE OF INVENTION: Cloning and Expression of
: TITLE OF INVENTION: Humanized Monoclonal Antibodies
: TITLE OF INVENTION: Against Human Interleukin-4
: NUMBER OF SEQUENCES: 69
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Schering-Plough Corporation
: STREET: 2000 Galloping Hill Road
: CITY: Kenilworth
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07033-0530
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Macintosh 6.0.5
: SOFTWARE: Microsoft Word 5.1A
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/290,793B
: FILING DATE: August 16, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/01301
: FILING DATE: 19-FEB-1992
: APPLICATION NUMBER: US 07/841,659
: FILING DATE: 19-FEB-1992
: APPLICATION NUMBER: US 07/782,784
: FILING DATE: 24-OCT-1991
: APPLICATION NUMBER: US 07/499,327
: FILING DATE: 21-MAY-1990
: APPLICATION NUMBER: PCT/US88/03631
: FILING DATE: 21-OCT-1988
: APPLICATION NUMBER: US 07/655,966
: FILING DATE: 14-FEB-1991
: APPLICATION NUMBER: US 07/113,623
: FILING DATE: 26-OCT-1987
: APPLICATION NUMBER: US 06/881,553
: FILING DATE: 03-JUL-1986
: APPLICATION NUMBER: US 06/843,958
: FILING DATE: 25-MAR-1986
: APPLICATION NUMBER: US 06/799,668
: FILING DATE: 19-NOV-1985
: ATTORNEY/AGENT INFORMATION:
: NAME: Foulke, Cynthia L.
: REGISTRATION NUMBER: 32,364
: REFERENCE/DOCKET NUMBER: 2409K7
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 908-298-5388
: TELEFAX: 908-298-2987
: INFORMATION FOR SEQ ID NO: 68:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-08-290-793B-68
:
: Query Match 55.9%; Score 33; DB 2; Length 10;
: Best Local Similarity 66.7%; Pred. No. 6.1;
: Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
:
: QY 1 GYFTSYDM 9
: 1:1:1:1:1
: DB 1 GYFTSYDM 9
:
: RESULT 5
: US-09-257-069-5
: Sequence 5, Application US/09257069
:
:
: Patent No. 6348580
: GENERAL INFORMATION:
: APPLICANT: Medical & Biological Laboratories Co., Ltd.
: TITLE OF INVENTION: Monoclonal Antibody Specific for
: FILE REFERENCE: M3-008-US
: CURRENT APPLICATION NUMBER: US/09/257,069
: PRIOR FILING DATE: 1999-02-24
: PRIOR APPLICATION NUMBER: JP 1998-252921
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 5
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Mus musculus
:
: US-09-257-069-5
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: Query Match 54.2%; Score 32; DB 4; Length 7;
: Best Local Similarity 71.4%; Pred. No. 1.9e+05;
: Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
:
: QY 1 GYFTSY 7
: 1:1:1:1
: DB 1 GYFTSY 7
:
: RESULT 6
: US-08-285-936-51
: Sequence 51, Application US/08285936
: Patent No. 5728821
: GENERAL INFORMATION:
: APPLICANT: Yelton, Dale
: APPLICANT: Glaser, Scott
: APPLICANT: Huse, William
: APPLICANT: Rosok, Mae J.
: TITLE OF INVENTION: No. 5728821e1 Mutant BR96 Antibodies and
: TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merchant & Gould
: STREET: 11150 Santa Monica Blvd., Suite 400
: CITY: Los Angeles
: STATE: CA
: COUNTRY: USA
: ZIP: 90025-3395
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/285,936
: FILING DATE: 04-AUG-1994
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Adriano, Sarah B.
: REGISTRATION NUMBER: 34,470
: REFERENCE/DOCKET NUMBER: 30436.160S01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 310-445-1140
: TELEFAX: 310-445-9031
: INFORMATION FOR SEQ ID NO: 51:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: MOLECULE TYPE: peptide
: TOPOLOGY: linear
:
: US-08-285-936-51
:
: Query Match 54.2%; Score 32; DB 1; Length 10;
: Best Local Similarity 50.0%; Pred. No. 9;
: Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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OY 1 GYFTSYDMH 10
 I:11:11:
 DB 1 GFTFSYDMH 10

RESULT 7

US-08-487-860-51
 ; Sequence 51, Application US/08487860
 ; Patent No. 5792456
 ; GENERAL INFORMATION:
 ; APPLICANT: Yelton, Dale
 ; APPLICANT: Glaser, Scott
 ; APPLICANT: Huse, William
 ; APPLICANT: Rosok, Mae J.
 ; TITLE OF INVENTION: No. 5792456el Mutant BR96 Antibodies and
 ; TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas
 ; NUMBER OF SEQUENCES: 62
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant & Gould
 ; STREET: 11150 Santa Monica Blvd., Suite 400
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90025-3395
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,860
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Adriano, Sarah B.
 ; REGISTRATION NUMBER: 34,470
 ; REFERENCE/DOCKET NUMBER: 30436.16US01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 310-445-1140
 ; TELEFAX: 310-445-9031
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-487-860-51

Query Match 54.2%; Score 32; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 9;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
 I:11:11:
 DB 1 GFTFSYDMH 10

RESULT 8

US-07-841-997A-39
 ; Sequence 39, Application US/07841997A
 ; Patent No. 5422254
 ; GENERAL INFORMATION:
 ; APPLICANT: Lonesborough, John
 ; APPLICANT: Vuorio, Outi
 ; TITLE OF INVENTION: A method to increase the trehalose content
 ; TITLE OF INVENTION: of organisms by transforming them with the
 ; TITLE OF INVENTION: structural genes for the short and long chains
 ; TITLE OF INVENTION: yeast trehalose synthase.
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Alko Ltd.
 ; STREET: PO Box 350

CITY: Helsinki
 STATE: Finland
 COUNTRY: Finland
 ZIP: SF-00101

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
 COMPUTER: IBM PC/XT/AT
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WP5.1 file exported as DOS text file
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/841,997A
 FILING DATE: 19920228
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/836,021
 FILING DATE: February 14, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Mary E. Gormley
 REGISTRATION NUMBER: 34409
 REFERENCE/DOCKET NUMBER: 920085A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)659-2930
 TELEFAX: (202)887-0357
 TELEX: 440142
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 HYPOTHEICAL: NO
 FRAGMENT TYPE: N-terminal
 US-07-841-997A-39

Query Match 50.8%; Score 30; DB 1; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.9e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 TFTSYD 8
 I:11:11:
 DB 1 TFTSYD 6

RESULT 9

US-08-290-301-39
 ; Sequence 39, Application US/08290301
 ; Patent No. 5792921
 ; GENERAL INFORMATION:
 ; APPLICANT: Lonesborough, John
 ; APPLICANT: Tunnele, Outi
 ; APPLICANT: Palva, Tupio
 ; APPLICANT: Holmstrom, Kjell-Ove
 ; APPLICANT: Melin, Bjorn
 ; TITLE OF INVENTION: Increasing the trehalose content
 ; TITLE OF INVENTION: of organisms by transforming them with combinations of
 ; TITLE OF INVENTION: the structural genes for trehalose synthase.
 ; NUMBER OF SEQUENCES: 85
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Alko Ltd.
 ; STREET: PO Box 350
 ; CITY: Helsinki
 ; STATE: Finland
 ; COUNTRY: Finland
 ; ZIP: SF-00101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
 ; COMPUTER: IBM PC/XT/AT
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WP5.1 file exported as DOS text file
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/290,301
 ; FILING DATE: 15 August 1994

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FI 943133
FILING DATE: 29 June 1994
APPLICATION NUMBER: PCT/FI93/00049
FILING DATE: 15 February 1993
APPLICATION NUMBER: 07/841,997
FILING DATE: 28 February 1992
APPLICATION NUMBER: 07/836,021
FILING DATE: 14 February 1992
ATTORNEY/AGENT INFORMATION:
NAME: Kubovcik, Ronald J.
NAME: Lydon, James C.
REGISTRATION NUMBER: 25,401
REFERENCE/DOCKET NUMBER: 30,082
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 467-6300
TELEFAX: (202) 466-2006
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-290-301-39

Query Match 50.8%; Score 30; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 TFTSYD 8
111:11
DB 1 TFTNYD 6

RESULT 10
US-09-013-598-39
Sequence 39, Application US/09013598
Patent No. 6323001
GENERAL INFORMATION:
APPLICANT: Lonsborough, John
APPLICANT: Tunela, Outi
APPLICANT: Palva, Tupio
APPLICANT: Holmstrom, Kjell-Ove
APPLICANT: Welin, Bjorn
TITLE OF INVENTION: Increasing the trehalose content
TITLE OF INVENTION: of organisms by transforming them with combinations of
TITLE OF INVENTION: the structural genes for trehalose synthase.
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alko Ltd.
STREET: PO Box 350
CITY: Helsinki
STATE: Finland
COUNTRY: Finland
ZIP: SF-00101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: PC-DOS
SOFTWARE: WP5.1 file exported as DOS text file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,598
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,301
FILING DATE:
APPLICATION NUMBER: PCT/FI93/00049

FILING DATE: 15 February 1993
APPLICATION NUMBER: 07/841,997
FILING DATE: 28 February 1992
APPLICATION NUMBER: 07/836,021
FILING DATE: 14 February 1992
ATTORNEY/AGENT INFORMATION:
NAME: Kubovcik, Ronald J.
NAME: Lydon, James C.
REGISTRATION NUMBER: 25,401
REFERENCE/DOCKET NUMBER: 30,082
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 467-6300
TELEFAX: (202) 466-2006
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-09-013-598-39

Query Match 50.8%; Score 30; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 TFTSYD 8
111:11
DB 1 TFTNYD 6

RESULT 11
US-08-208-886C-86
Sequence 86, Application US/0820886C
Patent No. 5597710
GENERAL INFORMATION:
APPLICANT: Dalie, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,886C
FILING DATE: March 10, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298 2987
TELEFAX: 908 298 5388
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-208-886C-86

Query Match 49.2% Score 29; DB 1; Length 10;
Best Local Similarity 55.6% Pred. No. 29;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYFTSYDM 9
1:1111
DB 1 GFSRYSYM 9

RESULT 12
US-08-704-744-88
Sequence 88, Application US/08704744
Patent No. 5705154

GENERAL INFORMATION:
APPLICANT: Daille, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,744
FILING DATE: 06-SEPT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208886
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: PCT/US/95/02400
FILING DATE: 08-MAR-1995

ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2987
TELEFAX: (908) 298-5388

TELEX:
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-744-88

Query Match 49.2% Score 29; DB 1; Length 10;
Best Local Similarity 55.6% Pred. No. 29;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYFTSYDM 9
1:1111
DB 1 GFSRYSYM 9

RESULT 13
US-08-469-557-67

Sequence 67, Application US/08469557
Patent No. 5770403

GENERAL INFORMATION:
APPLICANT: Daille, Barbara
APPLICANT: Le, Hung
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Nguyen, Hanh
APPLICANT: Tindall, Stephen
APPLICANT: Zavodny, Paul
TITLE OF INVENTION: Cloning and Expression of
Humanized Monoclonal Antibodies
TITLE OF INVENTION: Against Human Interleukin-4
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,557
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,793
FILING DATE: August 16, 1994
APPLICATION NUMBER: PCT/US93/01301
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/841,659
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/782,784
FILING DATE: 24-OCT-1991
APPLICATION NUMBER: US 07/499,327
FILING DATE: 21-MAY-1990

APPLICATION NUMBER: PCT/US88/03631
FILING DATE: 21-OCT-1988
APPLICATION NUMBER: US 07/655,966
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: US 07/113,623
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: US 06/881,553
FILING DATE: 03-JUL-1986
APPLICATION NUMBER: US 06/843,958
FILING DATE: 25-MAR-1986
APPLICATION NUMBER: US 06/799,668
FILING DATE: 19-NOV-1985
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: 2409K7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298-2987
TELEFAX: 908-298-5388

INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-557-67

Query Match 49.2% Score 29; DB 1; Length 10;
Best Local Similarity 55.6% Pred. No. 29;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYFTSYDM 9

Db 1 GFSFRSYAM 9

RESULT 14

US-08-290-793B-67

Sequence 67, Application US/08290793B

Patent No. 5863537

GENERAL INFORMATION:

APPLICANT: Dille, Barbara

APPLICANT: le, Hung

APPLICANT: Miller, Kenneth

APPLICANT: Murgolo, Nicholas

APPLICANT: Nguyen, Hanh

APPLICANT: Tindall, Stephen

APPLICANT: Zavadny, Paul

TITLE OF INVENTION: Cloning and Expression of

TITLE OF INVENTION: Humanized Monoclonal Antibodies

TITLE OF INVENTION: Against Human Interleukin-4

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schering-Plough Corporation

STREET: 2000 Galloping Hill Road

CITY: Kenilworth

STATE: New Jersey

COUNTRY: USA

ZIP: 07033-0530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 6.0.5

SOFTWARE: Microsoft Word 5.1A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,793B

FILING DATE: August 16, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/01301

FILING DATE: 19-FEB-1992

APPLICATION NUMBER: US 07/841,659

FILING DATE: 19-FEB-1992

APPLICATION NUMBER: US 07/782,784

FILING DATE: 24-OCT-1991

APPLICATION NUMBER: US 07/99,327

FILING DATE: 21-MAY-1990

APPLICATION NUMBER: PCT/US88/03631

FILING DATE: 21-OCT-1988

APPLICATION NUMBER: US 07/655,966

FILING DATE: 14-FEB-1991

APPLICATION NUMBER: US 07/113,623

FILING DATE: 26-OCT-1987

APPLICATION NUMBER: US 06/881,553

FILING DATE: 03-JUL-1986

APPLICATION NUMBER: US 06/843,958

FILING DATE: 25-MAR-1986

APPLICATION NUMBER: US 06/799,668

FILING DATE: 19-NOV-1985

ATTORNEY/AGENT INFORMATION:

NAME: Foulke, Cynthia L.

REGISTRATION NUMBER: 32,364

REFERENCE/DOCKET NUMBER: 2409K7

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908 298-2987

TELEFAX: 908-298-5388

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-290-793B-67

Query Match

Best Local Similarity 49.2%; Score 29; DB 2; Length 10;
55.6%; Pred. No. 29;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYFTSYDM 9

Db 1 GFSFRSYAM 9

RESULT 15

US-08-974-899-10

Sequence 10, Application US/08974899

Patent No. 6037454

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.

APPLICANT: Jardieu, Paula M.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,899

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/031971

FILING DATE: 11/27/96

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P1014R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/952-9881

TELEFAX: 650/225-1994

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-974-899-10

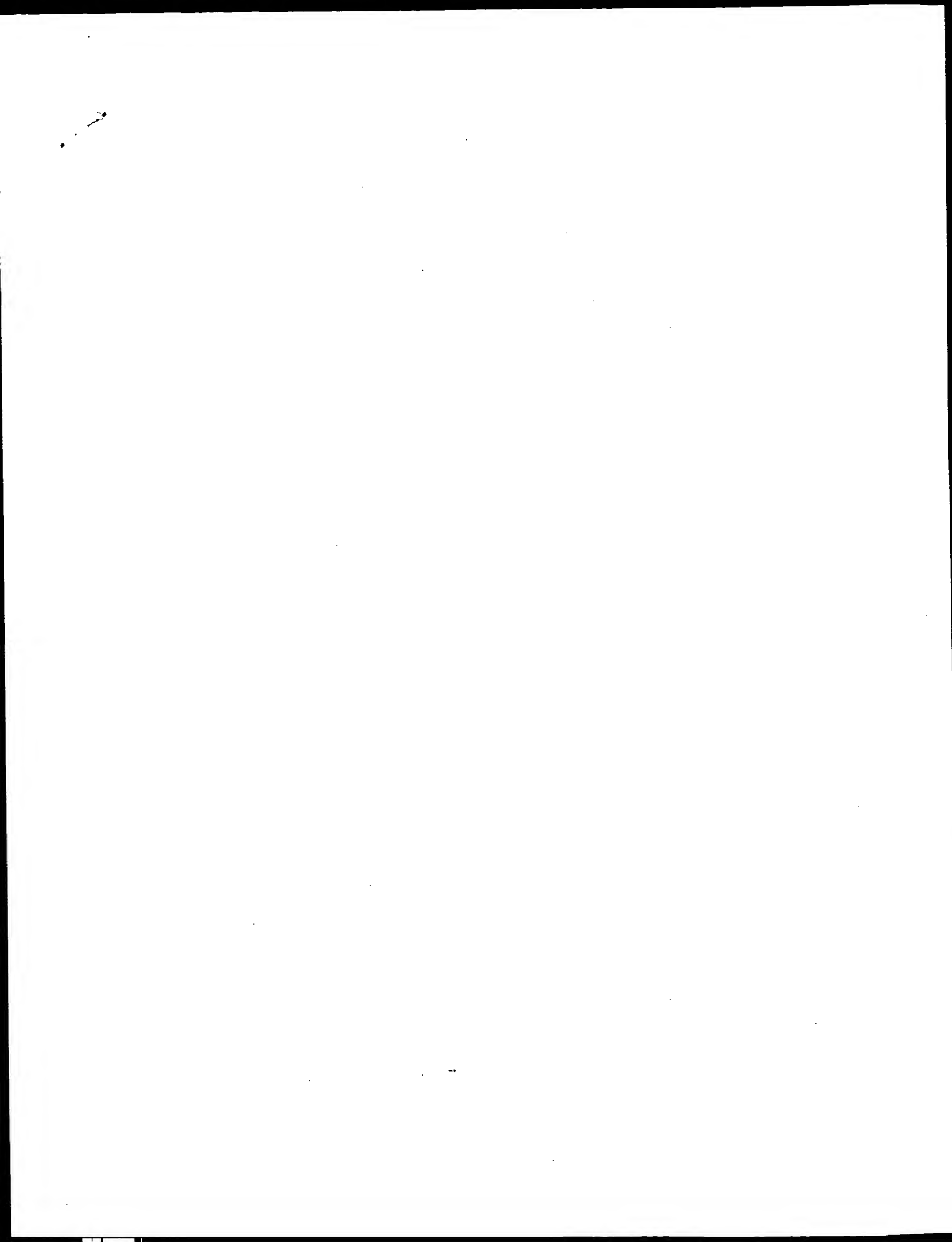
Query Match

Best Local Similarity 49.2%; Score 29; DB 3; Length 10;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYFTSYDM 10

Db 1 GYFTGHWMN 10

Search completed: February 25, 2003, 11:34:37
Job time: 31 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:37:31 ; Search time 14 Seconds
(without alignments)
116.735 Million cell updates/sec

Title: US-09-743-482a-10

Perfect score: 104

Sequence: 1 WYPCNGNTRKYNQKENG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 2988

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:***
2: PIR1:***
3: PIR2:***
4: PIR3:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	35	33.7	16	2	B45895	T-cell surface gly
2	31	29.8	17	2	S03533	Ig heavy chain J r
3	29	27.9	14	2	PH1322	Ig heavy chain DJ
4	29	27.9	15	2	B60763	endo-1,3-beta-gluc
5	26	25.0	15	2	PT0091	H+-transporting tw
6	25.5	24.5	17	2	PD0005	very-high-density
7	25	24.0	12	1	JTJG0	tremorogen A-10 -
8	25	24.0	12	2	PH1324	Ig heavy chain DJ
9	25	24.0	16	2	A49255	T-cell receptor be
10	24	23.1	9	2	S59802	glutathione transf
11	24	23.1	15	2	PH0808	T-cell receptor al
12	24	23.1	16	2	PH0763	T-cell receptor be
13	24	23.1	17	2	A27486	follicitropin inhibi
14	24	23.1	17	2	PH0809	T-cell receptor al
15	23	22.1	9	2	JP0073	ribosomal protein
16	23	22.1	10	2	PT0289	Ig heavy chain CRD
17	23	22.1	13	2	PC1149	equinatoxin 1A - s
18	23	22.1	13	2	S47362	T-cell antigen rec
19	23	22.1	13	2	PH0796	T-cell receptor al
20	23	22.1	14	2	S29486	GTP-binding protei
21	23	22.1	14	2	PH0135	T-cell receptor be
22	23	22.1	15	2	S47387	T-cell antigen rec
23	23	22.1	16	2	A42291	tail fiber protein
24	23	22.1	16	2	G24304	ribosomal protein
25	22	21.2	11	2	PT0218	T-cell receptor be
26	22	21.2	12	2	S10624	lipovitellin - Afr
27	22	21.2	12	2	PH1463	T-cell receptor be
28	22	21.2	12	2	PH1464	T-cell receptor be
29	22	21.2	12	2	PH1468	T-cell receptor be

30	22	21.2	13	2	JQ2309	hypothetical 1.6k
31	22	21.2	13	2	JQ2319	hypothetical 1.6k
32	22	21.2	13	2	PT0263	Ig heavy chain CRD
33	22	21.2	16	2	A49226	major outer membra
34	22	21.2	16	2	A61530	uridine-phosphate I
35	22	21.2	11	2	S68649	spermadhesin AQN-3
36	21	20.2	11	2	A33571	follicitropin - bovi
37	21	20.2	13	2	A46463	preabsorbing anti
38	21	20.2	14	2	S58862	botulinum neurotox
39	21	20.2	14	2	S58866	botulinum neurotox
40	21	20.2	15	2	S36889	ribosomal protein
41	21	20.2	15	2	PH0784	T-cell receptor al
42	21	20.2	16	2	PH0773	T-cell receptor be
43	21	20.2	17	2	PS0454	38k protein 3129 -
44	21	20.2	17	2	A61019	17k basolateral pl
45	20.5	19.7	10	1	RHA02	gonadotberin II -

ALIGNMENTS

RESULT 1

B45895
T-cell surface glycoprotein CD28 short form - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Feb-1994
C:Accession: B45895
R:Lee, K.P.; Taylor, C.; Petryniak, B.; Turka, L.A.; June, C.H.; Thompson, C.B.
J. Immunol. 145, 344-352, 1990
A:Title: The genomic organization of the CD28 gene. Implications for the regulation
A:Reference number: A45895; MUID:90293482; PMID:2162892
A:Accession: B45895
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <LEP>
A:Cross-References: GB:M37813
C:Keywords: glycoprotein

Query Match

Best Local Similarity 60.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 NTKYNQKENG 17

DB 3 NLSYNEKENG 12

RESULT 2

S03533
Ig heavy chain J region (JH-6) - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 21-Jul-2000
C:Accession: S03533
R:Schwager, J.; Grossberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian X

A:Reference number: S01558; MUID:89052653; PMID:2903824

A:Accession: S03533

A:Molecule type: DNA

A:Residues: 1-17 <SCH>

A:Cross-References: EMBL:X14918; NID:964805; PIDN:CA43045.1; PID:g1334659

Query Match

Best Local Similarity 29.8%; Score 31; DB 2; Length 17;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYPCNGN 8

DB 4 WDYGQGN 11

RESULT 3

PH1322

Ig heavy chain DJ region (clone C344-99) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PH1322
 R:Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A:Reference number: PH1302; MUID:93094761; PMID:1460419
 A:Accession: PH1322
 A:Molecule type: DNA
 A:Residues: 1-14 <MAS>
 C:Keywords: heterotrimer; immunoglobulin

Query Match 27.9%; Score 29; DB 2; Length 14;
 Best Local Similarity 62.5%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WIYPGNGN 8
 : | | | |
 DB 6 WDYWGCGN 13

RESULT 4
 B60763
 endo-1,3-beta-glucanase (EC 3.2.1.-), 40k - Bacillus circulans (strain WL-12) (fragment)
 C:Species: Bacillus circulans
 C>Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
 C:Accession: B60763
 R:Fiske, M.J.; Tobey-Fincher, K.L.; Fuchs, R.L.
 J. Gen. Microbiol. 136, 2377-2383, 1990
 A:Title: Cloning of two genes from Bacillus circulans WL-12 which encode 1,3-beta-glucan
 A:Reference number: A60763; MUID:91178514; PMID:2127800
 A:Accession: B60763
 A:Molecule type: protein
 A:Residues: 1-15 <FRIS>
 C:Comment: This bacillus produces up to six different 1,3-beta-glucanases for growth on
 C:Keywords: glycosidase; hydrolase

Query Match 27.9%; Score 29; DB 2; Length 15;
 Best Local Similarity 41.7%; Pred. No. 2.5e+02;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 6 NGNTKYNKQKNG 17
 : | | : | | | |
 DB 3 MNMLWMSDFENG 14

RESULT 5
 PR0091
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 03-Jun-2002
 C:Accession: PR0091
 R:Kawakami, T.; Uchida, T.; Sakai, T.; Kano, M.; Morimasa, T.; Tsugita, A.
 submitted to JFID, July 1998
 A:Description: Proteome analysis of mouse brain.
 A:Reference number: PR0091
 A:Accession: PR0091
 A:Molecule type: protein
 A:Residues: 1-15 <KAW>
 A:Experimental source: brain, striatum
 C:Keywords: hydrolase

Query Match 25.0%; Score 26; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 YPGN 6
 : | | | |
 DB 9 YPGN 12

RESULT 6

PD0005
 Very-high-density lipoprotein - sand crayfish (fragment)
 N:Alternate names: VHDL
 C:Species: Ibacus ciliatus (sand crayfish)
 C>Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999
 C:Accession: PD0005
 R:Komatsu, M.; Ando, S.
 Biosci. Biotechnol. Biochem. 62, 459-463, 1998
 A:Title: A very-high-density lipoprotein with clotting ability from hemolymph of sand
 A:Reference number: PD0005; MUID:98233268; PMID:9571775
 A:Accession: PD0005
 A:Molecule type: protein
 A:Residues: 1-17 <KOM>
 C:Comment: This protein plays an important role in the defense process of crustacea,1

Query Match 24.5%; Score 25.5; DB 2; Length 17;
 Best Local Similarity 31.2%; Pred. No. 1e+03;
 Matches 5; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

OY 2 IYPGNGNTKYNKQKNG 17
 : | | : | | : | | |
 DB 1 LQPG---LEYQYRYNG 13

RESULT 7
 JTRG0
 Tremorogen A-10 - jelly fungus (Tremella mesenterica)
 C:Species: Tremella mesenterica
 C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 07-Nov-1997
 C:Accession: A01642; A61313
 R:Sakagami, Y.; Yoshida, M.; Isogai, A.; Suzuki, A.
 Science 212, 1525-1527, 1981
 A:Title: Peptide sex hormones inducing conjugation tube formation in compatible mating
 A:Reference number: A94256
 A:Accession: A01642
 A:Molecule type: protein
 A:Residues: 1-12 <SAKI>
 A:Note: the farnesyl may instead be (2E,6E,10Z)-12-hydroxyfarnesyl
 R:Sakagami, Y.; Isogai, A.; Suzuki, A.; Tamura, S.; Tsuchiya, E.; Fukui, S.
 Agric. Biol. Chem. 42, 1301-1302, 1978
 A:Title: Amino acid sequence of tremorogen A-10, a peptidic hormone, inducing conjug
 A:Reference number: A61313
 A:Accession: A61313
 A:Molecule type: protein
 A:Residues: 1-12 <SAK2>
 C:Comment: Tremorogen A-10 is produced by the A mating-type cells and induces formati
 C:Superfamily: tremorogen a-13
 C:Keywords: extracellular protein; hormone; lipoprotein; methylated carboxyl end; phe
 F:12/Binding site: Farnesyl (Cys) (covalent) #status experimental
 F:12/Modified site: methyl ester carboxyl end (Cys) #status experimental

Query Match 24.0%; Score 25; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PGNG 7
 : | | | |
 DB 7 PGNG 10

RESULT 8
 PH1324
 Ig heavy chain DJ region (clone C510-100) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PH1324
 R:Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A:Title: Predominance of fetal type DJH joining in young children with B precursor ly
 A:Reference number: PH1302; MUID:93094761; PMID:1460419
 A:Accession: PH1324
 A:Molecule type: DNA
 A:Residues: 1-12 <MAS>

C:Keywords: heterotetramer; immunoglobulin

Query Match

24.0%; Score 25; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIYPGNG 7
| | | | |
Db 5 WYWMGOG 11

RESULT 9

T-cell receptor beta chain V-D-J-C region (V beta 7, J beta 1.6) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: A49255

R:Rosenberg, W.M.; Moss, P.A.; Bell, J.I.

A:Title: Variation in human T cell

A:Reference number: A49039; MUID:92164737; PMID:1311263

A:Accession: A49255

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-16 <ROS>

A:Note: sequence extracted from NCBI backbone (NCBIP:90722)

C:Keywords: T-cell receptor

Query Match

24.0%; Score 25; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YPGNGNT 9
| | | | |
Db 5 YPGTQNS 11

RESULT 10

glutathione transferase (EC 2.5.1.18) P - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S59902

R:Nishihira, J.; Hibiya, Y.; Sakai, M.; Nishl, S.; Kumazaki, T.; Ohki, S.; Sakamoto, W.

A:Title: The C-terminal region, Arg(201)-Gln(209), of glutathione transferase P contrib

A:Reference number: S59902; MUID:96049505; PMID:7578228

A:Accession: S59902

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <NIS>

C:Superfamily: glutathione transferase

C:Keywords: transferase

Query Match

23.1%; Score 24; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PGNGNFK 10
| | | | |
Db 2 PINGNCK 8

RESULT 11

PH0808

T-cell receptor alpha chain (C7) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0808

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0808

A:Molecule type: mRNA

A:Residues: 1-15 <CAS>

A:Cross-references: EMBL:X60918

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match

23.1%; Score 24; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YPGNGN 8
| | | | |
Db 5 YGSGGN 10

RESULT 12

T-cell receptor beta chain (F15) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0763

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0763

A:Molecule type: mRNA

A:Residues: 1-16 <CAS>

A:Cross-references: EMBL:X60857; NID:950933; PIDN:CAA43247.1; PID:950934

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match

23.1%; Score 24; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GNNTKY 11
| | | | |
Db 8 GNODTGY 14

RESULT 13

foliitropin inhibitor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 18-Jun-1993
C:Accession: A27486

R:Robertson, D.M.; Klein, R.; de Vos, F.L.; McLachlan, R.I.; Wettenhall, R.E.H.; Hear

A:Title: The isolation of polypeptides with FSH suppressing activity from bovine foli

A:Reference number: A27486; MUID:88106500; PMID:3122741

A:Accession: A27486

A:Molecule type: protein

A:Residues: 1-17 <ROB>

A:Note: residues 3 and 6 could not be determined with certainty; these residues could

Query Match

23.1%; Score 24; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 GNTKYNQKFG 17
| | | | |
Db 1 GNSTLRQAKNG 11

RESULT 14

PH0809

T-cell receptor alpha chain (RF3.10.3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PH0809
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-H
allelic exclusion and antigen specific repertoire
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0809
A:Molecule type: mRNA
A:Residues: 1-17 <CDS>
A:Cross-references: EMBL:X60920
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 23.1%; Score 24; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 YPGNGN 8
1 1:11
Db 7 YGSGSN 12

RESULT 15
JP0073
ribosomal protein L32 - Leuconostoc mesenteroides (fragment)
C:Species: Leuconostoc mesenteroides
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
C:Accession: JP0073
R:Oehl, K.
submitted to JIPID, February 1994
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pr
A:Reference number: JP0042
A:Accession: JP0073
A:Molecule type: protein
A:Residues: 1-9 <OCH>
C:Keywords: protein biosynthesis; ribosome

Query Match 22.1%; Score 23; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PGNNTK 10
1 1 1:1
Db 3 PSNKNSK 9

Search completed: February 25, 2003, 11:41:01
Job time : 14 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 25, 2003, 11:33:11 : Search time 11 seconds
(without alignments)

28.245 Million cell updates/sec

Title: US-09-743-482a-8

Perfect score: 59

Sequence: 1 GYFTSYDMH 10

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 25476

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEM_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCF_NEM_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEM_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/PCFUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEM_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEM_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	72.9	10	US-09-900-590-34	Sequence 34, Appl
2	42	71.2	10	US-09-056-1608-1	Sequence 1, Appl
3	41	69.5	10	US-09-900-590-52	Sequence 52, Appl
4	38	64.4	10	US-09-900-590-48	Sequence 48, Appl
5	38	64.4	10	US-09-900-590-50	Sequence 50, Appl
6	36	61.0	10	US-09-056-1608-130	Sequence 130, App
7	34	57.6	9	US-10-153-159-20	Sequence 20, Appl
8	34	57.6	9	US-10-153-176-20	Sequence 86, Appl
9	34	57.6	10	US-09-056-1608-86	Sequence 86, Appl
10	34	57.6	10	US-09-056-1608-88	Sequence 128, App
11	34	57.6	10	US-09-056-1608-128	Sequence 23, Appl
12	33	55.9	9	US-10-153-159-23	Sequence 5, Appl
13	33	55.9	9	US-10-153-176-23	Sequence 6, Appl
14	32	54.2	7	US-09-518-737-5	Sequence 19, Appl
15	32	54.2	10	US-09-924-099-6	Sequence 28, Appl
16	30	50.8	9	US-10-153-159-19	Sequence 19, Appl
17	30	50.8	9	US-10-153-159-28	Sequence 28, Appl
18	30	50.8	9	US-10-153-176-19	Sequence 28, Appl
19	30	50.8	9	US-10-153-176-28	Sequence 28, Appl

20	30	50.8	10	US-09-056-1608-90	Sequence 90, Appl
21	30	50.8	10	US-09-056-1608-91	Sequence 91, Appl
22	29	49.2	9	US-10-153-159-22	Sequence 22, Appl
23	29	49.2	9	US-10-153-159-30	Sequence 30, Appl
24	29	49.2	9	US-10-153-176-22	Sequence 22, Appl
25	29	49.2	9	US-10-153-176-30	Sequence 30, Appl
26	28	47.5	10	US-09-056-1608-87	Sequence 87, Appl
27	27	45.8	6	US-09-839-447A-52	Sequence 52, Appl
28	27	45.8	7	US-09-839-447A-51	Sequence 51, Appl
29	27	45.8	8	US-09-839-447A-50	Sequence 50, Appl
30	27	45.8	9	US-10-153-159-25	Sequence 25, Appl
31	27	45.8	9	US-10-153-176-25	Sequence 25, Appl
32	27	45.8	9	US-09-839-447A-49	Sequence 49, Appl
33	27	45.8	10	US-09-056-1608-89	Sequence 89, Appl
34	27	45.8	10	US-09-839-447A-48	Sequence 48, Appl
35	26	44.1	10	US-09-826-290-431	Sequence 431, App
36	26	44.1	10	US-09-791-389-209	Sequence 209, App
37	26	44.1	10	US-09-791-393-209	Sequence 209, App
38	26	44.1	10	US-09-791-378-487	Sequence 487, App
39	26	44.1	10	US-10-007-761-34	Sequence 34, Appl
40	26	44.1	10	US-10-007-761-37	Sequence 37, Appl
41	25	42.4	5	US-09-861-284-13	Sequence 13, Appl
42	25	42.4	9	US-10-153-159-21	Sequence 21, Appl
43	25	42.4	9	US-10-153-159-29	Sequence 29, Appl
44	25	42.4	9	US-10-153-176-21	Sequence 21, Appl
45	25	42.4	9	US-10-153-176-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1

US-09-900-590-34
Sequence 34, Application US/09900590
Publication No. US20030028009A1

GENERAL INFORMATION:
APPLICANT: Huse, William D.
Glaser, Scott M.

TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
Antibodies, Nucleic Acids Encoding Same and Methods of U

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:
ADDRESS: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego

STATE: California
COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/900,590
FILING DATE: 06-Jul-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/016,061
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

REFERENCE/DOCKET NUMBER: P-IX 2965

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-900-590-34

Query Match 72.9%; Score 43; DB 9; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.058;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTSYDM 9
1:111111
DB 1 GYFTSSYDM 9

RESULT 2
US-09-056-160B-1
Sequence 1, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:

APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Loman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9681
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-09-056-160B-1

Query Match 71.2%; Score 42; DB 10; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.087;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDM 10
11111111
DB 1 GYFTSYDM 10

RESULT 3
US-09-900-590-52
Sequence 52, Application US/0900590
Publication No. US20030028009A1
GENERAL INFORMATION:
APPLICANT: Huse, William D.
Glaser, Scott M.

TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
Antibodies, Nucleic Acids Encoding Same and Methods of U

NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentlin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/900,590
FILING DATE: 06-Jul-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/016,061
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1X 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-900-590-52

Query Match 69.5%; Score 41; DB 9; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDM 9
1:111111
DB 1 GYFTLSYDM 9

RESULT 4
US-09-900-590-48
Sequence 48, Application US/09900590
Publication No. US20030028009A1
GENERAL INFORMATION:
APPLICANT: Huse, William D.
Glaser, Scott M.

TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
Antibodies, Nucleic Acids Encoding Same and Methods of U

NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentlin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/900,590
FILING DATE: 06-Jul-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/016,061
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-900-590-48

Query Match
Best Local Similarity 64.4%; Score 38; DB 9; Length 10;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDM 9
DB 1 GTTFSYDM 9

RESULT 5
US-09-900-590-50
Sequence 50, Application US/09900590
Publication No. US20030028009A1
GENERAL INFORMATION:
APPLICANT: Huse, William D.
Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESSES:
ADDRESS: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/900,590
FILING DATE: 06-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/016,061
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-900-590-50

Query Match
Best Local Similarity 64.4%; Score 38; DB 9; Length 10;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTSYDM 9
DB 1 GTTFSYDM 9

RESULT 6
US-09-056-160B-130
Sequence 130, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-09-056-160B-130

Query Match
Best Local Similarity 61.0%; Score 36; DB 10; Length 10;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYFTSYDM 10
DB 1 GYFTSYDM 10

RESULT 7
US-10-153-159-20
Sequence 20, Application US/10153159
Patent No. US20020177170A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
APPLICANT: Hsieh, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Caili
TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY

TITLE OF INVENTION: SILICO
FILE REFERENCE: 26050-704
CURRENT APPLICATION NUMBER: US/10/153,159
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 20
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH CDR1 Variant
US-10-153-159-20

Query Match 57.6%; Score 34; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GYFTSYDM 9
DB 1 GYFTSYDM 9

RESULT 8
US-10-153-176-20
Sequence 20, Application US/10153176
Publication No. US20030022240A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
APPLICANT: Hsieh, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Calli
APPLICANT: Cao, Yicheng
APPLICANT: Li, Shengfeng
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
FILE REFERENCE: 26050-701
CURRENT APPLICATION NUMBER: US/10/153,176
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 20
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH CDR1 Variant
US-10-153-176-20

Query Match 57.6%; Score 34; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GYFTSYDM 9
DB 1 GYFTSYDM 9

RESULT 9
US-09-056-160B-86
Sequence 86, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.

APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinpatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-86

Query Match 57.6%; Score 34; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.2;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
DB 1 GYFTSYDMH 10

RESULT 10
US-09-056-160B-88
Sequence 88, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinpatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B

FILING DATE: 06-Apr-1998
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/054,856
 FILING DATE: 06-AUG-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28,616
 REFERENCE/DOCKET NUMBER: P1093R2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1896
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 88:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-056-160B-88

Query Match 57.6%; Score 34; DB 10; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.2;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GYFTSYDMH 10
 DB 1 GYFTHYGMN 10

RESULT 11
 US-09-056-160B-128
 Sequence 128, Application US/09056160B
 Patent No. US20020032315A1
 GENERAL INFORMATION:
 APPLICANT: Baca, Manuel
 APPLICANT: Wells, James A.
 APPLICANT: Presta, Leonard G.
 APPLICANT: Lowman, Henry B.
 APPLICANT: Chen, Yvonne M.
 TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
 NUMBER OF SEQUENCES: 131
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatlin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/056,160B
 FILING DATE: 06-Apr-1998
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/054,856
 FILING DATE: 06-AUG-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28,616
 REFERENCE/DOCKET NUMBER: P1093R2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1896
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 128:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-056-160B-128

Query Match 57.6%; Score 34; DB 10; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.2;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GYFTSYDMH 10
 DB 1 GYFTHYGMN 10

RESULT 12
 US-10-153-159-23
 Sequence 23, Application US/10153159
 Patent No. US20020177170A1
 GENERAL INFORMATION:
 APPLICANT: Luo, Peter
 APPLICANT: Hsieh, Mark
 APPLICANT: Zhong, Pingyu
 APPLICANT: Wang, Cailli
 TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY
 FILE REFERENCE: 26050-704
 CURRENT APPLICATION NUMBER: US/10/153,159
 CURRENT FILING DATE: 2002-05-20
 PRIOR APPLICATION NUMBER: US 10/125,687
 PRIOR FILING DATE: 2002-04-17
 PRIOR APPLICATION NUMBER: US 60/284,407
 PRIOR FILING DATE: 2001-04-17
 NUMBER OF SEQ ID NOS: 125
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 23
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: VH CDR1 variant
 US-10-153-159-23

Query Match 55.9%; Score 33; DB 9; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GYFTSYDM 9
 DB 1 GYDFTRYGM 9

RESULT 13
 US-10-153-176-23
 Sequence 23, Application US/10153176
 Publication No. US20030022240A1
 GENERAL INFORMATION:
 APPLICANT: Luo, Peter
 APPLICANT: Hsieh, Mark
 APPLICANT: Zhong, Pingyu
 APPLICANT: Wang, Cailli
 APPLICANT: Cao, Yicheng
 APPLICANT: Li, Shengfeng
 APPLICANT: Liu, Shengjiang
 TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
 FILE REFERENCE: 26050-701
 CURRENT APPLICATION NUMBER: US/10/153,176
 CURRENT FILING DATE: 2002-05-20
 PRIOR APPLICATION NUMBER: US 10/125,687
 PRIOR FILING DATE: 2002-04-17
 PRIOR APPLICATION NUMBER: US 60/284,407
 PRIOR FILING DATE: 2001-04-17
 NUMBER OF SEQ ID NOS: 125
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 23
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:

OTHER INFORMATION: VH CDRI Variant
US-10-153-176-23

Query Match 55.9%; Score 33; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0;

OY 1 GYFTTSYDM 9
1 1 1 1 1
Db 1 GYDFTRYGM 9

RESULT 14
US-09-518-737-5
; Sequence 5, Application US/09518737
; Publication No. US20030008321A1
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHIKA
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI
; APPLICANT: SAITO, NAOKI
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
; FILE REFERENCE: 1965/49618
; CURRENT APPLICATION NUMBER: US/09/518,737
; CURRENT FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 1999-250209
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-5

Query Match 54.2%; Score 32; DB 9; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.3e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0;

OY 1 GYFTTSY 7
1 1 1 1 1
Db 1 GFTFSY 7

RESULT 15
US-09-924-099-6
; Sequence 6, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-6

Query Match 54.2%; Score 32; DB 10; Length 10;
Best Local Similarity 71.4%; Pred. No. 4.9;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 GYFTTSY 7
1 1 1 1 1
Db 1 GYFTTDY 7

Search completed: February 25, 2003, 11:37:44
Job time : 12 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:22:50 ; Search time 83 seconds
(without alignments)
16.054 Million cell updates/sec

Title: us-09-743-482a-8

Perfect score: 59

Sequence: 1 GYFTSYDMH 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues 174064

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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2: /SID52/gcgdata/geneseq/emb1/AA1981.DAT:*
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22: /SID52/gcgdata/geneseq/emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/emb1/AA2002.DAT:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	10	21	AAV78322
2	45	76.3	9	21	AAAB39807
3	45	76.3	10	22	AAAB35295
4	43	72.9	10	19	AAW76007
5	43	72.9	10	22	AAAB1365
6	42	71.2	9	21	AAAB39779
7	42	71.2	10	19	AAW70611
8	42	71.2	10	23	ABP61180
9	42	71.2	10	23	AAAG80311
10	42	71.2	10	23	AAU72831

11	41	69.5	9	21	AAAB39808	Anti-hIL12 antbod
12	41	69.5	10	19	AAW76016	LM609 grafted anti
13	41	69.5	10	22	AAAB61374	Mutant VH CDR1 pep
14	40	67.8	9	21	AAAB39812	Anti-hIL12 antbod
15	39	66.1	9	21	AAAB39810	Anti-hIL12 antbod
16	38	64.4	9	21	AAAB39505	Anti-hIL-12 antbo
17	38	64.4	9	21	AAAB39513	Anti-hIL-12 antbo
18	38	64.4	9	21	AAAB39773	Anti-hIL12 antbod
19	38	64.4	9	21	AAAB39786	Anti-hIL12 antbod
20	38	64.4	9	21	AAAB39798	Anti-hIL12 antbod
21	38	64.4	9	21	AAAB39813	Anti-hIL12 antbod
22	38	64.4	9	21	AAAB39818	Anti-hIL12 antbod
23	38	64.4	10	19	AAW76015	LM609 grafted anti
24	38	64.4	10	22	AAW76014	LM609 grafted anti
25	38	64.4	10	22	AAAB1372	Mutant VH CDR1 pep
26	38	64.4	10	22	AAAB1373	Mutant VH CDR1 pep
27	37	62.7	9	21	AAAB39778	Anti-hIL12 antbod
28	37	62.7	9	21	AAAB39781	Anti-hIL12 antbod
29	37	62.7	9	21	AAAB39814	Anti-hIL12 antbod
30	36	61.0	9	21	AAAB39772	Anti-hIL12 antbod
31	36	61.0	9	21	AAAB39776	Anti-hIL12 antbod
32	36	61.0	9	21	AAAB39777	Anti-hIL12 antbod
33	36	61.0	9	21	AAAB39782	Anti-hIL12 antbod
34	36	61.0	9	21	AAAB39809	Anti-hIL12 antbod
35	36	61.0	9	21	AAAB39811	Anti-hIL12 antbod
36	36	61.0	9	21	AAAB39815	Anti-hIL12 antbod
37	36	61.0	9	21	AAAB39816	Anti-hIL12 antbod
38	36	61.0	9	21	AAAB39817	Anti-hIL12 antbod
39	36	61.0	10	19	AAW70700	Anti-VEGF antibody
40	36	61.0	10	21	AAAB10001	H. pylori 26 kDa p
41	36	61.0	10	22	AAU07457	Synthetic peptide
42	36	61.0	10	22	AAAB60402	ETB2-reactive VH
43	36	61.0	10	22	AAAB61587	Humanised Fab vers
44	36	61.0	10	23	ABP61269	Anti-VEGF antibody
45	36	61.0	10	23	AAU82523	Llama CDR1/H1 regi

ALIGNMENTS

RESULT 1
AAV78322
ID AAV78322 standard; Protein; 10 AA.
XX
AC AAV78322;
XX
DF 04-MAY-2000 (first entry)
DE
XX Anti-zeta-chain antibody 2-B-5 VH-region CDR1 protein sequence.
XX
KW Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
KW complementary determining region; CDR; autoimmunity; cytotoxic;
KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.
XX
OS Rattus norvegicus.
XX
PN WO200003016-A1.
XX
PD 20-JAN-2000.
XX
PR 09-JUL-1999; 99WO-EP04838.
XX
PR 10-JUL-1998; 98EP-0112867.
XX
PA (CONN-) CONNEX GMBH.
XX
PI Reiter C;
XX
DR WPI; 2000-160926/14.
XX
DR N-PSDB; AA288320.
XX
PF New oligonucleotide, polypeptide, antibody useful for treating

PT autoimmune disease, immune deficiencies, T-cell malignancies and
PT infectious diseases -
XX
XX
PS Claim 10; Fig 6; 79pp; English.
XX
CC The present invention describes a nucleic acid molecule (I) encoding at
CC least one complementary determining region (CDR) of a variable region of
CC an antibody which specifically interacts with the extracellular domain of
CC the human zeta-chain. The antibody whose CDR of a variable region is
CC encoded by (I), is obtained by immunising a rat with Jurkat cells and
CC subsequently with a conjugate comprising a carrier molecule and a
CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
CC anti-zeta-chain antibody is useful for the treatment and prevention of
CC autoimmune diseases, immune deficiencies, T-cell malignancies,
CC infectious diseases and the suppression of immune response preferably in
CC order to avoid graft rejection after organ transplantation, malignancies,
CC or viral infections. The antibody, and fragments of it, can be useful for
CC the enhancement or suppression of NK-cell dependent immunity or for the
CC treatment of NK-cell derived malignancies. It can also be useful for the
CC determination of zeta-chain or eta-chain expression on NK-cells,
CC T-lymphocytes or their precursors. The present sequence represents the
CC CDR1 of the V α -region of the anti-zeta-chain antibody 2-B-5, produced
CC by rats from the present invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 59; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTSYDMH 10
| | | | | | | | | |
Db 1 GYFTSYDMH 10

RESULT 2
AAB39807
ID AAB39807 standard; Peptide; 9 AA.
AC AAB39807;
XX
DT 05-FEB-2001 (first entry)
XX
DE Anti-IL12 antibody heavy chain CDR1 amino acid sequence SEQ ID 323.
XX
KW Human: neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiscclerotic; cardiac;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN WO200056772-A1.
XX
PD 28-SEP-2000.
XX
PF 24-MAR-2000; 2000MO-US07946.
XX
PR 25-MAR-1999; 99US-0126603.
XX
PA (BADI) BASF AG.
PA (GEM) GENETICS INST INC.
XX
PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakcalan Z, Laskovsky B, Sakorafas P, Friederich S, Myles A;
PI Vaidman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Hollett TL, Du Fou SL;
XX
DR WPI; 2000-638250/61.
XX
PT New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's

PT disease and multiple sclerosis -
XX
XX
PS Claim 34; Figure 2A; 377pp; English.
XX
XX
CC This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB3517-B39560 and AAB40064-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in
CC AAC1062-C61071. The antibody of the invention is a neutralising
CC antibody and has antirheumatic; antirheumatic; antiscclerotic;
CC antinflammatory; neuroprotective; antipsoriatic; antiscclerotic;
CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
CC The antibodies or antigen-binding fragments are useful in the treatment
CC of disorders associated with detrimental release of human IL-12,
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.
XX
SQ Sequence 9 AA;

Query Match 76.3%; Score 45; DB 21; Length 9;
Best Local Similarity 77.8%; Pred. No. 7.8e+05;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YTFSSYDMH 10
| | | | | | | | | |
Db 1 YTFSSYDMH 9

RESULT 3
AAB35295
ID AAB35295 standard; Peptide; 10 AA.
XX
AC AAB35295;
XX
DT 08-MAY-2001 (first entry)
XX
DE Murine PSCA antibody fragment #3.
XX
KW Prostate stem cell antigen; PSCA; human; mouse; prostate cancer;
KW diagnosis; treatment; chromosome 8q24.2.
XX
OS Mus sp.
XX
PN WO200105427-A1.
XX
PD 25-JAN-2001.
XX
PF 20-JUL-2000; 2000MO-US19967.
XX
PR 20-JUL-1999; 99US-0359326.
XX
PR 03-MAY-2000; 2000US-0564329.
XX
PA (REGC) UNIV CALIFORNIA.
PA (UROG-) UROGENESYS.
XX
PI Reiter R, Witte O, Saffran DC, Jakobovits A;
XX
DR WPI; 2001-159478/16.
XX
PT Antibodies binding to prostate stem cell antigen inhibit the growth of
PT cancer cells and are used to detect and treat prostate, pancreatic or
PT bladder cancers -
XX
XX
XX Example 21; Fig 61; 229pp; English.

CC The present invention describes a method of treating cancer associated
 CC with prostate stem cell antigen (PSCA) by administering an antibody which
 CC selectively binds to PSCA and inhibits the growth of the cancer cells.
 CC The PSCA gene is found on human chromosome 8q24.2. The invention provides
 CC the human and murine PSCA protein and coding sequences, which can be used
 CC not only in the treatment of, but also in detection and prognosis of
 CC prostate cancer.

CC Sequence 10 AA:

Query Match 76.3%; Score 45; DB 22; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.12;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDM 10
 1111111111
 Db 1 GYFTSSYMMH 10

RESULT 4

AAM76007 standard; Protein; 10 AA.

AC AAM76007;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR1 protein fragment #1.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

PN MO9833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI: 1998-437472/37.

DR N-PSDB; AAV49844.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Disclosure: Page 40; 129pp; English.

CC AAM76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.

SQ Sequence 10 AA:

Query Match 72.9%; Score 43; DB 19; Length 10;
 Best Local Similarity 77.8%; Pred. No. 0.27;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTSYDM 9
 1111111111
 Db 1 GYFTSSYDM 9

RESULT 5

AAB61365 standard; peptide; 10 AA.

AC AAB61365;

DT 03-APR-2001 (first entry)

DE LM609 VH CDR1 peptide.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

PN WO200078815-A1.

PD 28-DEC-2000.

PF 23-JUN-2000; 2000WO-US17454.

PR 24-JUN-1999; 99US-0339922.

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

PI Huse WD, Wu H;

DR WPI: 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX Claim 4; Page 39; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

SQ Sequence 10 AA:

Query Match 72.9%; Score 43; DB 22; Length 10;
 Best Local Similarity 77.8%; Pred. No. 0.27;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTSYDM 9
 1111111111
 Db 1 GYFTSSYDM 9

RESULT 6
 AAB39779 standard; Peptide; 9 AA.

XX AAB39779;
 AC 05-FEB-2001 (first entry)
 DT
 DE Anti-IL12 antibody heavy chain CDR1 amino acid sequence SEQ ID 295.
 XX
 XX Human: neutralising antibody; Interleukin-12; IL-12; antiinflammatory;
 KW complementarily determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antiproliferative; antitumour; cardiac;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 PN WO200056772-A1.
 PD 28-SEP-2000.
 XX
 XX 24-MAR-2000: 2000KO-US07946.
 PF
 XX 25-MAR-1999: 99US-0126603.
 PR
 XX (BADI) BASF AG.
 PA (GENY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakçalan Z, Labkovsky B, Sakorafas F, Friedlich S, Myles A;
 PI Veldman GM, Venturini A, Warner NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;
 XX WPI: 2000-638250/61.
 DR
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 PS
 XX Claim 34: Figure 2A: 377pp: English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarily determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAC61062-C61071. The antibody of the invention is a neutralising
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antiproliferative; antitumour;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 CC
 XX
 SQ Sequence 9 AA:
 Query Match 71.2%; Score 42; DB 21; Length 9;
 Best Local Similarity 77.8%; Pred. No. 7.8e+05;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

ID AAW70611 standard; peptide: 10 AA.
 XX
 AC AAW70611;
 XX
 XX 27-JAN-1999 (first entry)
 DT
 DE Anti-VEGF antibody heavy chain hypervariable region CDRH1.
 XX
 XX Heavy chain hypervariable region; murine; humanised antibody;
 KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
 KW VEGF-induced angiogenesis; tumour; retinal disorder;
 KW age-related macular degeneration; diabetic retinopathy;
 KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
 XX
 XX Synthetic.
 OS Mus sp.
 PN WO9845331-A2.
 PD 15-OCT-1998.
 XX
 XX 03-APR-1998: 98WO-US06604.
 PF
 XX 06-AUG-1997: 97US-0908469.
 PR 07-APR-1997: 97US-0833504.
 XX
 XX (GENY) GENENTECH INC.
 PA
 XX Baca M, Chen YM, Lowman HB, Presta LG, Wells JA;
 PI WPI: 1998-568337/48.
 DR
 XX New humanised antibody with affinity for vascular endothelial growth
 PT factor - for treatment of tumours, retinal disease and other
 PT angiogenic states, also related nucleic acid, vectors and
 PT transformed cells
 PS
 XX Claim 8: Page 79; 100pp: English.
 XX
 CC The present sequence represents a heavy chain hypervariable region of the
 CC murine anti-vascular endothelial growth factor (anti-VEGF) antibody. The
 CC sequence is used to construct the humanised anti-VEGF antibody of the
 CC invention. The humanised antibodies are used to inhibit VEGF-induced
 CC angiogenesis, particularly for treating or preventing tumours (of any
 CC type) and retinal disorders (e.g. age-related macular degeneration or
 CC diabetic retinopathy). They can also be used to treat other conditions
 CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
 CC atherosclerosis, Grave's disease, etc.
 CC
 XX
 SQ Sequence 10 AA:
 Query Match 71.2%; Score 42; DB 19; Length 10;
 Best Local Similarity 70.0%; Pred. No. 0.4;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YFTFTSYDMH 10
 :|||||
 1 FTFTSYGMH 9
 DB

RESULT 8
 AAB61180
 ID AAB61180 standard; peptide: 10 AA.
 XX
 AC AAB61180;
 XX
 XX 20-SEP-2002 (first entry)
 DT
 XX Humanised anti-VEGF antibody heavy chain variable domain, CDRH1.
 DE
 XX Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KW retinal disorder; intraocular neovascular disorder;

KW heavy chain; variable domain; CDRH1.
 XX Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 XX US2002032315-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 06-APR-1998; 98US-0056160.
 XX
 PR 06-AUG-1997; 97US-054856P.
 XX
 PA (BACA/) BACA M.
 PA (WELL/) WELLS J A.
 PA (PRES/) PRESTA L G.
 PA (LOHM/) LOWMAN H B.
 PA (CHEN/) CHEN Y M.
 XX
 PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 XX
 DR WPI; 2002-517920/55.
 XX
 PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 PT mammal, particularly for treating tumor or retinal disorders -
 XX
 PS Claim 8; Page 31; 47pp; English.
 XX
 CC The present invention relates to humanised anti-VEGF (vascular
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumour or a retinal disorder e.g. intraocular
 CC neovascular disorders. The present sequence is an exemplary heavy chain
 CC variable domain of the humanised anti-VEGF antibody of the invention.
 XX
 SQ Sequence 10 AA:
 Query Match 71.2%; Score 42; DB 23; Length 10;
 Best Local Similarity 70.0%; Pred. No. 0.4;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYTFSTYDMH 10
 1111111111
 DB 1 GYTFSTNYGMN 10
 1111111111
 RESULT 9
 AAG80311
 ID AAG80311 standard; peptide: 10 AA.
 XX
 AC AAG80311:
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Anti-human TNF-alpha CDR-H1 peptide.
 XX
 KW TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
 KW heavy chain; light chain; complementarity determining region; vasotropic;
 KW antiaerthritic; neuroprotective; prozoacide; toxic shock syndrome;
 KW rheumatoid arthritis; malaria; multiple sclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200179298-A1.
 XX
 PD 25-OCT-2001.
 XX
 PF 18-APR-2001; 2001WO-JP03308.
 XX
 PI 19-APR-2000; 2000JP-0117394.
 XX

XX
 PA (SUNR) SUNTORY LTD.
 XX
 PI Fukuda Y, Nagahira K, Nakanishi T;
 XX
 DR WPI; 2002-066345/09.
 XX
 PT Novel heavy and light-chain polypeptides of chimeric and humanised
 PT antibodies against human tumour necrosis factor alpha for
 PT low-immunogenicity treatment of TNF-related diseases such as toxic
 PT shock syndrome -
 XX
 PS Claim 1a; Page 25; 36pp; Japanese.
 XX
 CC This invention describes novel heavy chain and light chain polypeptides
 CC or their fragments of a recombinant antibody to human TNF-alpha which
 CC contain complementarity determining region (CDR) sequences. The products
 CC of the invention have vasotropic, antiaerthritic, neuroprotective and
 CC prozoacide activity. The antibodies act by neutralising TNF-alpha in
 CC vivo. The antibodies are used for producing chimeric and humanised
 CC antibodies that may be used for the treatment and prevention of TNF-alpha
 CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
 CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
 CC humans. This sequence represents the anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) heavy chain CDR1 designated CDR-H1.
 XX
 SQ Sequence 10 AA:
 Query Match 71.2%; Score 42; DB 23; Length 10;
 Best Local Similarity 70.0%; Pred. No. 0.4;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYTFSTYDMH 10
 1111111111
 DB 1 GYTFSTNYGMN 10
 1111111111
 RESULT 10
 AAU72831
 ID AAU72831 standard; Peptide: 10 AA.
 XX
 AC AAU72831:
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE Anti-NKG2D hybridoma 11B2D10 variable heavy chain CDR2.
 XX
 KW Human; NKG2D; receptor complex; cancer; infectious disease; tumour;
 KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
 KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
 KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
 KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI10;
 KW helminth; cytosolic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
 KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
 KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10XP4-3; 3B10XP4-14;
 KW P53 tetramerisation domain; 3B10XP5-2; 3B10XP5-23.
 XX
 OS Homo sapiens.
 XX
 PN WO200171005-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 26-MAR-2001; 2001WO-EP03414.
 XX
 PR 24-MAR-2000; 2000EP-0106467.
 XX
 PA (KUFE/) KUFEER P.
 XX
 PI Kufer P, Rietmueller G, Lutterbuese R, Borschert K, Kischel R;
 XX
 DR Mayer M, Hofmeister R;
 WPI; 2002-055119/07.
 XX

XX Multifunctional polypeptides comprising binding sites that specifically
 PT recognise extracellular groups of the NKG2D receptor complex and
 PT domains which function as receptors or ligands, useful for treating
 PT cancers and infectious diseases -

Example 3: Fig 16; 114pp; English.

XX The invention relates to a multifunctional polypeptide comprising a
 CC group with a binding site that specifically recognises an extracellular
 CC domain of the NKG2D receptor complex and a second domain which functions
 CC as a receptor or ligand. The polypeptide and its associated
 CC polynucleotide are used for the preparation of a pharmaceutical
 CC composition for the treatment of cancer, infections and/or autoimmune
 CC conditions. The cancer may be a tumour of the head and neck, stomach,
 CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
 CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
 CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
 CC The infectious diseases can be caused by viruses, bacteria, fungi,
 CC protozoa or helminths. The autoimmune diseases include multiple
 CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
 CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
 CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
 CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
 CC receptor and the polypeptides of the invention.

XX Sequence 10 AA:

Query Match 71.2%; Score 42; DB 23; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.4;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYFTSYDMH 10
 ID 1 GYFTSYDMH 10

RESULT 11
 AAB39808
 ID AAB39808 standard; Peptide; 9 AA.

XX AAB39808;
 DT 05-FEB-2001 (first entry)

DE Anti-IL12 antibody heavy chain CDR1 amino acid sequence SEQ ID 324.

XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neutroprotective; antipsoriatic; antilasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.

XX Homo sapiens.

XX WO200056772-A1.

XX 28-SEP-2000.

XX 24-MAR-2000; 2000WO-US07946.

XX 25-MAR-1999; 99US-0126603.

XX (BADI) BASF AG.

XX (GBMY) GENETICS INST INC.

XX Salfield JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Fiedrich S, Myles A,
 PI Veitman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;

XX WPI: 2000-638250/61.

PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -

PS Claim 34; Figure 2A; 377pp; English.

XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAB61062-C61071. The antibody of the invention is a neutralising
 CC antibody and has antirheumatic; antilasthmatic; antisclerotic;
 CC antidiabetic; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.

XX Sequence 9 AA:

Query Match 69.5%; Score 41; DB 21; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 YFTSYDMH 10
 ID 1 FTFSYDMH 9

RESULT 12
 AAW76016
 ID AAW76016 standard; Protein; 10 AA.

XX AAW76016;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR1 protein fragment #4.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI: 1998-437472/37.

XX N-PSDB: AAV49853.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 XX angiogenesis or restenosis
 XX
 PS Claim 60: Page 41: 129pp; English.
 XX
 CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
 CC antibodies contain non-murine framework regions so are suitable for use
 CC in humans. Enhanced types of LM609 have affinity more than 90 times
 CC greater than that of parent the parent antibody.
 CC
 SQ Sequence 10 AA:
 Query Match 69.5%; Score 41; DB 19; Length 10;
 Best Local Similarity 77.8%; Pred. No. 0.6;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYFTSYDM 9
 1 1 1 1 1 1 1 1 1 1
 Db 1 GFTFLSYDM 9
 1 1 1 1 1 1 1 1 1 1
 RESULT 13
 AAB61374
 ID AAB61374 standard; peptide; 10 AA.
 XX
 AC AAB61374;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Mutant VH CDR1 peptide #3.
 XX
 KW LM609: grafted antibody; alphaVbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI: 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 CC angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 CC osteoporosis -
 XX
 PS Disclosure: Page 41: 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 CC
 SQ Sequence 10 AA:
 Query Match 69.5%; Score 41; DB 22; Length 10;
 Best Local Similarity 77.8%; Pred. No. 0.6;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYFTSYDM 9
 1 1 1 1 1 1 1 1 1 1
 Db 1 GFTFLSYDM 9
 1 1 1 1 1 1 1 1 1 1
 RESULT 14
 AAB39812
 ID AAB39812 standard; peptide; 9 AA.
 XX
 AC AAB39812;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-IL12 antibody heavy chain CDR1 amino acid sequence SEQ ID 328.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US07946.
 XX
 PR 25-MAR-1999; 99US-0126603.
 XX
 PA (BADI) BASF AG.
 PA (GENEY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;
 XX
 DR WPI: 2000-638250/61.
 XX
 PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 CC disease and multiple sclerosis -
 XX
 PS Claim 34: Figure 2A: 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAC61062-C61071. The antibody of the invention is a neutralising
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.

CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.

XX Sequence 9 AA;

Query Match 67.8%; Score 40; DB 21; Length 9;
 Best Local Similarity 66.7%; Pred. NO. 7.8e+05;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 2 YTFSTYDMH 10
 :||:||||
 Db 1 FTFSYNMH 9

RESULT 15
 AAB39810
 ID AAB39810 standard; Peptide; 9 AA.

XX AAB39810;

DT 05-FEB-2001 (first entry)

XX Anti-hIL12 antibody heavy chain CDR1 amino acid sequence SEQ ID 326.

XX Human: neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarily determining region; CDR; antirheumatic; antiarthritic;
 KW antileukemic; neuroprotective; antiparasitic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.

XX Homo sapiens.

XX WO200056772-A1.

XX 28-SEP-2000.

XX 24-MAR-2000; 2000MO-US07946.

XX 25-MAR-1999; 9905-0126603.

XX (BADI) BASE AG.

XX (CEMY) GENETICS INST INC.

XX Salfield JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;

PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A; AR;

PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;

PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;

DR WPL: 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -

XX Claim 34; Figure 2A: 377pp; English.

XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarily determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAB61062-C61071. The antibody of the invention is a neutralizing
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;
 CC antileukemic; neuroprotective; antiparasitic; antiasthmatic;
 CC antiinflammatory; antiparasitic; antibacterial and immunosuppressive activity.

CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.

XX Sequence 9 AA;

Query Match 66.1%; Score 39; DB 21; Length 9;
 Best Local Similarity 66.7%; Pred. NO. 7.8e+05;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 YTFSTYDMH 10
 :||:||||
 Db 1 FTFSYNMH 9

Search completed: February 25, 2003, 11:32:14
 Job time : 84 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:29:11 : Search time 28 Seconds

(without alignments)
73.588 Million cell updates/sec

Title: US-09-743-482A-8

Sequence: 1 GYFTSYDMH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1224

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp-organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacterioph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	37.3	10	11 Q8VIL8	Q8VIL8 mus musculus
2	19	32.2	8	2 Q9S443	Q9S443 pseudomonas
3	18	30.5	9	4 Q9UKJ6	Q9UKJ6 homo sapien
4	18	30.5	9	16 Q8X4G1	Q8X4G1 escherichia
5	17	28.8	8	2 Q9S6D5	Q9S6D5 escherichia
6	17	28.8	8	2 P72221	P72221 pseudomonas
7	17	28.8	8	4 Q9UMH9	Q9UMH9 homo sapien
8	17	28.8	8	4 Q9UDZ4	Q9UDZ4 homo sapien
9	17	28.8	9	5 P82208	P82208 bombyx mori
10	17	28.8	9	8 Q94V10	Q94V10 varanus gilig
11	17	28.8	10	2 P83161	P83161 anabaena sp
12	16	27.1	8	2 P83158	P83158 anabaena sp
13	16	27.1	8	5 P82688	P82688 periplaneta
14	16	27.1	9	4 Q9BYF9	Q9BYF9 homo sapien
15	15	25.4	7	2 O07354	O07354 synecococc
16	15	25.4	9	4 Q14277	Q14277 homo sapien

17	15	25.4	9	4 Q96T78	Q96T78 homo sapien
18	15	25.4	10	4 Q96O19	Q96O19 homo sapien
19	15	25.4	10	4 Q9UCP3	Q9UCP3 homo sapien
20	15	25.4	10	13 Q9PRU9	Q9PRU9 sparus aura
21	14	23.7	7	10 P82445	P82445 nicotiana t
22	14	23.7	8	2 Q9R3X0	Q9R3X0 planktothrix
23	14	23.7	8	3 P87225	P87225 saccharomyc
24	14	23.7	8	5 P82686	P82686 periplaneta
25	14	23.7	8	7 Q9S213	Q9S213 oryctolagus
26	14	23.7	9	2 Q8RKC6	Q8RKC6 erwinia chr
27	14	23.7	9	2 Q9UCQ9	Q9UCQ9 homo sapien
28	14	23.7	9	5 P83276	P83276 macrobrachi
29	14	23.7	9	13 P83059	P83059 bombina ori
30	14	23.7	9	13 P83058	P83058 bombina var
31	14	23.7	9	13 P83057	P83057 bombina var
32	14	23.7	9	13 P83056	P83056 bombina var
33	14	23.7	10	6 P82923	P82923 bos taurus
34	14	23.7	10	10 P82443	P82443 nicotiana t
35	13	22.0	7	2 P72081	P72081 nocardia la
36	13	22.0	7	6 Q28742	Q28742 oryctolagus
37	13	22.0	8	2 Q9R5R2	Q9R5R2 shigella dy
38	13	22.0	8	4 Q16468	Q16468 homo sapien
39	13	22.0	8	5 P82685	P82685 periplaneta
40	13	22.0	8	5 P82687	P82687 periplaneta
41	13	22.0	9	2 Q43960	Q43960 azotobacter
42	13	22.0	9	10 Q9S8J8	Q9S8J8 oryza sativ
43	13	22.0	9	12 Q71066	Q71066 canine dist
44	13	22.0	9	12 Q71069	Q71069 canine dist
45	13	22.0	9	12 Q65711	Q65711 berne virus

ALIGNMENTS

RESULT 1	Q8VIL8	PRELIMINARY:	PRT:	10 AA.
ID	Q8VIL8			
AC	Q8VIL8:			
DT	01-MAR-2002 (TREMBlrel. 20, Created)			
DT	01-MAR-2002 (TREMBlrel. 20, Last sequence update)			
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
DE	Immediate early gene protein Homer1a (fragment).			
GN	HOMER1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/SV;			
RA	Bottai D., Guzowski J.F., Schwarz M.K., Kang S.H., Xiao B.,			
RA	Lanahan A., Worley P.F., Seeburg P.H.;			
RT	"Synaptic Activity-Induced Conversion of Intronic to Exonic Sequence			
RT	in Homer1 Immediate Early Gene Expression.";			
RL	J. Neurosci. 0:0-0(2002).			
DR	EMBL; AF425674; AAL34511.1; -			
DR	MGI; MGI:1347345; Homer1.			
FT	NON_TER			
SO	SEQUENCE	10 AA;	1187 MW;	CD7A2B905DC5B449 CRC64;
Query Match		37.3%;	Score 22;	DB 11;
Best Local Similarity		80.0%;	Pred. No. 1.1e+03;	Length 10;
Matches	4;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;
QY	2 YTFPS 6			
DB	1 YTFNS 5			
RESULT 2	Q9S443	PRELIMINARY:	PRT:	8 AA.
ID	Q9S443			
AC	Q9S443:			

```

DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Beta-lactamase (Fragment).
GN psr2.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R545;
RA Roy D., Coulombe M., Perron K., Roy P.H.;
RT "Characterization of a novel 6'-N-aminoglycoside acetyltransferase
RT gene aac(6')-IIC from the integration of a Chinese Pseudomonas aeruginosa
RT clinical isolate.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF162771; AAD46628.1; -.
FT NON_TER
SQ SEQUENCE 8 AA: 930 MW; EBD85DDDD9D1A336 CRC64;

Query Match 32.2%; Score 19; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 TFTSY 7
   1 1
Db 3 TFAAY 7

RESULT 3
ID 09UKJ6 PRELIMINARY; PRT; 9 AA.
AC 09UKJ6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Androgen receptor (Fragment).
GN AR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Li X.Q., Wu Q.F.;
RT "A splice-site mutation in Androgen Receptor gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF159087; AAF04001.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 9 AA: 1272 MW; 6F2B8415B31E684 CRC64;

Query Match 30.5%; Score 18; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 YDMH 10
   1 1
Db 1 YRMH 4

RESULT 4
ID 08X4G1 PRELIMINARY; PRT; 9 AA.
AC 08X4G1;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical protein 22947.
GN 22947.
OS Escherichia coli O157:H7.

```

```

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed-11206551;
RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocists K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
DR EMBL, AE005411; AAG56883.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 9 AA: 1107 MW; 8F6CB72699D1B41 CRC64;

Query Match 30.5%; Score 18; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YTF 4
   1 1
Db 3 YTF 5

RESULT 5
ID 09S6D5 PRELIMINARY; PRT; 8 AA.
AC 09S6D5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Putative IS30 transposase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A295B;
RX MEDLINE=99194747; PubMed-10094716;
RA Rahn A., Drummel-Smith J., Whitfield C.;
RT "Conserved organization in the cps gene clusters for expression of
RT biosynthesis locus and the cps genes: relationship to the colanic acid
RT U. Bacteriol. 181:2307-2313(1999).
DR EMBL, AF118251; AAD30008.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA: 1011 MW; F21DC1A9D1B41406 CRC64;

Query Match 28.8%; Score 17; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 TFTS 6
   1 1
Db 4 TFTA 7

RESULT 6
ID P72221 PRELIMINARY; PRT; 8 AA.
AC P72221;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Alginase lyase (Fragment).
GN ALY.
OS Pseudomonas sp. (strain OS-ALG-9).
OC Bacteria; Proteobacteria.

```

OX NCBI_TaxID=86038;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OS-ALG-9;
 RA Fujiyama K.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OS-ALG-9;
 RX MEDLINE=93329366; PubMed=8336113;
 RA Maki H., Mori A., Fujiyama K., Kinoshita S., Yoshida T.;
 RT "Cloning, sequence analysis and expression in *Escherichia coli* of a
 RT gene encoding an alginate lyase from *Pseudomonas* sp. OS-ALG-9.";
 RL J. Gen. Microbiol. 139:987-993(1993).
 DR EMBL: D38469; BAA21704.1; -;
 RN Lyase.
 KW NON_TER
 FT NON_TER
 SO SEQUENCE 8 AA; 841 MW; 461DDC5A5B041BB CRC64;
 Query Match 28.8%; Score 17; DB 4; Length 8;
 Best Local Similarity 60.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 TSYDMH 6
 DB 1 TDIYHM 5

RESULT 7
 ID O9UMH9 PRELIMINARY; PRT; 8 AA.
 AC O9UMH9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE RHC protein (Fragment).
 GN RHC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RX MEDLINE=97260406; PubMed=9106526;
 RA Matassi G., Cherif-Zahar B., Moura I., Carttron J.P.;
 RT "Characterization of the recombination hot spot involved in the
 RT genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
 RT phenotype.";
 RL Am. J. Hum. Genet. 60:808-817(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RX MEDLINE=90349591; PubMed=1696722;
 RA Cherif-Zahar B., Bloy C., Le Van Kim C., Blanchard D., Bailly P.,
 RA Hermand P., Salmon C., Carttron J.-P., Colin Y.;
 RT "Molecular cloning and protein structure of a human blood group Rh
 RT polypeptide.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6243-6247(1990).
 DR EMBL: Z97030; CAB09726.1; -;
 FT NON_TER
 FT NON_TER
 SO SEQUENCE 8 AA; 1049 MW; C007244691FBSAB1 CRC64;

Query Match 28.8%; Score 17; DB 4; Length 8;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 TSYDMH 10
 DB 1 TDIYHM 6

RESULT 8
 ID O9UD24 PRELIMINARY; PRT; 8 AA.
 AC O9UD24;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RHD protein (Fragment).
 GN RHD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RX MEDLINE=97260406; PubMed=9106526;
 RA Matassi G., Cherif-Zahar B., Moura I., Carttron J.P.;
 RT "Characterization of the recombination hot spot involved in the
 RT genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
 RT phenotype.";
 RL Am. J. Hum. Genet. 60:808-817(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RX MEDLINE=93066356; PubMed=1438298;
 RA Le Van Kim C., Moura I., Cherif-Zahar B., Raynal V., Cherrier C.,
 RA Carttron J.P., Colin Y.;
 RT "Molecular cloning and primary structure of the human blood group Rh
 RT polypeptide.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10925-10929(1992).
 DR EMBL: Z97031; CAB09727.1; -;
 FT NON_TER
 FT NON_TER
 SO SEQUENCE 8 AA; 1042 MW; D296944691FBSAB1 CRC64;

Query Match 28.8%; Score 17; DB 4; Length 8;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 TSYDMH 10
 DB 1 TDIYHM 6

RESULT 9
 ID P82208 PRELIMINARY; PRT; 9 AA.
 AC P82208;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Bombycoidea; Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=XINHANG X KEMING; TISSUE=BODY WALL, AND FAT BODY;
 RX MEDLINE=21177481; PubMed=11280994;
 RA Zhong B.X.;
 RT "Protein database for several tissues derived from five instar of
 RT silkworm.";
 RL I Chuan Hsueh Pao 28:217-224(2001).
 FT NON_TER
 FT NON_TER
 SO SEQUENCE 9 AA; 1009 MW; 377C3AB845B042D7 CRC64;

Query Match 28.8%; Score 17; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SYD 8
111
Db 5 SYD 7

RESULT 10

Q94V10 PRELIMINARY; PRT; 9 AA.

AC 094V10: 094V10: PRELIMINARY; PRT; 9 AA.
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CYTOCHROME C oxidase subunit I (Fragment).
GN COL.
OS Varanus giganteus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
OX NCBI_TaxID=62041;
RN 11
RP SEQUENCE FROM N.A.
RA Ast J.C.: "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL: AF407498; AAL10048.1; -.
KM Mitochondrion.
FT NON_TER

QY 3 TETSY 7
111
Db 2 TETRW 6

Query Match 28.8%; Score 17; DB 8; Length 9;
Best Local Similarity 60.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 11

P83161 PRELIMINARY; PRT; 10 AA.

AC P83161: 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative RNA-binding protein rbpA (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN 11
RP SEQUENCE.
RA Apté S.K., Uhlemann E., Schmid R., Alenddorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
DR InterPro: IPR000504; RNA_rec_mot.
DR PROSITE: PS00030; RRM_RNP_1; PARTIAL.
KM RNA-binding.
FT NON_TER

QY 6 SYD 8
111
Db 8 SYD 10

Query Match 28.8%; Score 17; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12

P83158 PRELIMINARY; PRT; 8 AA.

AC P83158: 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Photosystem I Iron-sulfur center (Photosystem I subunit VII) (9 kDa polypeptide) (PSI-C) (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN 11
RP SEQUENCE.
RA Apté S.K., Uhlemann E., Schmid R., Alenddorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -1- FUNCTION: APOPROTEIN FOR THE IRON-SULFUR CENTERS FA AND FB OF THE PHOTOSYSTEM I COMPLEX.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
DR InterPro: IPR001450; 4FE4S_FERREDOXIN.
DR PROSITE: PS00198; 4FE4S_FERREDOXIN; PARTIAL.
KM Photosynthesis: Photosystem I; Iron-sulfur; 4Fe-4S; Metal-binding.
FT NON_TER

QY 2 YTTSTD 8
111
Db 2 HTVKYD 8

Query Match 27.1%; Score 16; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 13

P82688 PRELIMINARY; PRT; 8 AA.

AC P82688: 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Klnin-4 (PEA-K-4).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN 11
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Raps J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight klnins from the retrocerebral complex of the American cockroach, Periplaneta americana.";
RL Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KM Neuropeptide; Amidation.
FT MOD_RES

QY 1 GYTTSY 7
111
Db 1 GAQFSSW 7

Query Match 27.1%; Score 16; DB 5; Length 8;
Best Local Similarity 42.9%; Pred. No. 6.7e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 14

Q9BYF9

ID Q9BYF9 PRELIMINARY; PRT; 9 AA.
 AC Q9BYF9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Cyokeratin 19 (Fragment).
 GN K19.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21339745; Pubmed=11682035;
 RA Kagaya M., Kaneko S., Ohno H., Inamura K., Kobayashi K.;
 RT "Cloning and characterization of the 5'-flanking region of human
 cyokeratin 19 gene in human cholangiocarcinoma cell line."
 RL J. Hepatol. 35:504-511(2001).
 DR EMBL: AB045973; BAB40770.1; -.
 KW Keratin.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1122 MW; 9E9FC41B45AB45A1 CRC64;

Query Match 27.1%; Score 16; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

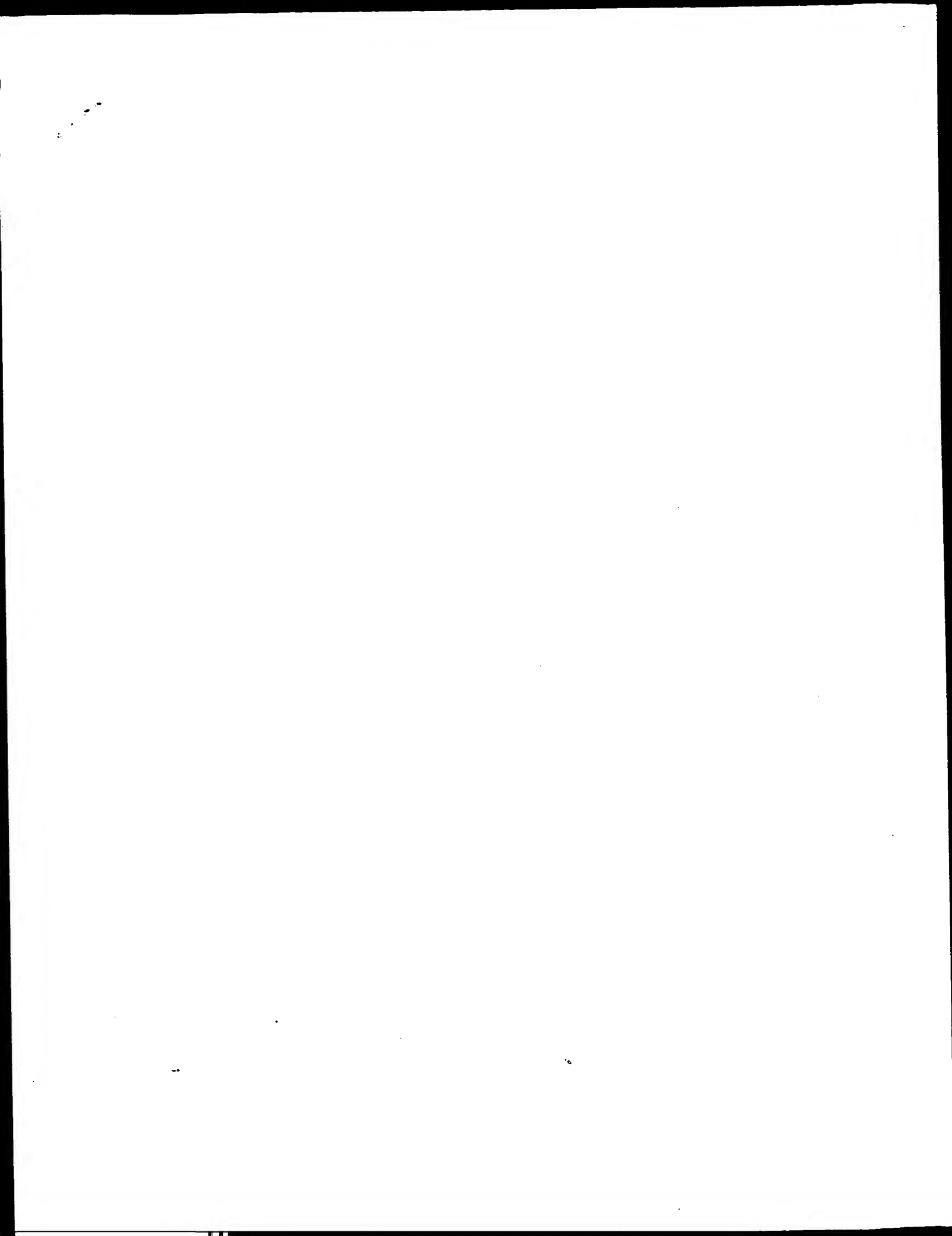
QY 5 TSY 7
 |||
 Db 2 TSY 4

RESULT 15
 ID 007354 PRELIMINARY; PRT; 7 AA.
 AC 007354;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Nifk (Fragment).
 GN NIFK.
 OS Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanophyceae PCC 8801).
 OC Bacteria; Cyanobacteria; Chroococcales; Cyanophyce.
 OX NCBI_TaxID=41431;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RF-1;
 RX MEDLINE=99231861; Pubmed=10217509;
 RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
 RT "Organization and expression of nitrogen-fixation genes in the aerobic
 nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
 RF-1."
 RL Microbiology 145:743-753(1999).
 DR EMBL: AF003700; AAC35193.1; -.
 FT NON_TER
 SQ SEQUENCE 7 AA; 849 MW; 7A12C72AA9D5B030 CRC64;

Query Match 25.4%; Score 15; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 SYDM 9
 |||
 Db 2 SFDL 5

Search completed: February 25, 2003, 11:33:07
 Job time : 30 secs



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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:23:15 : Search time 10 Seconds

(without alignments)
41.476 Million cell updates/sec

Title: US-09-743-482a-8

Perfect score: 59

Sequence: 1 GYTFSTYDMH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 346

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	32.2	10	1	TKNK_PIG
2	18	30.5	8	1	ALL5_CYPDO
3	18	30.5	10	1	ESTA_SCHGA
4	16	27.1	8	1	AKH_TYBAT
5	16	27.1	8	1	HIF2_PERAM
6	16	27.1	10	1	HIF2_CARMO
7	16	27.1	10	1	HFE_HELZE
8	16	27.1	10	1	HFE_TYBAT
9	16	27.1	10	1	LPK2_LOCM1
10	15	25.4	8	1	LCK5_LEUMA
11	15	25.4	9	1	PELR_DIAB
12	15	25.4	9	1	TAL3_PICJA
13	15	25.4	9	1	UN19_CLOPA
14	15	25.4	10	1	SLAP_BACG
15	15	25.4	10	1	TPIS_NICPL
16	14	23.7	5	1	ALL4_CARMA
17	14	23.7	5	1	PSK_DAUCA
18	14	23.7	7	1	HY7_PIG
19	14	23.7	8	1	AL15_CARMA
20	14	23.7	8	1	AL17_CARMA
21	14	23.7	8	1	AL18_CARMA
22	14	23.7	8	1	ALL3_CYPDO
23	14	23.7	8	1	ALL4_CALVO
24	14	23.7	8	1	ALL4_CYPDO
25	14	23.7	8	1	COXG_RAT
26	14	23.7	10	1	AL19_CARMA
27	14	23.7	10	1	AMPN_HELMA
28	14	23.7	10	1	UH05_RAT
29	13	22.0	5	1	PAP2_PARMA
30	13	22.0	6	1	LOK1_LOCM1
31	13	22.0	7	1	ALL2_CARMA
32	13	22.0	7	1	ALL3_CARMA
33	13	22.0	7	1	ALL4_CARMA

34	13	22.0	7	1	ALL5_CARMA	P81808 carcinos ma
35	13	22.0	7	1	ALL7_CYPDO	P82158 cydia pomon
36	13	22.0	8	1	ALL2_CARMA	P81815 carcinos ma
37	13	22.0	8	1	ALL1_CYPDO	P82152 cydia pomon
38	13	22.0	8	1	ALL5_CALVO	P81841 calliphora
39	13	22.0	8	1	ALL6_CYPDO	P82157 cydia pomon
40	13	22.0	8	1	ALL7_CARMA	P82157 carcinos ma
41	13	22.0	8	1	ALL8_CARMA	P81809 carcinos ma
42	13	22.0	8	1	ALL9_CARMA	P81812 carcinos ma
43	13	22.0	8	1	LCK2_LEUMA	P21141 leucophaea
44	13	22.0	8	1	LCK7_LEUMA	P19989 leucophaea
45	13	22.0	8	1	LCK8_LEUMA	P19990 leucophaea

ALIGNMENTS

```

RESULT 1
TKNK_PIG
ID TKNK_PIG STANDARD: PRT: 10 AA.
AC P01292:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurokinin B (NKB) (Neuromedin K).
GN TAC3 OR NKNB
OS Sus scrofa (Pig), and
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823, 8406;
RN [1]
RP SEQUENCE.
RC SPECIES=Pig; TISSUE=Spinal cord;
RX MEDLINE=83282812; PubMed=6576785;
RA Kangawa K., Minemino N., Fukuda A., Matsuo H.;
RT "Neuromedin K: a novel mammalian tachykinin identified in porcine
RL spinal cord.";
RT Blochem. Biophys. Res. Commun. 114:533-540(1983).
RN [2]
RP SEQUENCE.
RC SPECIES=R. ridibunda; TISSUE=Brain;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lomas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Renikinin: a novel NKT tachykinin receptor agonist isolated with
RL neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091(1991).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ. 1.
FT Tachykinin; Neuropeptide; Amidation.
FT MOD RES 10
SQ SEQUENCE 10 AA: 1211 MW: 114706262939CAAI CRC64;
Query Match 32.2% Score 19; DB 1; Length 10;
Best local similarity 100.0% Pred. No. 6.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
ALL5_CYPDO STANDARD: PRT: 8 AA.
ID ALL5_CYPDO
AC P82156:

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 5.
 OS Cydia pomonella (Coddling moth).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 OC Ditrysia; Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=96054539; PubMed=9392829;
 RA Duve H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Amidation.
 KM MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 898 MW; 922879CAB58640D CRC64;

Query Match 30.5%; Score 18; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYTF 4
 DB 3 GYDF 6

RESULT 3

ESTR_SCHGA STANDARD; PRT: 10 AA.
 ID ESTR_SCHGA
 AC P81012;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Esterase 52 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)
 DE (Fragment).
 OS Schizaphis graminum (Aphid).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
 OC Aphidiformes; Aphidoidea; Aphididae; Aphidini; Schizaphis.
 OX NCBI_TaxID=13262;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97468499; PubMed=9327586;
 RA Siegfried B.D., Ono M., Swanson J.J.;
 RT "Purification and characterization of a carboxylesterase associated
 with organophosphate resistance in the greenbug, Schizaphis graminum
 (Homoptera: Aphididae)."
 RL Arch. Insect Biochem. Physiol. 36:229-240(1997).
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O -> an alcohol + a
 carboxylic anion.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC InterPro: IPR002018; Carboxylesterase.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; PARTIAL.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B.2; PARTIAL.
 KM Hydrolase; Serine esterase.
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1025 MW; 018ABE587865A2C0 CRC64;

Query Match 30.5%; Score 18; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 9.4e+02;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYTF 4
 DB 7 GYDF 10

RESULT 4
 AKH_TABAT STANDARD; PRT: 8 AA.
 ID AKH_TABAT
 AC P14595;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
 DE (DCC I).
 OS Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Tabanomorpha; Tabanidae; Tabanus.
 OX NCBI_TaxID=7207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90046758; PubMed=2813985;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 hypotrehalosemic activity isolated from the corpora cardiaca of horse
 flies (Diptera)."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: A33995; A33995.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KM Neuropeptide; Amidation; Flight.
 FT MOD_RES 1
 FT MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 27.1%; Score 16; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTF 5
 DB 3 TTF 5

RESULT 5

HTE2_PERAM STANDARD; PRT: 8 AA.
 ID HTE2_PERAM
 AC P04349;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypertrehalosemic factor II (Neuropeptide M-II) (Periplaneta
 (bea-CAH-II) (Led-CC-II) (Hypertrehalosemic neuropeptide II).
 OS Periplaneta americana (American cockroach).
 OS Lepidoptera decemlineata (Colorado potato beetle), and
 Blattella orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattellidae; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L., Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 bombardment mass spectrometry."
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.

RC SPECIES-P.americana;
 RX MEDLINE-84298179; PubMed-6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardiolaccinase activity and hyperglycemic activity from the corpora
 RT cardiaca of *Periplaneta americana*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [13]
 RP SEQUENCE.
 RC SPECIES-L.deceunlineata; TISSUE=corpora cardiaca;
 RX MEDLINE-90160053; PubMed-2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289(1989).
 RN [14]
 RP SEQUENCE.
 RC SPECIES-B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE-90253659; PubMed-2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrihaloasemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches *Leucophaea maderae*,
 RT *Gromphodrhina portenosia*, *Blattella germanica* and *Blatta orientalis*
 RT and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
 RT atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: HYPERTRIHALOASEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: A05170; A05170.
 DR PIR: S08996; S08996.
 DR PIR: B44960; B44960.
 DR PIR: B49823; B49823.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 DR Neuropeptide; Amidation.
 KW MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD.RES 8 8 AMIDATION.
 FT SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;
 SQ

Query Match 27.1%; Score 16; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TFT 5
 DB 3 TFT 5

RESULT 6
 HTF2_CARMO STANDARD; PRT; 10 AA.
 ID HTF2_CARMO
 AC P1385;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Hypertrihaloasemic factor II (HTF-II) (HRTN-II) (Hypertrihaloasemic
 DE neuropeptide II).
 OS Carausius morosus (Indian stick insect), and
 OS Extatosoma tiaratum (Stick insect).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Phasmatoidea;
 CC Heteronemidae; Carausius.
 OX NCBI_TaxID=7022, 7024;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;
 RX MEDLINE-87157103; PubMed-3828678;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structure of the Indian stick insect, *Carausius morosus*,
 RT corpus cardiaca of the Indian stick insect, *Carausius morosus*,

RT determined by fast atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).
 RN [12]
 RP SEQUENCE.
 RC SPECIES-E.tiaratum; TISSUE=Corpora cardiaca;
 RX MEDLINE-90253659; PubMed-2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrihaloasemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches *Leucophaea maderae*,
 RT *Gromphodrhina portenosia*, *Blattella germanica* and *Blatta orientalis*
 RT and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
 RT atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 RN [13]
 RP CARBOHYDRATE-LINKAGE SITE.
 RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;
 RX MEDLINE-93129188; PubMed-1482345;
 RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
 RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
 RT a stick insect corpus cardiaca.";
 RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
 CC -1- FUNCTION: HYPERTRIHALOASEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- MASS SPECTROMETRY: MM=1308.61; METHOD=FA-MS.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: S07157; S07157.
 DR PIR: S09138; S09138.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 DR Neuropeptide; Amidation; Glycoprotein.
 KW MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD.RES 8 8 C-LINKED (MAN) (PROBABLE).
 FT MOD.RES 10 10 AMIDATION.
 FT SEQUENCE 10 AA; 989036745771A9D1 CRC64;
 SQ

Query Match 27.1%; Score 16; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TFT 5
 DB 3 TFT 5

RESULT 7
 HTF_HELZE STANDARD; PRT; 10 AA.
 ID HTF_HELZE
 AC P16353;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypertrihaloasemic hormone (hez-HRTN).
 OS Heliothis zea (corn earworm) (Bollworm).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 CC Diptera; Noctuidae; Noctuidae; Heliothinae; Helioverpa.
 OX NCBI_TaxID=7113;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE-88326324; PubMed-3415690;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
 RA Tseng C.M., Zhang Y.S., Hayes D.K.;
 RT "Isolation and primary structure of a neuropeptide hormone from
 RT *Heliothis zea* with hypertrihaloasemic and adipokinetic activities.";
 RL Biochem. Biophys. Res. Commun. 155:344-350(1988).
 CC -1- FUNCTION: HYPERTRIHALOASEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: A31571; A31571.
 DR InterPro: IPR002047; AKH.

DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide: Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SO SEQUENCE 10 AA; 1096 MW; BE70367865A5B9D1 CRC64;
 Query Match 27.1%; Score 16; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TFFT 6
 DB 3 TFFT 6

RESULT 8
 HTF_TABAT STANDARD; PRT; 10 AA.
 ID HTF_TABAT
 AC P14596;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypertrichalosemic factor (HOTH) (Dipteran corpora cardiaca factor II)
 DE (DCC II).
 OS Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Tabanomorpha; Tabanidae; Tabanus.
 OX NCBI_TaxID=7207;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90046758; PubMed=2813385;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 Vogt V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypertrichalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -1- FUNCTION: HYPERTRICHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: B33995; B33995.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide: Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SO SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;
 Query Match 27.1%; Score 16; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TFFT 5
 DB 3 TFFT 5

RESULT 9
 LPK2_LOCM1 STANDARD; PRT; 10 AA.
 ID LPK2_LOCM1
 AC P41488;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustapyrokinin 2 (LOW-PK-2) (EXPR-amlide).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
 OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;

RN (1)
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=94094539; PubMed=7903606;
 RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
 de Loof A.;
 RT "Isolation, identification and synthesis of locustapyrokinin II from
 RT locusta migratoria, another member of the EXPR-amlide peptide
 RT family.";
 RL Comp. Biochem. Physiol. 106C:103-109(1993).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC
 CC ACTIVITY).
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro: IPR001484; Pyrokinin.
 DR PROSITE: PS00539; PYROKININ; 1.
 KW Neuropeptide: Amidation; Pyrokinin.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SO SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;
 Query Match 27.1%; Score 16; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TFFT 5
 DB 5 TFFT 7

RESULT 10
 LCK5_LEUMA STANDARD; PRT; 8 AA.
 ID LCK5_LEUMA
 AC P19987;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Leucokinin V (L-V).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidae; Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Head;
 RX MEDLINE=87052651; PubMed=2877794;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
 RT myotropic peptides of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:27-30(1987).
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
 DR PIR: JS0315; JS0315.
 KW Neuropeptide: Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SO SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;
 Query Match 25.4%; Score 15; DB 1; Length 8;
 Best Local Similarity 42.9%; Pred. No. 1.1e+05;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GYFTSY 7
 DB 1 GSGFSW 7

RESULT 11
 PGLR_DIAAB STANDARD; PRT; 9 AA.
 ID PGLR_DIAAB
 AC P81179;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Endo-polygalacturonase (PG) (EC 3.2.1.15) (Fragment).
 OS Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 OC Cucujiformia; Phycophaga; Curculionidae; Entiminae; Entimini;
 OC Diaprepes.
 NC NCB1_TaxID=13040;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Larval gut;
 RA Doostdar H., McCollum T.G., Mayer R.T.;
 RT "Purification and characterization of an endo-polygalacturonase from
 the gut of West Indies sugarcane rootstalk borer weevil (Diaprepes
 abbreviatus L.) larvae."
 RL Comp. Biochem. Physiol. 118B:861-867(1997).
 CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
 galactosiduronic linkages in pectate and other galacturonans.
 CC -1- INDUCTION: INHIBITED BY CITRUS PGIP.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
 9.4, ITS MW IS: 44.5 kDa.
 CC -1- SIMILARITY: WEAK, TO OTHER POLYGALACTURONASES.
 KW Hydrolase; Glycosidase; Cell wall.
 FT NON_TER
 SQ SEQUENCE 9 AA: 1041 MW: 1F49087042DB41B CRC64;

Query Match 25.4%; Score 15; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 YTF 4
 DB 11;
 2 YTY 4

RESULT 12
 TAL3_PICJA STANDARD; PRT; 9 AA.
 AC P17441;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transaldolase III (EC 2.2.1.2) (Fragment).
 OS Pichia jadinii (Yeast) (Candida utilis).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Pichia.
 NC NCB1_TaxID=4903;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=75145197; PubMed=1092268;
 RA Tsolas O., Sun S.C.;
 RT "Isolation of a peptide containing a histidinyl-cysteiny sequence
 from the active center of transaldolase.";
 RL Arch. Biochem. Biophys. 167:525-533(1975).
 CC -1- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
 METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
 CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
 3-phosphate -> D-erythrose 4-phosphate + D-fructose 6-phosphate.
 CC -1- PATHWAY: Pentose phosphate pathway; nonoxidative part.
 CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
 DR InterPro: IPR001585; Transaldolase.
 DR PROSITE: PS00958; TRANSALDOLASE_2; PARTIAL.
 DR PROSITE: PS01054; TRANSALDOLASE_1; PARTIAL.
 KW Transferase; Pentose shunt.
 FT NON_TER
 SQ SEQUENCE 9 AA: 1033 MW: 325A31A44EB1E058 CRC64;

Query Match 25.4%; Score 15; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 YDMH 10
 DB 11;
 1 YGIH 4

RESULT 13
 UN19_CLOPA STANDARD; PRT; 9 AA.
 AC P81355;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 19 from 2D-page (Fragment).
 OS Clostridium pasteurianum.
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 CC Clostridium.
 NC NCB1_TaxID=1501;
 RN (1)
 RP SEQUENCE.
 RC STRAIN=W5.
 RX MEDLINE=96291870; PubMed=9629918;
 RA Flensburg R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 sequence analysis of proteins from Clostridium pasteurianum W5."
 RL Electrophoresis 19:802-806(1998).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 6.5, ITS MW IS: 38.0 kDa.
 CC VARIANT 8 8
 FT NON_TER
 SQ SEQUENCE 9 AA: 1128 MW: E33E9B0AF5BB19DA CRC64;

Query Match 25.4%; Score 15; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 FTSYDM 9
 DB 11;
 3 FESXEM 8

RESULT 14
 SLAP_BACTG STANDARD; PRT; 10 AA.
 AC P49325;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE S-layer protein (surface layer protein) (Fragment).
 OS Bacillus thuringiensis (subsp. galleriae).
 CC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 NC NCB1_TaxID=29338;
 RN (1)
 RP SEQUENCE.
 RC STRAIN=NRRL 4045;
 RA MEDLINE=90078111; PubMed=2592346;
 RX Luckevich M.D., Beveridge T.J.;
 RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
 RL J. Bacteriol. 171:6656-6667(1989).
 CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
 OF PROTEIN WHICH COAT THE SURFACE OF BACTERIA.
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
 CELL WALL; S-LAYER. (P2) SYMMETRY.
 KW Cell wall; S-layer.
 FT NON_TER
 SQ SEQUENCE 10 AA: 1080 MW: 57AECAAB769D1A3 CRC64;

Query Match 25.4%; Score 15; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYTF 4
 DB 11;
 2 GRTF 5

RESULT 15

TPIS.NICPL

ID TPIS.NICPL STANDARD; PRT: 10 AA.

AC P19118; 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).

OS Nicotiana glauca (leaflet) (leadwort-leaved tobacco).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; eusterids I; Solanales; Solanaceae; Nicotiana.

OX NCBI_TaxID=4092;

RN [1]

RP SEQUENCE.

RA Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;

RT "Alterations in the phenotype of plant cells studied by NH2-terminal

RT amino acid-sequence analysis of proteins electrophoretically

RT dimensional gel-separated total extracts."

RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).

CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone

CC phosphate.

CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.

CC -1- SUBUNIT: HOMODIMER.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

CC -1- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC

CC AND PLASTID.

CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.

CC PIR: A27617; A27617.

DR InterPro: IPR000652; Triophos_1smrse.

DR PROSITE: PS00171; TIM; PARTIAL.

KW isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;

KW Pentose shunt.

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1140 MW; 80B9D37862C9C9D1 CRC64;

QY

1 GYTF 4

1 1 1

Db

1 GRTF 4

1 1 1

1 GRTF 4

1 1 1

1 GRTF 4

1 1 1

1 GRTF 4

1 1 1

1 GRTF 4

1 1 1

1 GRTF 4

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1 GRTF 4

1 1 1

1 GRTF 4

1 1 1

1 GRTF 4

Search completed: February 25, 2003, 11:32:31
 Job time : 10 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:20:35 ; Search time 13 seconds

(without alignments)
20.370 Million cell updates/sec

Title: US-09-743-482a-6

Perfect score: 49

Sequence: 1 LQRYSNPNT 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 66399

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	53.1	9	1	US-08-649-272A-3
2	26	53.1	9	2	US-08-350-260A-438
3	26	53.1	9	3	US-09-105-799-3
4	25	51.0	9	1	US-07-955-905A-18
5	24	49.0	7	6	5200320-23
6	24	49.0	9	4	US-09-644-600-58
7	24	49.0	9	4	US-09-644-600-81
8	24	49.0	9	5	PCT-US93-08435-26
9	24	49.0	9	5	PCT-US93-08435-39
10	24	49.0	9	6	5521296-4
11	23	46.9	9	1	US-08-318-970B-22
12	23	46.9	9	2	US-08-814-806-7
13	23	46.9	9	4	US-08-918-148-24
14	22	44.9	8	4	US-08-444-818-675
15	22	44.9	8	4	US-08-444-818-676
16	22	44.9	9	1	US-08-360-125-21
17	22	44.9	9	2	US-08-450-578-21
18	22	44.9	9	2	US-08-896-176-10
19	22	44.9	9	2	US-09-017-628-21
20	22	44.9	9	2	US-09-014-880-21
21	22	44.9	9	3	US-08-599-226-25
22	22	44.9	9	4	US-09-125-098-25
23	22	44.9	9	4	US-09-227-357-432
24	22	44.9	9	4	US-08-450-363-21
25	21	42.9	7	1	US-08-044-547-10
26	21	42.9	7	1	US-09-150-133-21
27	21	42.9	7	3	US-09-150-141-21

28	21	42.9	7	4	US-09-374-493-21	Sequence 21, Appl
29	21	42.9	7	4	US-09-374-824-21	Sequence 21, Appl
30	21	42.9	7	4	US-09-374-492-21	Sequence 21, Appl
31	21	42.9	8	6	5514646-14	Patent No. 5514646
32	21	42.9	9	1	US-08-300-386A-51	Sequence 51, Appl
33	21	42.9	9	1	US-08-787-547-91	Sequence 91, Appl
34	21	42.9	9	3	US-08-159-339A-233	Sequence 233, App
35	21	42.9	9	3	US-08-931-645-51	Sequence 51, Appl
36	21	42.9	9	4	US-08-197-484-38	Sequence 38, Appl
37	21	42.9	9	5	PCT-US94-01258-51	Sequence 51, Appl
38	21	42.9	9	5	PCT-US95-02121-38	Sequence 38, Appl
39	21	42.9	9	5	PCT-US95-11235-51	Sequence 51, Appl
40	21	42.9	9	6	5210180-6	Patent No. 5210180
41	20	40.8	6	2	US-08-932-376A-9	Sequence 9, Appl1
42	20	40.8	6	2	US-08-637-759B-498	Sequence 498, App
43	20	40.8	6	3	US-08-871-355A-498	Sequence 498, App
44	20	40.8	6	4	US-09-201-945-498	Sequence 498, App
45	20	40.8	6	5	PCT-US93-08435-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-649-272A-3
; Sequence 3, Application US/08649272A
; Patent No. 5763393
; GENERAL INFORMATION:
; APPLICANT: MOSKAL, Joseph R
; APPLICANT: YAMAMOTO, Hirotsuka
; APPLICANT: COLLEY, Patricia A
; TITLE OF INVENTION: Neuroactive peptides
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,272A
; FILING DATE: 17-May-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAO, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 95,1204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note="NT3"
; US-08-649-272A-3

Query Match 53.1%; Score 26; DB 1; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRYSNPNT 9
1 1 1 1 1
Db 2 QHYSNPT 9

RESULT 2

US-08-350-260A-438

Sequence 438, Application US/08350260A

Patent No. 5962255

GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 438:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-438

Query Match 53.1%; Score 26; DB 2; Length 9;

Best Local Similarity 55.6%; Pred. No. 2e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQRYSNPNT 9
1 1 1 1 1
Db 1 MORIEFPNT 9

RESULT 3

US-09-105-799-3

Sequence 3, Application US/09105799

Patent No. 6107271

GENERAL INFORMATION:

APPLICANT: MOSKAL, Joseph R
APPLICANT: YAMAMOTO, Hirokazu
APPLICANT: COLLEY, Patricia A
TITLE OF INVENTION: Neuroactive Peptides
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & ALLEGRETTI, LTD.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,799
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/649,272
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: CHAO, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 95,1204
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1234
FAX: 312-715-1000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: No. 6107271 Relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /note="NT3"

US-09-105-799-3

Query Match 53.1%; Score 26; DB 3; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRYSNPNT 9
1 1 1 1 1
Db 2 QHYSNPT 9

RESULT 4

US-07-955-905A-18

Sequence 18, Application US/07955905A

Patent No. 5770433

GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: RECOMBINANT 47 AND 31 KD COCOA PROTEINS AND

TITLE OF INVENTION: PRECURSOR
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/955,905A
FILING DATE: 21-JAN-1993
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: CDS
LOCATION: 1..9
OTHER INFORMATION: /product="Cyanogen bromide peptide"
US-07-955-905A-18

Query Match
Best Local Similarity 51.0%; Score 25; DB 1; Length 9;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 RYSNP 9
DB 4 ANPNT 8

RESULT 5
5200320-23
Patent No. 5200320
APPLICANT: SETTE, ALESSANDRO;BUIUS, SOREN;GREY, HOWARD M.
TITLE OF INVENTION: METHOD FOR IDENTIFYING USEFUL
POLYPEPTIDE VACCINES
NUMBER OF SEQUENCES: 41
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-07/130,036
FILING DATE: 7-DEC-1987
SEQ ID NO:23:
LENGTH: 7
5200320-23

Query Match
Best Local Similarity 49.0%; Score 24; DB 6; Length 7;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYSNP 7
DB 2 QREGP 7

RESULT 6
US-09-644-600-58
Sequence 58, Application US/09644600
Patent No. 6451500
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotochi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/09/644,600
CURRENT FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: 09/027,337
PRIOR FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 58

LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 665-673 of the TADG-15 protein
US-09-644-600-58

Query Match
Best Local Similarity 49.0%; Score 24; DB 4; Length 9;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RYSNP 7
DB 1 RYSDP 5

RESULT 7
US-09-644-600-81
Sequence 81, Application US/09644600
Patent No. 6451500
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotochi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/09/644,600
CURRENT FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: 09/027,337
PRIOR FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 81
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 664-672 of the TADG-15 protein
US-09-644-600-81

Query Match
Best Local Similarity 49.0%; Score 24; DB 4; Length 9;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RYSNP 7
DB 2 RYSDP 6

RESULT 8
PCT-US93-08435-26
Sequence 26, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Confering Passive
IMMUNITY Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Morrilstown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-08435-26

Query Match 49.0%; Score 24; DB 5; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 QRYSNPNT 9
1 1 1 1 1
DB 2 QVSYSPRT 9

RESULT 9
PCT-US93-08435-39
Sequence 39, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: Smithline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
TITLE OF INVENTION: Novel Antibodies for Confering Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen In Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids

TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-08435-39

Query Match 49.0%; Score 24; DB 5; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 QRYSNPNT 9
1 1 1 1 1
DB 2 QVSYSPRT 9

RESULT 10
5521296-4
Patent No. 5521296
APPLICANT: OKADA, HIDECHIKA, OKADA, NORIKO; NAGAMI, YOICHI;
TAKAHASHI, KAZUHIRO; TAKIZAWA, HISAO; KONDO, JUN CODING THEREFOR
TITLE OF INVENTION: GLYCOPROTEIN AND GENE CODING THEREFOR
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,211
FILING DATE: 01-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 376,828
FILING DATE: 07-JUL-1989
SEQ ID NO: 4
LENGTH: 9
5521296-4

Query Match 49.0%; Score 24; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LQRYSNPN 8
1 1 1 1 1
DB 1 LQCYNCPN 8

RESULT 11
US-08-318-970B-22
Sequence 22, Application US/08318970B
Patent No. 5589573
GENERAL INFORMATION:
APPLICANT: HIDEAKI HAGIMARA, et al.
TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: Dell System 210; Intel 80 285 Microprocessor
OPERATING SYSTEM: MS DOS 3.3
SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,970B
FILING DATE: October 6, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: S-2371
TELEPHONE: (703) 549-2282
TELEFAX: (703) 836-0106

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: L CDR3-4
OTHER INFORMATION: hypervariable region
US-08-318-970B-22

Query Match 46.9%; Score 23; DB 1; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRYSNPT 9
Db 2 QVYSSPPT 9

RESULT 12
US-08-814-806-7
Sequence 7, Application US/08814806
Patent No. 5986065
GENERAL INFORMATION:
APPLICANT: Wong, Hing C.
APPLICANT: Jiao, Jin-an
APPLICANT: Esperanza, Nieves
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
TITLE OF INVENTION: COAGULATION AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,806
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F.
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-814-806-7

Query Match 46.9%; Score 23; DB 2; Length 9;

Best Local Similarity 62.5%; Pred. No. 2e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QRYSNPT 9
Db 2 QVYSSPPT 9

RESULT 13
US-08-918-148-24
Sequence 24, Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camella
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Rendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 24
LENGTH: 9
TYPE: PPT
ORGANISM: artificial
FEATURE:
NAME/KEY: 5S5scfv, 10D10scfv, 12B5scfv VL CDR3
LOCATION: 1-9
OTHER INFORMATION: also 12D5scfv VL CDR3
US-08-918-148-24

Query Match 46.9%; Score 23; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 2e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QRYSN 6
Db 1 QQYSN 5

RESULT 14
US-08-444-818-675
Sequence 675, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiton Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbld, Alisha A.
REGISTRATION NUMBER: 33,895

Sat Mar 1 08:16:45 2003

us-09-743-482a-6.closed.ra1

Page 6

Search completed: February 25, 2003, 11:22:47
Job time : 14 secs

REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 675:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-675

Query Match 44.9%; Score 22; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 2e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0;

OY 1 LORISNP 7
DB 2 MTRYGAP 8

RESULT 15
US-08-444-818-676
Sequence 676, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 676:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-676

Query Match 44.9%; Score 22; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 2e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0;

OY 1 LORISNP 7
DB 1 MTRYGAP 7

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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:22:30 : Search time 32 Seconds
(without alignments)
8.738 Million cell updates/sec

Title: US-09-743-482a-6
Perfect score: 49
Sequence: 1 LQRYSNPT 9

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Gapop 10.0, Gapext 0.5

Searched: 156504 seqs, 31069816 residues
Total number of hits satisfying chosen parameters: 21285

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	67.3	9	US-09-968-561A-144	Sequence 144, App
2	33	67.3	9	US-09-968-561A-300	Sequence 300, App
3	33	67.3	9	US-09-968-561A-318	Sequence 318, App
4	33	67.3	9	US-09-192-854-84	Sequence 84, App
5	29	59.2	9	US-09-192-854-98	Sequence 98, App
6	28	57.1	9	US-09-968-561A-18	Sequence 18, App
7	28	57.1	9	US-09-968-561A-72	Sequence 72, App
8	28	57.1	9	US-09-968-561A-78	Sequence 78, App
9	28	57.1	9	US-09-968-561A-216	Sequence 216, App
10	28	57.1	9	US-09-968-561A-222	Sequence 222, App
11	28	57.1	9	US-09-968-561A-240	Sequence 240, App
12	28	57.1	9	US-09-192-854-48	Sequence 48, App
13	28	57.1	9	US-09-192-854-13	Sequence 13, App
14	28	57.1	9	US-09-968-561A-96	Sequence 96, App
15	27	55.1	9	US-09-968-561A-192	Sequence 192, App
16	27	55.1	9	US-09-968-561A-198	Sequence 198, App
17	27	55.1	9	US-09-968-561A-264	Sequence 264, App
18	27	55.1	9	US-09-968-561A-276	Sequence 276, App
19	27	55.1	9	US-09-968-561A-276	Sequence 276, App

20	27	55.1	9	US-09-968-561A-288	Sequence 288, App
21	27	55.1	9	US-09-192-854-59	Sequence 59, App
22	27	55.1	9	US-09-192-854-111	Sequence 111, App
23	27	55.1	9	US-09-192-854-150	Sequence 150, App
24	25	51.0	9	US-09-423-800-61	Sequence 61, App
25	25	51.0	9	US-09-968-561A-90	Sequence 90, App
26	25	51.0	9	US-09-968-561A-132	Sequence 132, App
27	25	51.0	9	US-09-968-561A-150	Sequence 150, App
28	24	49.0	9	US-09-968-561A-270	Sequence 270, App
29	24	49.0	9	US-09-968-561A-284	Sequence 284, App
30	24	49.0	9	US-09-968-561A-126	Sequence 126, App
31	24	49.0	9	US-09-968-561A-138	Sequence 138, App
32	24	49.0	9	US-09-968-561A-150	Sequence 150, App
33	24	49.0	9	US-09-968-561A-270	Sequence 270, App
34	24	49.0	9	US-09-968-561A-284	Sequence 284, App
35	24	49.0	9	US-09-192-854-28	Sequence 28, App
36	24	49.0	9	US-09-192-854-55	Sequence 55, App
37	24	49.0	9	US-09-192-854-81	Sequence 81, App
38	23	46.9	9	US-10-001-934-21	Sequence 21, App
39	23	46.9	9	US-09-968-561A-36	Sequence 36, App
40	23	46.9	9	US-09-293-854-7	Sequence 7, App
41	23	46.9	9	US-09-808-037-20	Sequence 20, App
42	23	46.9	9	US-09-192-854-25	Sequence 25, App
43	22	44.9	9	US-09-968-561A-102	Sequence 102, App
44	22	44.9	9	US-09-983-802-432	Sequence 432, App
45	22	44.9	9	US-09-192-854-63	Sequence 63, App

ALIGNMENTS

RESULT 1
US-09-968-561A-144
Sequence 144, Application US/09968561A
Patent No. US2002016462A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
FILE REFERENCE: 8039/10738
CURRENT APPLICATION NUMBER: US/09/968, 561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065, 248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066, 729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511, 939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 144
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-144
Query Match
Best Local Similarity 67.3%; Score 33; DB 9; Length 9;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 QRYSNPT 9
DB 2 QRYSNPT 9
RESULT 2
US-09-968-561A-300
Sequence 300, Application US/09968561A
Patent No. US2002016462A1

GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 300
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-300

Query Match 67.3%; Score 33; DB 9; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QRYSNPNT 9
1 1 1 1 1 1
Db 2 QSYSTPNT 9

RESULT 3
US-09-968-561A-318
Sequence 318, Application US/09968561A
Patent No. US2002016462A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 318
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-318

Query Match 67.3%; Score 33; DB 9; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QRYSNPNT 9
1 1 1 1 1 1
Db 2 QSYSTPNT 9

RESULT 4

US-09-192-854-84
Sequence 84, Application US/09192854
Patent No. US20020068276A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Greg
TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 84
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-192-854-84

Query Match 67.3%; Score 33; DB 10; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QRYSNPNT 9
1 1 1 1 1 1
Db 2 QSYSTPNT 9

RESULT 5
US-09-968-561A-174
Sequence 174, Application US/09968561A
Patent No. US2002016462A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
FILE REFERENCE: 8039/1073B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 174
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-174

Query Match 59.2%; Score 29; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 QRYSNPNT 9
1 1 1 1 1 1
Db 2 QRYTNPNT 9

RESULT 6
US-09-192-854-98
Sequence 98, Application US/09192854
Patent No. US20020068276A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Greg

APPLICANT: Tomlinson, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 98
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-192-854-98

Query Match 59.2%; Score 29; DB 10; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ORYSNPNT 9
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Db 2 QSYSTPST 9

RESULT 7
US-09-968-561A-18
Sequence 18, Application US/09968561A
Patent No. US20020164642A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/10738
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 18
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-18

Query Match 57.1%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 ORYSNPNT 9
| | | | |
Db 2 QSYSTPST 9

RESULT 8
US-09-968-561A-72
Sequence 72, Application US/09968561A
Patent No. US20020164642A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/10738
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01

PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 72
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-72

Query Match 57.1%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 ORYSNPNT 9
| | | | |
Db 2 QSYSTPST 9

RESULT 9
US-09-968-561A-78
Sequence 78, Application US/09968561A
Patent No. US20020164642A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
FILE REFERENCE: 8039/10738
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 78
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-78

Query Match 57.1%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 ORYSNPNT 9
| | | | |
Db 2 QSYSTPST 9

RESULT 10
US-09-968-561A-216
Sequence 216, Application US/09968561A
Patent No. US20020164642A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand

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; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 216
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-216
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Query Match          57.1% Score 28; DB 9; Length 9;
Best Local Similarity 62.5% Pred. No. 1.3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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OY 2 QRYSNPNT 9
    1 1 1 1 1
Db 2 QSYSTPST 9
```

```
RESULT 11
US-09-968-561A-222
; Sequence 222, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 222
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-222
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Query Match          57.1% Score 28; DB 9; Length 9;
Best Local Similarity 62.5% Pred. No. 1.3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
OY 2 QRYSNPNT 9
    1 1 1 1 1
Db 2 QSYSTPST 9
```

```
RESULT 12
US-09-968-561A-240
; Sequence 240, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
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; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-240
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```
Query Match          57.1% Score 28; DB 9; Length 9;
Best Local Similarity 62.5% Pred. No. 1.3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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OY 2 QRYSNPNT 9
    1 1 1 1 1
Db 2 QSYSTPST 9
```

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RESULT 13
US-09-192-854-13
; Sequence 13, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-13
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Query Match          57.1% Score 28; DB 10; Length 9;
Best Local Similarity 62.5% Pred. No. 1.3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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OY 2 QRYSNPNT 9
    1 1 1 1 1
Db 2 QSYSTPST 9
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RESULT 14
US-09-192-854-48
; Sequence 48, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
```

```

; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 48
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-48

```

```

Query Match          57.1%; Score 28; DB 10; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2 QSYSNPNT 9
   1 1 1 1 1
Db 2 QSYSNPNT 9

```

```

RESULT 15
US-09-968-561A-96
; Sequence 96, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phase Display Libraries with Different Ligands
; FILE REFERENCE: 8039/10738
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 96
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-96

```

```

Query Match          55.1%; Score 27; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

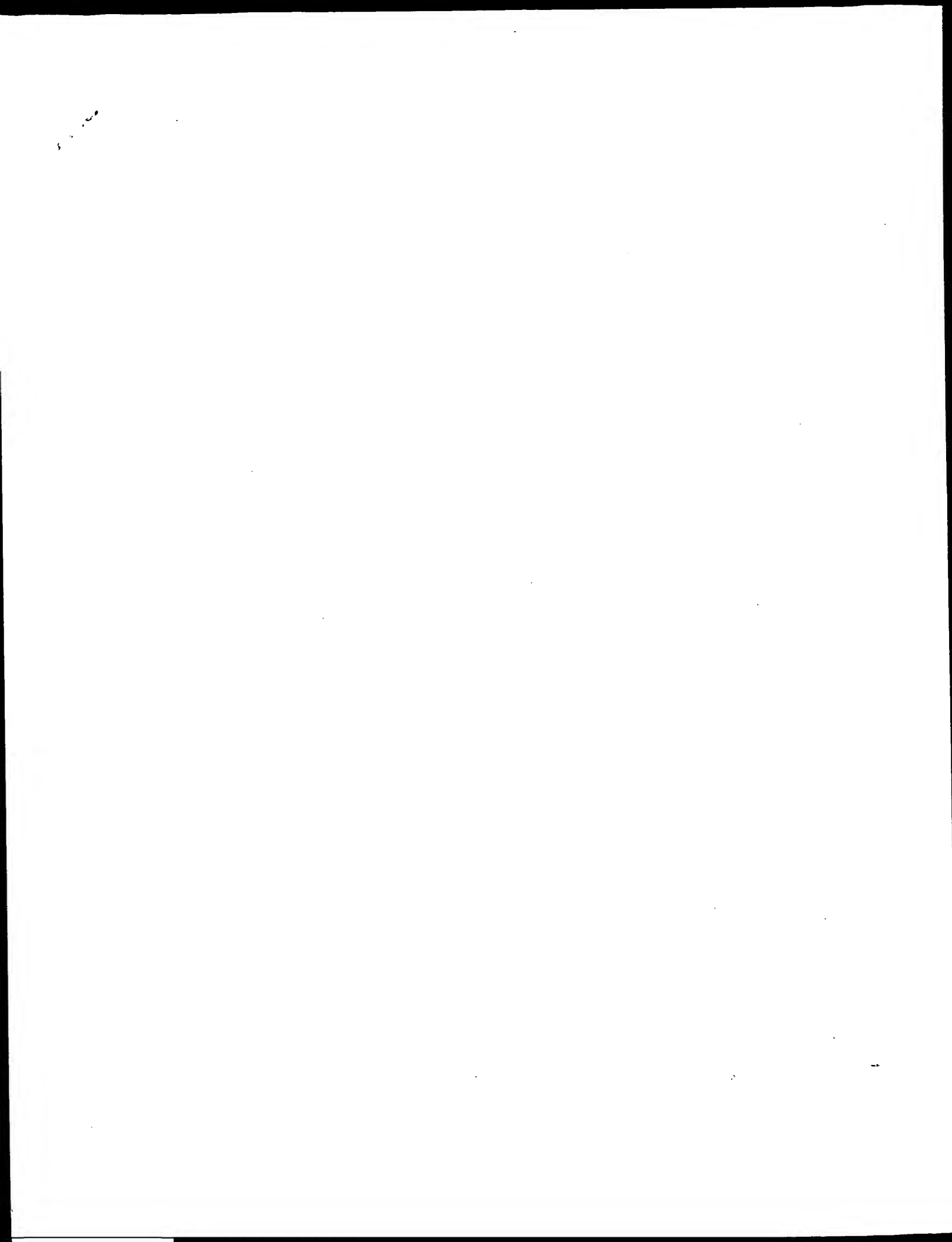
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QY 2 QSYSNPNT 9
   1 1 1 1 1
Db 2 QSYSNPNT 9

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Search completed: February 25, 2003, 11:30:44
 Job time : 33 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:17:25 ; Search time 34 Seconds

(without alignments)
35.272 Million cell updates/sec

Title: US-09-743-482a-6

Perfect score: 49

Sequence: 1 LQRYSNPNT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 segs, 133250620 residues

Total number of hits satisfying chosen parameters: 130868

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	49	100.0	21	AAV78321
2	29	59.2	22	AAU02668
3	29	59.2	9	AAE16429
4	27	55.1	9	AAW13932
5	26	53.1	7	AAE12150
6	26	53.1	9	AAW47103
7	26	53.1	9	AAW50682
8	25	51.0	7	AAW44991
9	25	51.0	9	AAW44991
10	25	51.0	9	AAW44991
			17	AAW99014

11	25	51.0	9	AAW62191
12	25	51.0	9	AAW57579
13	25	51.0	9	AAW02549
14	25	51.0	9	AAW09631
15	25	51.0	9	AAW77517
16	25	51.0	9	AAW67115
17	25	51.0	9	AAW63397
18	25	51.0	9	AAW64779
19	25	51.0	9	AAW68993
20	25	51.0	9	AAW69912
21	25	51.0	9	AAW69912
22	25	51.0	9	AAW69912
23	25	51.0	9	AAW69912
24	25	51.0	9	AAW69912
25	25	51.0	9	AAW69912
26	25	51.0	9	AAW69912
27	25	51.0	9	AAW69912
28	25	51.0	9	AAW69912
29	25	51.0	9	AAW69912
30	25	51.0	9	AAW69912
31	25	51.0	9	AAW69912
32	25	51.0	9	AAW69912
33	25	51.0	9	AAW69912
34	25	51.0	9	AAW69912
35	25	51.0	9	AAW69912
36	25	51.0	9	AAW69912
37	25	51.0	9	AAW69912
38	25	51.0	9	AAW69912
39	25	51.0	9	AAW69912
40	25	51.0	9	AAW69912
41	25	51.0	9	AAW69912
42	25	51.0	9	AAW69912
43	25	51.0	9	AAW69912
44	25	51.0	9	AAW69912
45	25	51.0	9	AAW69912

ALIGNMENTS

RESULT 1	AAV78321	standard; Protein; 9 AA.
ID	AAV78321	
AC	AAV78321	
XX		
DT	04-MAY-2000	(first entry)
XX		
DE	Anti-zeta-chain antibody 2-B-5; VL-region CDR3 protein sequence.	
KW	Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;	
KW	complementary determining region; CDR; autoimmune disease; cytotoxic;	
KW	immune deficiency; T-cell malignancy; infectious disease; antiviral;	
KW	immunosuppressive; antimicrobial; immune response modulator; NK-cell.	
OS	Rattus norvegicus.	
XX		
PN	WO200003016-A1.	
XX		
PD	20-JAN-2000.	
XX		
PF	09-JUL-1999;	99WO-EF04838.
XX		
PR	10-JUL-1998;	98EP-0112867.
XX		
PA	(CONN-) CONNEX GMBH.	
XX		
PI	Reiter C;	
XX		
DR	WPI: 2000-160926/14.	
DR	N-PDB: AA288319.	
XX		
PT	New oligonucleotide, polypeptide, antibody useful for treating	

PT autoimmune disease, immune deficiencies, T-cell malignancies and
 PT infectious diseases -
 XX
 XX
 XX Claim 10; Fig 7; 79pp; English.
 XX
 CC The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is
 CC encoded by (I), is obtained by immunizing a rat with jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,
 CC infectious diseases and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC or viral infections. The antibody, and fragments of it, can be useful for
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC treatment of NK-cell derived malignancies. It can also be useful for the
 CC determination of zeta-chain or eta-chain expression on NK-cells.
 CC T-lymphocytes or their precursors. The present sequence represents the
 CC CDR3 of the VL-region of the anti-zeta-chain antibody 2-B-5, produced
 CC by rats from the present invention.
 CC
 SQ Sequence 9 AA:
 Query Match 100.0%; Score 49; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LQRYSNPNT 9
 1 LQRYSNPNT 9
 DB 1 LQRYSNPNT 9
 RESULT 2
 AAU02668
 ID AAU02668 standard; Peptide; 9 AA.
 AC AAU02668;
 XX
 XX 29-AUG-2001 (first entry)
 DE CDR region of anti-adipocyte antibody heavy chain, FAT 29.
 XX
 XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 XX
 XX WO200127279-A1.
 PN 19-APR-2001.
 PD 11-OCT-2000; 2000WO-GB03900.
 PF 12-OCT-1999; 99US-0158812.
 PR (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA Edwards BM, Main SH, Vaughan TJ;
 XX
 XX WPI: 2001-282031/29.
 DR N-PSDB: AAS03440.
 XX
 XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity
 PT related diseases -
 PS Example 7; Page 77; 182pp; English.
 XX
 CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light

CC chain, and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease.
 CC
 SQ Sequence 9 AA:
 Query Match 59.2%; Score 29; DB 22; Length 9;
 Best Local Similarity 44.4%; Pred. No. 7.8e+05;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 1 LQRYSNPNT 9
 1 LQRYSNPNT 9
 DB 1 VNRYSNPT 9
 RESULT 3
 AAEL6429
 ID AAEL6429 standard; peptide; 9 AA.
 AC AAEL6429;
 XX
 XX 09-APR-2002 (first entry)
 DE Mouse antibody 2A4 light chain variable region CDR #3.
 XX
 XX Mouse; antibody 2A4; light chain variable region; osteopathic; psoriasis;
 KW cytostatic; antiinflammatory; osteoporosis; bone cancer; immune disease;
 KW inflammatory bowel disease; multiple sclerosis; osteopenic disease; CDR;
 KW complementarity determining region; rheumatoid arthritis; diabetes.
 XX
 OS Mus sp.
 XX
 XX WO200191793-A1.
 PN 06-DEC-2001.
 PD 24-MAY-2001; 2001WO-US16865.
 PF 26-MAY-2000; 2000US-207628P.
 PR (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Blake SM, Sweet RW, Taylor AH, Wattam TA;
 PI
 XX
 XX WPI: 2002-122040/16.
 DR N-PSDB: AAD26951.
 XX
 XX New anti-RANK ligand monoclonal antibodies, useful for treating or
 PT preventing osteopenic diseases (e.g. arthritis, osteoporosis or bone
 PT cancer) or immune disease (e.g. psoriasis, inflammatory bowel disease
 PT or multiple sclerosis) -
 PS Claim 5; Page 47; 50pp; English.
 XX
 CC The invention relates to anti-RANK monoclonal antibodies which has the
 CC identifying characteristics of monoclonal antibody 2A4. The antibody or
 CC polypeptide is useful for treating or preventing osteopenic diseases
 CC (e.g., rheumatoid arthritis, osteoporosis, metastatic and primary bone
 CC cancer, wear debris induced osteolysis or osteoarthritis) or immune
 CC diseases (e.g., psoriasis, insulin dependent, diabetes, inflammatory

CC bowel disease or multiple sclerosis). The antibody is also useful for
 CC treating and diagnosing conditions mediated by the RANK ligand. The
 CC present sequence is mouse antibody 2A4 light chain variable region
 CC complementarity determining region (CDR).

SO Sequence 9 AA:

Query Match 59.2%; Score 29; DB 23; Length 9;
 Best Local Similarity 62.5%; Pred. No. 7.8e+05;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 QRYSNPMT 9
 1 1 1 1 1
 DB 2 QHYSSPRT 9

RESULT 4

AAW13932
 ID AAW13932 standard; Protein; 9 AA.

AC AAW13932;

DT 15-MAY-1997 (first entry)

DE CDR-3 fragment of light chain of anti-HB virus antibody #1.

XX Antibody: heavy chain; light chain; variable region; human; monoclonal;
 KW complementarity determining region; human; adr type hepatitis B virus;
 KM HB virus; CDR: virus antigen; anti-HB antibody; vaccine.

OS Homo sapiens.

PN JF09020798-A.

PD 21-JAN-1997.

PF 11-JUL-1995; 95JP-0174752.

PR 11-JUL-1995; 95JP-0174752.

PA (ASAH) ASAH KASEI KOGYO KK.

DR WPI; 1997-140911/13.

DR N-PSDB; AAT60127.

PT Human anti-Hepatitis B antibody - used in a adr type HB virus
 PT vaccine

PS Example 1; Page 11; 20pp; Japanese.

CC AAW13929-W13943 represent fragments of the complementarity determining
 CC regions of the heavy and light chains of the human monoclonal antibodies
 CC of the invention. The antibody of the invention preferably contains the
 CC sequence represented by AAW13912 in the complementarity determining
 CC region-1 (CDR-1) of the heavy chain variable region. The antibody of
 CC the invention also contains the sequence represented by AAW13913 in the
 CC CDR-3 of the light chain variable region. The antibody is capable of
 CC binding to adr type hepatitis B (HB) virus antigen. A human anti-HB
 CC virus monoclonal antibody preparation which is highly safe and is
 CC effective to adr type HB virus can be provided, using the monoclonal
 CC antibody. It can also be used as a vaccine against HB infection.

SO Sequence 9 AA:

Query Match 55.1%; Score 27; DB 18; Length 9;
 Best Local Similarity 62.5%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 QRYSNPMT 9
 1 1 1 1 1
 DB 2 QSYSPRT 9

RESULT 5

AAE12150

ID AAE12150 standard; peptide; 7 AA.

AC AAE12150;

DT 15-JAN-2002 (first entry)

DE Bacillus subtilis strain AQ713 bacillomycin F cyclic peptide.

XX Agrastatin; iturin C; plipastatin A2; surfactin; pesticide; insecticide;
 KW antibacterial; antifungal; anti-corn rootworm activity; cyclic;
 KM bacillomycin F.

OS Bacillus subtilis AQ713.

Key Location/Qualifiers

FT Modified-site

/note= "This residue is attached to
 R(CH2)8-12CHNCH2CO group where R = CH3, CH(CH3)2,
 CH3CH2CHCH3; linked to Thr at position 7 to
 form a cyclic structure"

FT Misc-difference

2..3

FT Modified-site

/note= "D-form residues"
 /note= "This residue is linked to Asn at position 1
 to form a cyclic structure"

US6291426-B1.

18-SEP-2001.

14-MAY-1999; 99US-0312314.

08-MAY-1998; 98US-0074870.

09-MAY-1997; 97US-0853753.

(AGRA-) AGRAQUEST INC.

Heins SD, Manker DC, Jimenez DR, McCoy RJ, Marrone PG, Orjala JE;

WPI; 2001-647228/74.

New agrastatin produced by a new Bacillus strain useful for controlling
 fungal and bacterial infections including corn rootworm infestation -

Disclosure; Column -; 19pp; English.

XX The invention relates to a novel antibiotic and metabolite
 CC producing Bacillus subtilis strain AQ713 exhibiting antibacterial,
 CC antifungal and anti-corn rootworm activities. The invention also
 CC provides novel compounds, agrastatins produced by B. subtilis
 CC strain AQ713 and a novel combination of compounds comprising
 CC iturin A, plipastatin, surfactin and agrastatin. The compounds
 CC of the invention are useful for controlling fungal and bacterial
 CC infections caused by Phytophthora infestans, Venturia pyrina,
 CC Rhizoctonia solani, Cladosporium cucumerinum, Botrytis cinerea,
 CC Alternaria solani, Colletotrichum cocodes, Alternaria brassicicola,
 CC Monilia fructicola, Sphaerotheca fuliginea, Acidovorax avenae,
 CC Pseudomonas syringae, Xanthomonas campestris, Erwinia carotovora,
 CC Clavibacter michiganense, Plasmodiopsis viticola, Uncinula necator,
 CC Pythium ultimum and Peronospora parasitica and corn rootworm
 CC infestation. The invention further provides methods for treating
 CC or protecting plants from bacterial, fungal and corn rootworm
 CC infections. The present sequence is B. subtilis strain AQ713
 CC bacillomycin F cyclic peptide. This peptide belongs to the iturin
 CC family.
 CC Note: This sequence is not shown in the specification but is
 CC derived from the peptide sequence shown in Column 3 of the
 CC specification.

SO Sequence 7 AA:

Query Match 53.1%; Score 26; DB 22; Length 7;
Best Local Similarity 66.7%; Pred. No. 7.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 YSNPNT 9
I: | | |
DB 2 YNOPT 7

RESULT 6
AAM47103

ID AAM47103 standard; peptide; 9 AA.

AC AAM47103;

DT 18-MAY-1998 (first entry)

DE NMDA receptor binding neuroactive peptide 3.

KM NMDA receptor; neuroactive; glycine co-agonist; learning; memory;

KM N-methyl-D-aspartate; pharmaceutical.

OS Synthetic.

OS Ratus sp.

PN WO9743306-A1.

PD 20-NOV-1997.

PF 16-MAY-1997; 97MO-US08667.

PR 17-MAY-1996; 96US-0649272.

PA (NEUR-) NEUROTERAPEUTICS LP.

PI Colley PA, Moskal JR, Yamamoto H;

DR WPI: 1998-008795/01.

PT New neuro-active polypeptide(s) for enhancing learning and memory -

PT have NMDA receptor agonist activity at the glycine binding site

PS Claim 1; Page 23; 38pp; English.

CC This neuroactive peptide can bind to a N-methyl-D-aspartate (NMDA)

CC receptor and is included in a pharmaceutical composition comprising an

CC effective NMDA receptor binding amount of a polypeptide. The products

CC bind to the NMDA receptor at the glycine co-agonist site and effect at

CC least the same biological activity from the NMDA receptor as the binding

CC of glycine. They can be used as NMDA receptor agonists for enhancing

CC learning and memory. They can also be used for the isolation and

CC characterisation of NMDA receptor activity, NMDA receptor tissue

CC localisation and correlation with disease, injury or other

CC pharmacological effects.

CC

CC

CC

CC

CC

CC

Sequence 9 AA;

Query Match 53.1%; Score 26; DB 19; Length 9;

Best Local Similarity 62.5%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 QRSNPNT 9
I: | | |
DB 2 QHSTPPT 9

RESULT 7
AAM50682

ID AAM50682 standard; Peptide; 9 AA.

AC AAM50682;

PN 08-APR-2002 (first entry)

XX Neuroactive peptide NT-3, for hypoxia treatment.

DE Neuroactive peptide; NT-3; hypoxia; ischaemia; therapy;

KM antihypoxic.

OS Synthetic.

PN WO200198367-A2.

PD 27-DEC-2001.

PF 22-JUN-2001; 2001WO-US19839.

PR 22-JUN-2000; 2000US-213614P.

PA (NYXI-) NYXI NEURO THERAPIES INC.

PI Moskal JR, Yamamoto H, Colley PA;

DR WPI: 2002-098225/13.

PT Use of peptide or amino acid compositions for the treatment of hypoxia

PT and ischaemia -

PS Claim 1; Page 31; 41pp; English.

CC The present sequence is that of neuroactive peptide NT-3, which is

CC capable of binding to the N-methyl-D-aspartate (NMDA) receptor.

CC NT-3 is one of a set of NT family peptides (see AAM50680-92) that

CC can be used to treat hypoxia and ischaemia. A method of treating

CC hypoxia by administering a peptide or amino acid composition

CC comprising a neuroactive peptide, DNA molecules encoding the

CC neuroactive peptides, and a method of treating the effects of

CC hypoxia in the central nervous system by administering a

CC neuroactive peptide such as NT-3 are claimed. The neuroactive

CC peptides may be cyclized and may contain (preferably conservative)

CC amino acid substitutions. A preferred neuroactive peptide is NT-13

CC (see AAM50692).

CC

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CC

Sequence 9 AA;

Query Match 53.1%; Score 26; DB 23; Length 9;

Best Local Similarity 62.5%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 QRSNPNT 9
I: | | |
DB 2 QHSTPPT 9

RESULT 8
AAM44991

ID AAM44991 standard; Peptide; 7 AA.

AC AAM44991;

DT 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #1262.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;

KW immunogenically cross-reactive; cancer; immunogenic cancer cell;

KW cytotoxic; vaccine; tumour-specific immunogenic response inducer;

KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;

XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.

OS Homo sapiens.

OS Synthetic.

PN CA2290722-A1.

PD 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.
XX 08-DEC-1999; 99CA-2290722.
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX Kaplan HA, Maltl PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated
XX antigen-binding fragments of an antibody that binds specifically to the
XX complex
XX
XX Example 4; Page 105; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPPC) associated with tumors that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPPCs specific to target cancer (TC). Also described is an isolated
XX antigen-binding fragment of an antibody that binds specifically to SPPCs
XX or a population of different SPPCs consisting of immunogenic cancer cell
XX surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX used in vaccine production and as a tumour-specific immunogenic response
XX inducer. (I) is useful for treating 71 types of cancers or tumors in a
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
XX Sequence 7 AA:
SQ
Query Match 51.0%; Score 25; DB 22; Length 7;
Best Local Similarity 71.4%; Pred. No. 7.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LQRYSNP 7
1:|||||
1 LKRYSTIP 7
DB
RESULT 9
AAR99011
ID AAR99011 standard; peptide: 9 AA.
XX
XX AAR99011;
XX
XX 24-OCT-1996 (first entry)
XX
XX Anti-thyroid peroxidase antibody clone 6F light chain CDR3.
XX
XX Mutagenesis; Ig; immunoglobulin; FR: framework region; variable; CDR;
XX complementarity determining region; light; heavy chain; PCR;
XX polymerase chain reaction; antibody library; diversity; affinity;
XX immunospecificity; ds.
XX
XX Synthetic.
XX
XX WO9607754-A1.
XX
XX 14-MAR-1996.
XX
XX 01-SEP-1995; 95WO-US11235.
XX
XX 02-SEP-1994; 94US-0300386.
XX
XX (SCRI) SCRIPPS RES INST.
PA

XX
XX Barbas CF, Burton DR, Lerner RA;
XX WPI; 1996-171625/17.
XX
XX Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain
XX gene CDR - useful for prodn. of Ig heavy and light chain
XX combinatorial antibody libraries
XX
XX Example 9C; Page 76; 125pp; English.
XX
XX AAR99009-R99011 are light chain complementarity determining regions
XX (CDRs) 1, 2 and 3, respectively of an anti-thyroid peroxidase (TPO)
XX antibody clone 6F. Several anti-TPO clones were made using mutagenic
XX primers which induce mutations in the CDRs of the light and heavy
XX chain variable regions, the primers pref. mutate CDR3 of a human
XX Ig light chain. The mutagenic primers have sequences at their 3' and
XX 5' ends both capable of binding different framework regions linked by
XX a sequence 6 to 50 nucleotides long. Different immunoglobulins produced
XX using the primers may be used to produce antibody libraries having
XX diverse and novel immunospecificities and affinities. By using
XX mutagenic ONS an extremely large population of different randomised
XX binding sites can be created and use of the universal light chain
XX increases the number of combinations which yield functional
XX heterodimeric antibodies.
XX
XX Sequence 9 AA:
SQ
Query Match 51.0%; Score 25; DB 17; Length 9;
Best Local Similarity 62.5%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 QRYSNPNT 9
1:|||||
2 QYSTPTPT 9
DB
RESULT 10
AAR99014
ID AAR99014 standard; peptide: 9 AA.
XX
XX AAR99014;
XX
XX 24-OCT-1996 (first entry)
XX
XX Anti-thyroid peroxidase antibody clone SP1.2 light chain CDR3.
XX
XX Mutagenesis; Ig; immunoglobulin; FR: framework region; variable; CDR;
XX complementarity determining region; light; heavy chain; PCR;
XX polymerase chain reaction; antibody library; diversity; affinity;
XX immunospecificity; ds.
XX
XX Synthetic.
XX
XX WO9607754-A1.
XX
XX 14-MAR-1996.
XX
XX 01-SEP-1995; 95WO-US11235.
XX
XX 02-SEP-1994; 94US-0300386.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CF, Burton DR, Lerner RA;
XX WPI; 1996-171625/17.
XX
XX Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain
XX gene CDR - useful for prodn. of Ig heavy and light chain
XX combinatorial antibody libraries
XX
XX Example 9C; Page 76; 125pp; English.
PS

XX AAR9012-R99014 are light chain complementarity determining regions
 CC (CDRs) 1, 2 and 3, respectively of an anti-thyroid peroxidase (TPO)
 CC antibody clone SPI.2. Several anti-TPO clones were made using mutagenic
 CC primers which induce mutations in the CDRs of the light and heavy
 CC chain variable regions, the primers pref. mutate CDR3 of a human
 CC 19 light chain. The mutagenic primers have sequences at their 3' and
 CC 5' ends both capable of binding different framework regions linked by
 CC a sequence 6 to 50 nucleotides long. Different immunoglobulins produced
 CC using the primers may be used to produce antibody libraries having
 CC diverse and novel immunospecificities and affinities. By using
 CC mutagenic ONS an extremely large population of different randomised
 CC binding sites can be created and use of the universal light chain
 CC increases the number of combinations which yield functional
 CC heterodimeric antibodies.

XX Sequence 9 AA:

Query Match 51.0%; Score 25; DB 17; Length 9;

Best Local Similarity 62.5%; Pred. No. 7.8e+05;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QRSNPNT 9

DB 2 QRYSSPPT 9

RESULT 11

ID AAW62191 standard; peptide; 9 AA.

XX AAW62191;

DT 21-SEP-1998 (first entry)

XX Mouse anti-HM1.24 antibody L chain V region CDR 3.

XX Mouse; human; humanised; anti-HM1.24 antibody; myeloma; FR; CDR;

XX framework region; complementarity determining region; antigenicity.

XX Mus sp.

XX MO9814580-A1.

XX 09-APR-1998.

XX 03-OCT-1997; 97WO-JP03553.

XX 04-OCT-1996; 96JP-0264756.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Koshihara Y, Kosaka M, Ohtomo T, Ono K, Tsuchiya M;

XX Yoshimura Y;

XX WPI; 1998-286421/25.

XX Humanised anti-HM1.24 antibody - for treatment of myeloma

XX Claim 10; Page 103; 210pp; Japanese.

XX A humanised anti-HM1.24 antibody has been developed which comprises
 CC human L and H chain C regions, and L and/or H chain V regions
 CC containing material originating in mouse anti-HM1.24 antibody. The V
 CC regions contain framework (FR) regions of human origin and
 CC complementarity determining regions (CDR) of mouse origin, leading to
 CC a reshaped humanised antibody. The C regions are human Ck (L-chain) and
 CC human C gamma (especially C gamma 1) (H-chain). The FR regions of the
 CC L chain V region are derived from human subtype HSG1 (e.g. from human
 CC antibody RE1) and the FR regions of the H chain V region are derived
 CC from human subtype HSG1 (e.g. FR1-3 from human antibody Hg3 and FR4
 CC from human antibody JH6). The present sequence represents mouse L chain
 CC V region CDR 3 from the present invention. The antibodies are used for

CC the treatment of myeloma, especially by injection, intravenously,
 CC intramuscularly or subcutaneously. The antibodies are used at 0.01-1000
 CC (especially 5-100) mg/kg body weight. The humanised antibody has low
 CC antigenicity and is therefore effective therapeutically in humans.

XX Sequence 9 AA:

Query Match 51.0%; Score 25; DB 19; Length 9;

Best Local Similarity 62.5%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRSNPNT 9

DB 2 QRYSSPPT 9

RESULT 12

ID AAW57579 standard; peptide; 9 AA.

XX AAW57579;

DT 03-SEP-1998 (first entry)

XX Chimeric L chain V region CDR-3 for an antibody against hPTRP.

XX Chimeric; antibody; human parathormone related peptide; hPTRP; mouse;

XX L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;

XX hypophosphataemia; pathogen; vitamin D resistance; V region; C region;

XX humanised.

XX Synthetic.

XX Chimeric - Mus sp.

XX Chimeric - Homo sapiens.

XX WO9813388-A1.

XX 02-APR-1998.

XX 24-SEP-1997; 97WO-JP03382.

XX 24-JUL-1997; 97JP-0214168.

XX 26-SEP-1996; 96JP-0255196.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Sato K, Wakahara Y, Yabuta N;

XX WPI; 1998-230640/20.

XX New chimeric antibodies against human parathormone related

XX peptide(s) - useful for, e.g. treatment of hypercalcaemia and other

XX disorders caused by malignant neoplasms(s)

XX Claim 9; Page 124; 182pp; Japanese.

XX New antibodies have been developed which are specific for human
 CC parathormone related peptides (hPTRP). The antibodies comprise chimeric
 CC L and/or H chains, where the C region is of human and L region of mouse,
 CC origin. The present sequence represents a specifically claimed region of
 CC an antibody of the invention. Host cells, transformed with vectors
 CC containing DNA encoding antibodies of the invention, can be used to
 CC produce the antibodies. The antibodies may be used to treat
 CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of
 CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
 CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They
 CC may also be used for treatment of hypophosphataemia such as that due to
 CC pathogens or to vitamin D resistance.

XX Sequence 9 AA:

Query Match 51.0%; Score 25; DB 19; Length 9;

Best Local Similarity 62.5%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ORYSNPNT 9
 1 1 1 1 1
 Db 2 QHSTPPT 9

RESULT 13
 AAY02549
 ID AAY02549 standard; Peptide: 9 AA.

XX AC AAY02549;

XX DT 16-JUL-1999 (first entry)

XX DE Artificial CDR(3) of L chain V region of antiHML.24 antibody.

XX KW Reconstituted human antibody; peptide antigen HML.24; framework region:
 XX complementary determining region: CDR; anti-HML.24 antibody; myeloma.

XX OS Synthetic.

XX PN W09918212-A1.

XX PD 15-APR-1999.

XX PF 02-OCT-1998; 98WO-JP04469.

XX PR 03-OCT-1997; 97JP-0271726.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Tsuchiya M;

XX DR WPI: 1999-277273/23.

XX PT Reconstituted human antibody useful in the treatment of myeloma

XX PS Disclosure: Page 83; 256pp; Japanese.

XX CC The specification describes a reconstituted human antibody recognizing
 CC the peptide antigen HML.24. This human antibody contains natural human
 CC framework regions modified by amino acid substitutions to provide
 CC homogeneity with a previously designed framework region (which may
 CC arise from a human or non-human source); and complementary determining
 CC regions (CDR) derived from a non-human anti-HML.24 antibody. The
 CC reconstituted antibody is useful in the treatment of diseases in which
 CC the surface antigen HML.24 is implicated such as myeloma. The present
 CC sequence is used in the creation of the antibodies of the invention.

XX SQ Sequence 9 AA;

Query Match 51.0%; Score 25; DB 20; Length 9;
 Best Local Similarity 62.5%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ORYSNPNT 9
 1 1 1 1 1
 Db 2 QHSTPPT 9

RESULT 14
 AAW89631
 ID AAW89631 standard; peptide: 9 AA.

XX AC AAW89631;

XX DT 14-APR-1999 (first entry)

XX DE Mouse humanised antibody #23-57-137-1 light chain CDS3 peptide.

XX KW Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
 XX inhibitor; humanised.

XX OS Mus sp.
 OS Synthetic.
 XX PN W09851329-A1.

XX PD 19-NOV-1998.

XX PF 13-MAY-1998; 98WO-JP02116.

XX PR 18-JUL-1997; 97JP-0194445.

XX PR 15-MAY-1997; 97JP-0125505.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Ishii K, Sato K, Tuenari T;

XX DR WPI: 1999-070101/06.

XX PT Inhibitors of binding of parathyroid hormone related peptide to its
 XX receptor - useful for, e.g. treatment of cachexia arising from
 XX cancer or other diseases

XX PS Example 2: Page 85; 125pp; Japanese.

XX CC The present invention describes compositions for the treatment of
 XX cachexia containing a substance which inhibits the binding of a
 XX parathyroid hormone related peptide (PTHrP) to its receptor, as an
 XX active component. This substance may be an antagonist to the receptor,
 XX or an antibody (preferably monoclonal) or antibody fragment,
 XX recognising PTHrP. The antibody is preferably humanised or chimeric.
 XX The present invention also describes a humanised antibody prepared
 XX by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for
 XX the treatment of cachexia arising in connection with diseases such as
 XX cancer, thereby improving the quality of life of the patient. The
 XX present sequence represents mouse humanised antibody light chain CDS3
 XX from #23-57-137-1 from the present invention.

XX SQ Sequence 9 AA;

Query Match 51.0%; Score 25; DB 20; Length 9;
 Best Local Similarity 62.5%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ORYSNPNT 9
 1 1 1 1 1
 Db 2 QHSTPPT 9

RESULT 15
 AAY7517
 ID AAY7517 standard; peptide: 9 AA.

XX AC AAY7517;

XX DT 26-APR-2000 (first entry)

XX DE Antibody H chain V region CDR3 peptide seq ID No: 61.

XX KW Hypercalcaemic crisis; parathyroid hormone related peptide; PTHrP; tumour.

XX OS Homo sapiens.

XX PN W0200000219-A1.

XX PD 06-JAN-2000.

XX PF 25-JUN-1999; 99WO-JP03433.

XX PR 26-JUN-1998; 98JP-0180143.

XX PA (CHUS) CHUGAI SEIYAKU KK.

PI Salo K, Tsunenari T;
XX
DR WPI: 2000-117115/10.
XX Treatment of hypercalcemic crisis with a substance inhibiting binding
PT of parathyroid hormone related peptide to its receptor -
XX
XX Example 2: Page 100; 120pp; Japanese.
PS
XX The invention relates to a method of treatment of hypercalcemic crisis.
CC A composition for the treatment of hypercalcemic crisis contains as
CC active component a substance which inhibits the binding of parathyroid
CC hormone related peptide (PTHrP) to its receptor. The inhibitor is used
CC for the treatment of hypercalcemic crisis, such as that associated with
CC a malignant tumour.
XX
SQ Sequence 9 AA;
Query Match 51.0%; Score 25; DB 21; Length 9;
Best Local Similarity 62.5%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 QRYSNPNT 9
| | | | |
DB 2 QHYSTPPT 9

Search completed: February 25, 2003, 11:21:35
Job time : 35 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:20:10 ; Search time 28 Seconds

(without alignments)
66.229 Million cell updates/sec

Title: US-09-743-482a-6

Perfect score: 49

Sequence: 1 LORSNPNT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 686

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	44.9	9	8	094VC6
2	20	40.8	8	8	094VB5
3	20	40.8	8	8	094VB2
4	20	40.8	8	8	094VA7
5	20	40.8	9	12	067605
6	20	40.8	9	12	067606
7	18	36.7	8	8	09TKES
8	18	36.7	9	7	031415
9	18	36.7	9	8	09TKG1
10	18	36.7	9	8	09TKG1
11	17	34.7	8	11	062527
12	16	32.7	7	2	034028
13	16	32.7	7	2	013591
14	16	32.7	9	6	09TK77
15	16	32.7	9	12	069473
16	16	32.7	9	15	012096

17	16	32.7	9	15	012098	012098 caprine art
18	16	32.7	9	15	012100	012100 caprine art
19	16	32.7	9	15	012102	012102 caprine art
20	16	32.7	9	15	012104	012104 caprine art
21	15	30.6	8	8	035792	035792 saccharomyc
22	15	30.6	8	8	09MD43	09MD43 raltus norv
23	15	30.6	8	8	094VB2	094VB2 varanus yuw
24	14	28.6	7	2	047505	047505 escherichia
25	14	28.6	8	2	051594	051594 escherichia
26	14	28.6	8	4	09HC00	09HC00 homo sapien
27	14	28.6	8	11	08R4D8	08R4D8 mus musculu
28	14	28.6	9	4	09U0A3	09U0A3 homo sapien
29	14	28.6	9	10	08VZ23	08VZ23 pinus radia
30	14	28.6	9	11	09QW70	09QW70 mus musculu
31	13	26.5	8	2	09X3K1	09X3K1 prochloroco
32	13	26.5	8	2	09AGP4	09AGP4 arthroacte
33	13	26.5	8	2	049534	049534 mycoplasma
34	13	26.5	8	4	015893	015893 homo sapien
35	13	26.5	8	4	09Y4J3	09Y4J3 homo sapien
36	13	26.5	8	8	09Y4M4	09Y4M4 begonia for
37	13	26.5	8	8	09MSX1	09MSX1 jurinea hum
38	13	26.5	8	8	09P2Y3	09P2Y3 begonia tai
39	13	26.5	8	8	09T2Y2	09T2Y2 begonia apt
40	13	26.5	8	8	09T2Y1	09T2Y1 begonia nan
41	13	26.5	8	10	09XGL9	09XGL9 begonia chl
42	13	26.5	8	10	09XGL8	09XGL8 begonia pal
43	13	26.5	8	10	09STD5	09STD5 mus spretus
44	13	26.5	8	11	09ETI8	09ETI8 mus spretus
45	13	26.5	8	11	09ETI7	09ETI7 mus caroll

ALIGNMENTS

RESULT 1

094VC6 PRELIMINARY; PRT; 9 AA.

AC 094VC6; 01-DEC-2001 (TREMUREL. 19, Created)

DT 01-DEC-2001 (TREMUREL. 19, Last sequence update)

DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)

DE Cytochrome c oxidase subunit I (fragment).

GN COI.

OS Varanus pilbarensis.

OC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Anguilliformes; Varanus.

OX NCBI_TaxID-62048;

ON [1]

RP SEQUENCE FROM N.A.

RA Ast J.C.;

RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";

RL Cladistics 17:0-0(2001).

DR EMBL: AF407518; AAL10108.1; -.

KW Mitochondrion.

FT NON_TER

SQ SEQUENCE 9 AA; 1064 MW; 874CA5A36411A735 CRC64;

Query Match 44.9%; Score 22; DB 8; Length 9;
Best Local Similarity 57.18; Pred. No. 6.7e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LORSNP 7
Db 3 LTRWSSP 9

RESULT 2

094VB5 PRELIMINARY; PRT; 8 AA.

ID 094VB5; 01-DEC-2001 (TREMUREL. 19, Created)

DT 01-DEC-2001 (TREMUREL. 19, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Varanus salvator cuningi.
 OC Mitochondrion.
 CC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OX NCBI_TaxID=169830;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL: AF407523; AAL10122.1; .
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 8 AA; 992 MW; EFC775A5A36411A6 CRC64;

Query Match 40.8%; Score 20; DB 8; Length 8;
 Best Local Similarity 42.9%; Pred. No. 6.7e+05;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQRYSNP 7
 DB 1 MTRWSSP 7

RESULT 3

ID 094VB2 PRELIMINARY; PRT; 8 AA.
 AC 094VB2;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Varanus salvator togianus.
 CC Mitochondrion.
 CC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OX NCBI_TaxID=169832;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL: AF407524; AAL10125.1; .
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 8 AA; 992 MW; EFC775A5A36411A6 CRC64;

Query Match 40.8%; Score 20; DB 8; Length 8;
 Best Local Similarity 42.9%; Pred. No. 6.7e+05;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQRYSNP 7
 DB 1 MTRWSSP 7

RESULT 4

ID 094VA7 PRELIMINARY; PRT; 8 AA.
 AC 094VA7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Varanus salvator salvator.
 CC Mitochondrion.
 CC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OX NCBI_TaxID=169831;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL: AF407526; AAL10130.1; .
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 8 AA; 992 MW; EFC775A5A36411A6 CRC64;

OX NCBI_TaxID=169831;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL: AF407526; AAL10130.1; .
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 8 AA; 992 MW; EFC775A5A36411A6 CRC64;

Query Match 40.8%; Score 20; DB 8; Length 8;
 Best Local Similarity 42.9%; Pred. No. 6.7e+05;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQRYSNP 7
 DB 1 MTRWSSP 7

RESULT 5

ID 067605 PRELIMINARY; PRT; 9 AA.
 AC 067605;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE AL1 protein (Fragment).
 GN AL1.
 OS Squash leaf curl virus.
 CC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV-R;
 RX MEDLINE=91082450; PubMed=1984669;
 RA Lazarowitz S.G.;
 RT "Molecular characterization of two bipartite geminiviruses causing squash leaf curl disease: Role of viral replication and movement functions in determining host range.";
 RT Virology 180:70-80(1991).
 DR EMBL: M63155; AAA47823.1; .
 FT NON_TER
 SQ SEQUENCE 9 AA; 1118 MW; 2B30D5B457645417 CRC64;

Query Match 40.8%; Score 20; DB 12; Length 9;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 NPNT 9
 DB 4 NPNS 7

RESULT 6

ID 067606 PRELIMINARY; PRT; 9 AA.
 AC 067606;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE AL1 protein (Fragment).
 GN AL1.
 OS Squash leaf curl virus.
 CC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV-E;
 RX MEDLINE=91082450; PubMed=1984669;
 RA Lazarowitz S.G.;
 RT "Molecular characterization of two bipartite geminiviruses causing squash leaf curl disease: Role of viral replication and movement

RT functions in determining host range."
 RL Virology 180:70-80(1991).
 DR EMBL: M63157; AAA47822.1; -
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1118 MW; 2B30D5B457645417 CRC64;

Query Match 40.8%; Score 20; DB 12; Length 9;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 NPNT 9
 DB 4 NPNT 7

RESULT 7
 O9TKES PRELIMINARY; PRT; 8 AA.
 AC O9TKES; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE ATPB (Fragment).
 GN ATPB.
 OS Leptospermum erubescens.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Myrtaceae; Leptospermum.
 OX NCBI_TaxID=106049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
 RL Aust. J. Bot. 48:0-0(2000).
 DR EMBL: AF184690; AAF03860.1; -
 KW Chloroplast.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 876 MW; ECA1B1B764405056 CRC64;

Query Match 36.7%; Score 18; DB 8; Length 8;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 NPNT 9
 DB 4 NPNT 7

RESULT 8
 O31415 PRELIMINARY; PRT; 9 AA.
 ID O31415;
 AC O31415;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-JAN-1999 (TREMBlrel. 01, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE MHC class I antigen (Fragment).
 OX Gallus gallus (Chicken).
 OS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kanki T., Kuwasawa N., Sekiya Y., Ichikawa Y.;
 RT "Responsive expression of a MHC class I epitope and genes following
 Marek's disease virus infection."
 RL Submitted (JAN-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D90399; BA14395.1; -
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 859 MW; 8A55A76455B861B5 CRC64;

Query Match 36.7%; Score 18; DB 7; Length 9;

Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 SNPN 8
 DB 5 SNPN 8

RESULT 9
 O9TKG1 PRELIMINARY; PRT; 9 AA.
 AC O9TKG1;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE ATPB (Fragment).
 GN ATPB.
 OS Calothamnus validus.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Myrtaceae; Calothamnus.
 OX NCBI_TaxID=106037;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
 RL Aust. J. Bot. 48:0-0(2000).
 DR EMBL: AF184667; AAF03837.1; -
 KW Chloroplast.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1075 MW; 712CA1B1B7644044 CRC64;

Query Match 36.7%; Score 18; DB 8; Length 9;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 NPNT 9
 DB 4 NPNT 7

RESULT 10
 O9TKD9 PRELIMINARY; PRT; 9 AA.
 ID O9TKD9;
 AC O9TKD9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE ATPB (Fragment).
 GN ATPB.
 OS Pericalymma crassipes.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Myrtaceae; Pericalymma.
 OX NCBI_TaxID=106067;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
 RL Aust. J. Bot. 48:0-0(2000).
 DR EMBL: AF184701; AAF03870.1; -
 KW Chloroplast.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1044 MW; 77EE31B1B7644044 CRC64;

Query Match 36.7%; Score 18; DB 8; Length 9;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 NPNT 9
 DB 4 NPNT 7

DB 4 NPPT 7

RESULT 11

ID 062527 PRELIMINARY: PRT: 8 AA.

AC 062527; 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE Transhyelin (Prealbumin) (Fragment).
 GN TTR.
 OS Mus. spretus (Western wild mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10096;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRET/ET;
 RX MEDLINE=94319082; PubMed=8043949;
 RA Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maezaki Y.,
 Nadeau J.H.;
 RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR."
 RL Mamm. Genome 5:349-355(1994).
 CC -1- FUNCTION: THYROID HORMONE-BINDING PROTEIN. PROBABLY TRANSPORTS
 CC THYROXINE FROM THE BLOODSTREAM TO THE BRAIN.
 CC -1- SUBUNIT: HOMOTETRAMER.
 DR EMBL: U05689; AAB60461.1; -.
 DR MGD: MGI:98865; Ttr.
 KW Albumin; Transport; Retinol-binding; Vitamin A; Thyroid hormone.
 FT NON_TER
 SQ SEQUENCE 8 AA; 828 MW; 9156C76455A2D2CD CRC64;

Query Match 34.7%; Score 17; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12

ID 034028 PRELIMINARY: PRT: 7 AA.

AC 034028; 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Catechol-2,3-dioxygenase (Fragment).
 GN PHE.
 OS Sphingomonas chungbukensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 OC Sphingomonas.
 OX NCBI_TaxID=56193;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=DJ77;
 RL Kim Y.-C.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U88298; AAB66311.1; -.
 KW Dioxygenase.
 FT NON_TER
 SQ SEQUENCE 7 AA; 868 MW; 71A452D1A699D460 CRC64;

Query Match 32.7%; Score 16; DB 2; Length 7;
 Best Local Similarity 42.9%; Pred. NO. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 RYSNPNT 9
 DB 1 RFTVNT 7

RESULT 13

ID 013591 PRELIMINARY: PRT: 8 AA.

AC 013591; 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE ORF YNL337W (Fragment).
 GN YNL337W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
 OX NCBI_TaxID=4932;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Obermaier B., Piravandi E., Rinke M.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z71612; CA96271.2; -.
 DR SGD: S0005281; YNL337W.
 FT NON_TER
 SQ SEQUENCE 8 AA; 1005 MW; 5CA441E449C9C720 CRC64;

Query Match 32.7%; Score 16; DB 3; Length 8;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 YSNPNT 9
 DB 3 FNNHT 8

RESULT 14

ID 09T77 PRELIMINARY: PRT: 9 AA.

AC 09T77; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Wilm's tumor protein 1 (Fragment).
 GN WT1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21015404; PubMed=11130975;
 RA Brouillette J.A., Andrew J.R., Venta P.J.;
 RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
 method."
 RL Mamm. Genome 11:1079-1086(2000).
 DR EMBL: AF202074; AAF20919.1; -.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1231 MW; 58DDF41416D1F403 CRC64;

Query Match 32.7%; Score 16; DB 6; Length 9;
 Best Local Similarity 33.3%; Pred. NO. 6.7e+05;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 LQRYSNPNT 9
 DB 1 LKRRORRHT 9

RESULT 15

ID 069473


```

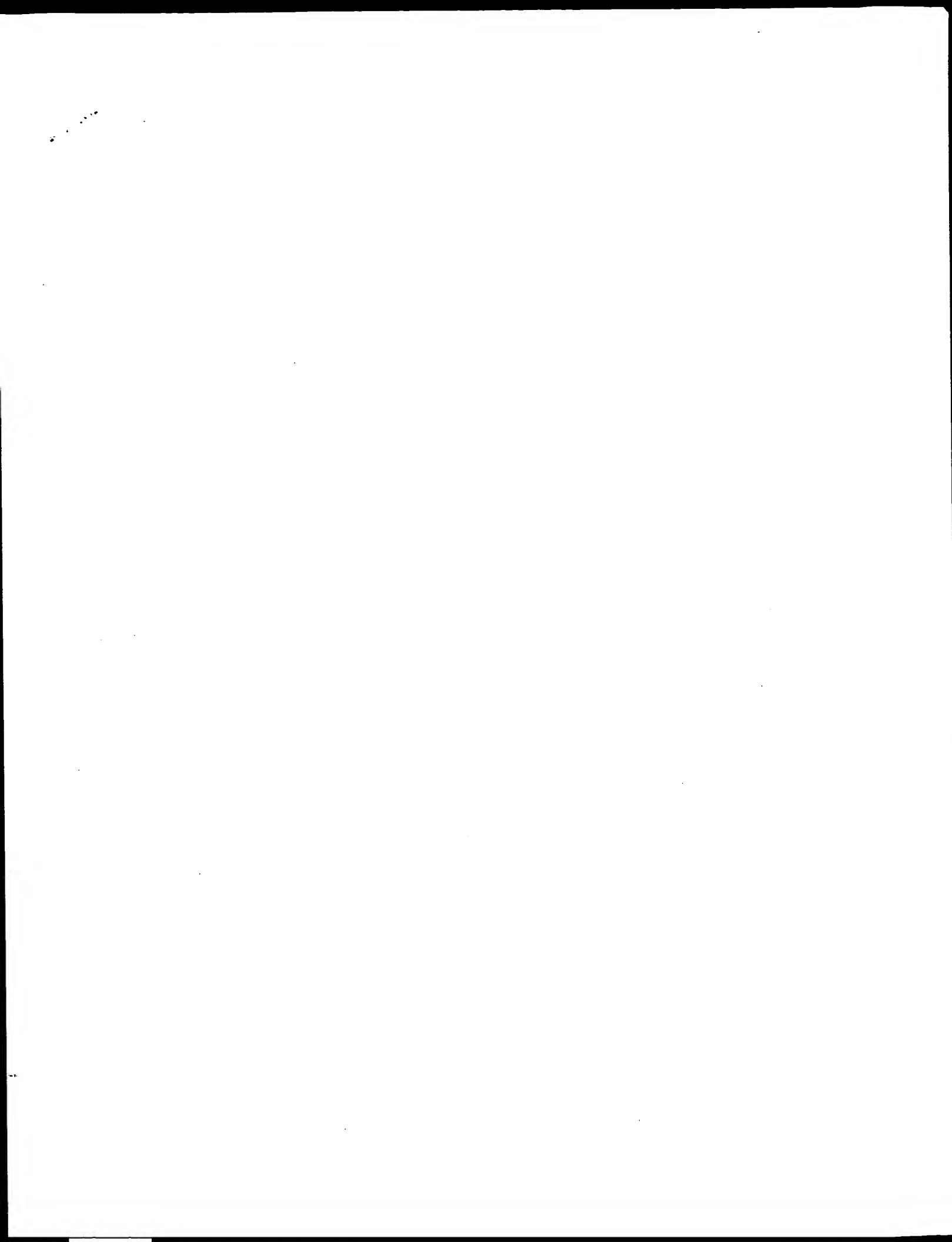
ID 069473      PRELIMINARY;      PRT;      9 AA.
AC 069473;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Immediate-early transactivator 110 (Fragment).
GN ICP0.
OS human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MP;
RX PubMed=11725047;
RA Chang Y., Jeang K., Lietman T., Hayward G.S.;
RT "Structural Organization of the Spliced Immediate-Early Gene Complex
RT that Encodes the Major Acidic Nuclear (IE1) and Transactivator (IE2)
RT Proteins of African Green Monkey Cytomegalovirus.";
RL J. Biomed. Sci. 2:105-130(1995).
DR EMBL; U18080; AAA75442.1; -.
FT NON_TER      1
FT NON_TER      1
SQ SEQUENCE      9 AA; 1029 MW; 797BB867740DDB04 CRC64;

Query Match      32.7%; Score 16; DB 12; Length 9;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ORYSNP 7
DB 1 QREARP 6

```

Search completed: February 25, 2003, 11:22:27
 Job time : 30 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:18:04 ; Search time 10 seconds

(without alignments)
37.329 Million cell updates/sec

Title: US-09-743-482a-6
Perfect score: 49
Sequence: 1 LQRYSNPNT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 231

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	38.8	7	1	CHOX_ALCSP
2	18	36.7	8	1	FAR1_PANRE
3	15	30.6	7	1	MNP1_LEPDE
4	15	30.6	7	1	FAR2_PANRE
5	14	28.6	6	1	VP19_HSVIK
6	14	28.6	8	1	HTF1_PERAM
7	14	28.6	7	1	HTF_TENMO
8	13	26.5	6	1	TMOF_SARBU
9	13	26.5	7	1	AL15_CARMA
10	13	26.5	7	1	FAR4_PANRE
11	13	26.5	7	1	UN06_PINPS
12	13	26.5	8	1	ANG2_BOTUA
13	13	26.5	8	1	HTF2_PERAM
14	13	26.5	8	1	NPR_BOVIN
15	13	26.5	8	1	UF06_MOUSE
16	13	26.5	8	1	UF09_RAT
17	13	26.5	9	1	BUR_CLOPA
18	13	26.5	9	1	FAR4_CALVO
19	13	26.5	9	1	FARA_CALVO
20	13	26.5	9	1	MGMT_BOVIN
21	13	26.5	9	1	URAF6_HUMAN
22	12	24.5	5	1	FARP_ARTTR
23	12	24.5	5	1	PRCT_PERAM
24	12	24.5	8	1	AL17_CARMA
25	12	24.5	9	1	LPCA_STAV
26	12	24.5	9	1	YBFR_AZOVI
27	11	22.4	6	1	AL14_CARMA
28	11	22.4	6	1	UN06_CLOPA
29	11	22.4	7	1	ICAO_DACOE
30	11	22.4	8	1	AKH_MEIML
31	11	22.4	8	1	AL15_CARMA
32	11	22.4	8	1	AL16_CARMA
33	11	22.4	8	1	AL18_CARMA

34	11	22.4	8	1	ALL3_CYPDO	P82154 cydia pomon
35	11	22.4	8	1	ALL4_CALVO	P41840 calliphora
36	11	22.4	8	1	ALL4_CYPDO	P82155 cydia pomon
37	11	22.4	8	1	B44K_PORGI	P81886 porphyromon
38	11	22.4	8	1	FAR4_HOMAM	P41487 homarus ame
39	11	22.4	8	1	LCK8_LEUMA	P19990 leucophaea
40	11	22.4	9	1	ALL0_CARMA	P81813 carcius ma
41	11	22.4	9	1	OXYA_SCYCA	P42996 scyllorhinu
42	11	22.4	9	1	OXYA_SQUCA	P42999 squalus aca
43	11	22.4	9	1	OXYF_SCYCA	P42997 scyllorhinu
44	11	22.4	9	1	TAL3_PICCA	P17441 picchia jadi
45	11	22.4	9	1	ULAD_HUMAN	P31929 homo sapien

ALIGNMENTS

RESULT 1

CHOX_ALCSP
ID CHOX_ALCSP STANDARD: PRT: 7 AA.
AC P16101:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Alcaligenes.
OX NCBI_TaxID=512;
RN [1]

RP MEDLINE=81006769; PubMed=6997283;
RA Ohta-Fukuyama M., Miyake Y., Eml S., Yamano T.;
RT "Identification and properties of the prosthetic group of choline
oxidase from Alcaligenes sp.";
RL J. Biochem. 88:197-203(1980).
CC -I- CATALYTIC ACTIVITY: Choline + O(2) -> betaine aldehyd + H(2)O(2).
DR PIR: A15398; A15398.
KW Oxidoreductase.
FT NON_TER
SQ SEQUENCE 7 AA: 839 MW: 741581E457644AC0 CRC64;

Query Match 38.8%; Score 19; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NPN 8
Db 2 NPN 4

RESULT 2
FAR1_PANRE
ID FAR1_PANRE STANDARD: PRT: 8 AA.

AC P41872;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide PFI (SDPNLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdittida;
OC Panagrellidae; Panagrellinae; Panagrelliinae; Panagrellus.
OX NCBI_TaxID=6233;

RN [1]

RP MEDLINE=93027659; PubMed=1408999;

RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,

Garison R.D., Williams J.F., Friedman A.R.;

RT "Two FMRFamide-like peptides from the free-living nematode

Panagrellus redivivus";

Peptides 13:209-214(1992).

CC -I- FUNCTION: MYOACTIVE.

-I- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED

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CC CAUDALLY TO THE BASE OF THE PHARYNX.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; Amidation.
KM MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA: 995 MW: 66D40729C4576AB5 CRC64:

Query Match 36.7%; Score 18; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 SNP 8
   1:11
Db 1 SDPN 4

RESULT 3
MNPL_LEPDE STANDARD; PRT: 7 AA.
ID MNPL_LEPDE
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE MYOTROPIC NEUROPEPTIDE 1 (Led-MNP-1).
OS Leptinotarsa decemlineata (Colorado potato beetle).
CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
CC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
CC Cucujiformia; Phytophaga; Chrysomeloidea; Chrysomelidae;
CC Chrysomellinae; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=95380343; PubMed=7651886;
RA Spiltzels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leuven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotropic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata."
RL Peptides 16:365-374(1995).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
CC Neuropeptide; Amidation.
KM MOD_RES 7 7 AMIDATION.
FT SEQUENCE 7 AA: 705 MW: 6DD73768745B5DB0 CRC64:
SQ SEQUENCE 7 AA: 705 MW: 6DD73768745B5DB0 CRC64:

Query Match 30.6%; Score 15; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 YSNP 7
   1:1
Db 2 YNCP 5

RESULT 4
FAR2_PANRE STANDARD; PRT: 9 AA.
ID FAR2_PANRE
AC P41873;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide PF2 (SADPNFLRF-amide).
OS Panagrellus redivivus.
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
CC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE.
RX MEDLINE=93027659; PubMed=1408999;
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
RA Garlison R.D., Williams J.F., Friedman A.R.;
RT "Two FMRFamide-like peptides from the free-living nematode

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RT Panagrellus redivivus."
RL Peptides 13:209-214(1992).
CC -1- FUNCTION: MYOACTIVE.
CC -1- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
CC CAUDALLY TO THE BASE OF THE PHARYNX.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KM Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1066 MW: DA0B0729C4576AAD CRC64:

Query Match 30.6%; Score 15; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 SNP 8
   1:11
Db 2 ADPN 5

RESULT 5
VP19_HSV1K STANDARD; PRT: 6 AA.
ID VP19_HSV1K
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Capsid assembly and DNA maturation protein (Virion protein UL38)
DE (Capsid protein VP19c) (Fragment).
GN UL38.
OS Herpes simplex virus (type 1 / strain KOS).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly."
RL J. Virol. 65:769-786(1991).
CC -1- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSID ARE
CC EMBEDDED. BINDS DNA.
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M57646; AAA45830.1;
KM Capsid assembly; Coat protein; DNA-binding.
FT NON_TER 6 6
SQ SEQUENCE 6 AA: 703 MW: 67376451A336F000 CRC64:

Query Match 28.6%; Score 14; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 SNP 7
   1:1
Db 3 TNP 5

RESULT 6
HTFL_PERAM STANDARD; PRT: 8 AA.
ID HTFL_PERAM
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)

```

DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypertrihaloasemic factor I (Neuropeptide M-I) (Periplaneta CC-1)
 DE (Per-CAH-1) (led-CC-1) (Hypertrihaloasemic neuropeptide I).
 OS Periplaneta americana (American cockroach),
 OS Lepidoptera decemlineata (Colorado potato beetle), and
 OS Blatta orientalis (Oriental cockroach).
 OC Eukaryota: Metazoa: Arthropoda: Mandibulata: Pancrustacea: Hexapoda:
 OC Insecta: Pterygota: Neoptera: Orthopteroidea: Dictyoptera: Blattaria:
 OC Blattodea: Blattidae: Periplaneta.
 OX NCBI_Taxid=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P. americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L. Jr.,
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry".
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P. americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarbrough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.,
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana".
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L. decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.,
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical".
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=B. orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.,
 RT "Primary structures of hypertrihaloasemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gryllodromia portosa, Blattella germanica and Blatta orientalis
 RT and of the stick insect Extradosia tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry".
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: HYPERTRIHALOASEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / RPH / RPH FAMILY.
 DR PIR: A05169; A05169.
 DR PIR: S08995; S08995.
 DR PIR: A49823; A49823.
 DR PIR: A44960; A44960.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1
 FT MOD_RES 8 8
 FT SEQUENCE 8 AA: 991 MW; 86745775B9C452D6 CRC64;
 SQ PYRROLIDONE CARBOXYLIC ACID.
 AMIDATION.
 PYRROLIDONE CARBOXYLIC ACID.
 Query Match 28.6%; Score 14; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 HTF_TEMNO
 ID HTF_TEMNO STANDARD; PRT; 8 AA.
 AC P25419;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypertrihaloasemic factor (HOTH) (Hypertrihaloasemic neuropeptide).
 OS Tenebrio molitor (Yellow mealworm), and
 OS Zophobas rugipes.
 OC Eukaryota: Metazoa: Arthropoda: Mandibulata: Pancrustacea: Hexapoda:
 OC Insecta: Pterygota: Neoptera: Endopterygota: Coleoptera: Polyphaga:
 OC Cucujiformia: Tenebrionidae: Tenebrio.
 OX NCBI_Taxid=7067, 7073;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90341081; PubMed=2381871;
 RA Gaede G., Rosinski G.,
 RT "The primary structure of the hypertrihaloasemic neuropeptide from
 RT tenebrionid beetles: a novel member of the AKH/RPH family".
 RL Peptides 11:455-459(1990).
 CC -1- FUNCTION: HYPERTRIHALOASEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / RPH / RPH FAMILY.
 DR PIR: A43976; A43976.
 DR PIR: B43976; B43976.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1
 FT MOD_RES 8 8
 FT SEQUENCE 8 AA: 1005 MW; 86745775B9C44736 CRC64;
 SQ PYRROLIDONE CARBOXYLIC ACID.
 AMIDATION.
 PYRROLIDONE CARBOXYLIC ACID.
 Query Match 28.6%; Score 14; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 28.6%; Score 14; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 TMOF_SARBU
 ID TMOF_SARBU STANDARD; PRT; 6 AA.
 AC P41495;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Trypsin-modulating oostatic factor (TMOF).
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota: Metazoa: Arthropoda: Mandibulata: Pancrustacea: Hexapoda:
 OC Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Brachyera:
 OC Muscomorpha: Oestroidea: Sarcophagidae: Sarcophaga.
 OX NCBI_Taxid=7385;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=ovary;
 RX MEDLINE=94211930; PubMed=8159807;
 RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
 RA de Loof A.,
 RT "Sequencing and characterization of trypsin modulating oostatic
 RT factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
 RT (Sarcophaga) bullata".
 RL Regul. Pept. 50:61-72(1994).
 CC -1- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
 CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
 CC CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
 CC DEVELOPMENT.
 CC -1- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
 CC EPITHELIUM AFTER A BLOOD MEAL.

KW Hormone.
SQ SEQUENCE 6 AA: 695 MW: 61E72451B7642000 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NP 7
DB 1 NP 2

RESULT 9

ALIS_CARMA STANDARD; PRT: 7 AA.

ID ALIS_CARMA
AC P81808;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Carcinustatin 5
OS Carcinus maenas (Common shore crab) (Green crab)
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_Taxid=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duye H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 7
FT MOD_RES 7
SQ SEQUENCE 7 AA: 781 MW: 672879CDBA76420 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NP 7
DB 1 NP 2

RESULT 10

FAR4_PANRE STANDARD; PRT: 7 AA.

ID FAR4_PANRE
AC P41875;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide pp4 (KPNIRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimidae; Panagrolaimidae; Panagrellus.
OX NCBI_Taxid=6233;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95232026; PubMed=7716079;
RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
RA Thim L., Kublik T.W., Martin R.A., Geary T.G.;
RT "Isolation and preliminary biological characterization of
RT KPNIRFamide, a novel FMRFamide-related peptide from the free-living
RT nematode, Panagrellus redivivus.";
RL Peptides 16:87-93(1995).
CC -1- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT
CC MUSCLE TENSION INCREASE.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)

CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA: 921 MW: 69D40059CA576350 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PN 8
DB 2 PN 3

RESULT 11

UN06_PINPS STANDARD; PRT: 7 AA.

ID UN06_PINPS
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_Taxid=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Plomieu C., Bauw G., Dubos C., Bahman N., Kremer A.,
RA Frigerio J.-M., Plomieu C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA: 823 MW: 69D7672448B5740 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 YSN 6
DB 2 YSN 4

RESULT 12

ANG2_BOTJA STANDARD; PRT: 8 AA.

ID ANG2_BOTJA
AC O10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Bothrops jararaca; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Scleroglossa; Serpentes; Colubroidae;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_Taxid=8724;
RN [1]
RP SEQUENCE.
RX MEDLINE=96208937; PubMed=8829801;
RA Bogheres R.A.M.B., Dalle Lucce J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC Interpro: IPR000215; Serpin.

DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT NON_TER 8
 SQ SEQUENCE 8 AA: 1046 MW: DDD761E04B42D40A CRC64;

Query Match 26.5%; Score 13; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 YSNP 7
 DB 4 YINP 7

RESULT 13
 HTF2_PERAM
 ID HTF2_PERAM STANDARD; PRT; 8 AA.
 AC P04549;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hyperthrehalosaeamic factor II (Neuropeptide M-II) (Periplaneta CC-2)
 DE (Pea-CAH-II) (led-CC-II) (Hyperthrehalosaeamic neuropeptide II).
 OS Periplaneta americana (American cockroach),
 OS Lepidoptera decemlineata (Colorado potato beetle), and
 OS Blattella orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pearygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RC MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L., Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry."
 RT Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RL [2]
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RC MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana."
 RT Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RL [3]
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RC MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RT "Type metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical."
 RT Peptides 10:1287-1289(1989).
 RL [4]
 RN [4]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RC MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L., Jr.;
 RT "Primary structures of hyperthrehalosaeamic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gryllotalpa porteri, Blattella germanica and Blattella orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry."
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: HYPERTHREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: A05170; A05170.

DR PIR: S08996; S08996.
 DR PIR: B4960; B4960.
 DR PIR: B49823; B49823.
 DR InterPro: IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 1006 MW: 86745771A9D1A736 CRC64;
 PYRROLIDONE CARBOXYLIC ACID.
 AMIDATION.

Query Match 26.5%; Score 13; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PN 8
 DB 6 PN 7

RESULT 14
 NPB_BOVIN
 ID NPB_BOVIN STANDARD; PRT; 8 AA.
 AC P15507;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE Neuropeptide B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RC MEDLINE=86067985; PubMed=3865193;
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
 RT "Isolation, sequencing, synthesis, and pharmacological
 RT characterization of two brain neuropeptides that modulate the action
 RT of morphine."
 RT Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
 RL [1]
 RN [1]
 RP FUNCTION: MODULATES THE ACTION OF MORPHINE.
 CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
 DR PIR: B24749; B24749.
 KW Neuropeptide; Amidation.
 FT MOD_RES 5
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 1082 MW: 87d416c776d9c729 CRC64;
 TO NEUROPEPTIDE A (AA 5-8) (IDENTICAL).
 AMIDATION.

Query Match 26.5%; Score 13; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 QRY 4
 DB 6 QRF 8

RESULT 15
 UF06_MOUSE
 ID UF06_MOUSE STANDARD; PRT; 8 AA.
 AC P38644;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RC MEDLINE=95009907; PubMed=7523108;

RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.:
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
FT NON_TER 8
SQ SEQUENCE 8 AA: 817 MW: A35DD878676B05B1 CRC64:

Query Match 26.5%; Score 13; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSNP 7
DB 1 HSEP 4

Search completed: February 25, 2003, 11:21:51
Job time : 10 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:21:10 : Search time 15 seconds
(without alignments)
57.681 Million cell updates/sec

Title: US-09-743-482a-6
Perfect score: 49
Sequence: 1 LQRYSNPNT 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 789

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	22	44.9	8	P00701	unidentified 6.5/3
2	19	38.8	7	A15398	choline oxidase (E
3	19	38.8	8	A4117	acetylcholinestera
4	18	36.7	7	I50210	gene c-rel protein
5	18	36.7	9	J00914	MHC class I histoc
6	17	34.7	8	S71919	alcohol dehydrogen
7	17	34.7	8	I49404	prealbumin - weste
8	17	34.7	9	S66608	guinoline 2-oxidor
9	17	34.7	9	PT0299	Ig heavy chain CRD
10	16	32.7	9	JF0073	ribosomal protein
11	16	32.7	9	G56978	collagen alpha 1(I
12	16	32.7	9	P00443	3-oxoacid CoA-tran
13	15	30.6	6	A44916	mosquitocidal toxi
14	15	30.6	9	PH0921	T-cell receptor be
15	14	28.6	5	I38964	ribosomal protein
16	14	28.6	5	I39966	ribosomal protein
17	14	28.6	5	I39965	microcin C7 - Esch
18	14	28.6	7	S45311	hypertrehalosemic
19	14	28.6	8	S08995	adipokinetic hormo
20	14	28.6	8	A49823	neuropeptide Led-C
21	14	28.6	8	A44960	hypertrehalosemic
22	14	28.6	8	A43976	hypertrehalosemic
23	14	28.6	8	B43976	chitin-binding pro
24	14	28.6	8	S22428	inulinase (EC 3.2.
25	14	28.6	8	PT0030	neuropeptide M-I
26	14	28.6	8	A05169	protamine PI - Cer
27	13	26.5	4	I61883	protamine PI - sav
28	13	26.5	4	I37013	
29	13	26.5	4	I84439	

30	13	26.5	6	P00008	angiotensin-conver
31	13	26.5	6	I37027	protamine PI - gor
32	13	26.5	7	S21230	dermorhin (Trp-4,
33	13	26.5	7	PT0087	ribulose-bisphosph
34	13	26.5	7	I56695	hypothetical L2 pr
35	13	26.5	8	S08996	hypertrehalosemic
36	13	26.5	8	B49823	adipokinetic hormo
37	13	26.5	8	B44960	neuropeptide B - b
38	13	26.5	8	B24749	neuropeptide 8 - b
39	13	26.5	8	A42689	major postsynaptic
40	13	26.5	9	A61357	phyllocaerulein -
41	13	26.5	9	S63491	dissimilatory sulf
42	13	26.5	9	S70345	amine oxidase (cop
43	13	26.5	9	A44787	calliFERamide 10
44	13	26.5	9	D41978	calliFERamide 4 -
45	13	26.5	9	PT0288	Ig heavy chain CRD

ALIGNMENTS

RESULT 1

P00701 unidentified 6.5/3IK protein [imported] - rice (fragment)

C:Species: Oryza sativa (rice)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: P00701

R:Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A:Title: A rice protein library; a data-file of rice proteins separated by two-dimens

A:Reference number: P00696

A:Accession: P00701

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <KOM>

Query Match 44.9%; Score 22; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 2; Indels 1; Gaps 0;

QY 4 YSNPNT 9

DB 1 YGNPVT 6

RESULT 2

A15398 choline oxidase (EC 1.1.3.17) - Alcaligenes sp. (tentative sequence) (fragment)

C:Species: Alcaligenes sp.

C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000

C:Accession: A15398

R:Ohita-Fukuyama, M.; Miyake, Y.; Eml, S.; Yamano, T.

J. Biochem. 88, 197-203, 1980

A:Title: Identification and properties of the prosthetic group of choline oxidase fro

A:Reference number: A15398; MUID:81006769; PMID:6997283

A:Accession: A15398

A:Molecule type: protein

A:Residues: 1-7 <OHT>

C:Keywords: oxidoreductase

Query Match 38.8%; Score 19; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NPN 8

DB 2 NPN 4

RESULT 3

A4117 acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)

C:Species: Naja naja oxilana (Asian cobra, Oxa cobra)

C>Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 23-Jun-1993
C:Accession: A4117
R:Kreienkamp, H.J.; Weise, C.; Raba, R.; Avviksaar, A.; Huch, F.
Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
A:Title: Anticatalytic center of acetylcholinesterase from Torpedo
A:Reference number: A4117; MID:91296772; PMID:2068091
A:Accession: A4117
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <KRP>
C:Keywords: carboxylic ester hydrolase

Query Match 38.8%; Score 19; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NPN 8
DB 6 NPN 8

RESULT 4
150210
gene c-rel protein - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Feb-1997
C:Accession: 150210
R:Kobayashi, N.; Bumstead, N.; Hayman, M.J.; Enrietto, P.J.
Mol. Cell. Biol. 10, 4788-4794, 1990
A:Title: Characterization of a novel promoter insertion in the c-rel locus.
A:Reference number: 150210; MID:9035595; PMID:2167440
A:Accession: 150210
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <KAB>
A:Cross-references: GB:M55577; NID:955438; PID:9211061
C:Genetics:
A:Gene: c-rel

Query Match 36.7%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PNT 9
DB 5 PNT 7

RESULT 5
JQ0914
MHC class I histocompatibility antigen heavy chain - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Feb-1995
C:Accession: JQ0914
R:Kanki, T.; Kuwasawa, N.; Sekiya, Y.; Ichikawa, Y.
Submitted to JIPID, May 1991
A:Description: Responsive expression of a MHC class I epitope and genes following Marek
A:Reference number: JQ0914
A:Accession: JQ0914
A:Molecule type: mRNA
A:Residues: 1-9 <KAN>
A:Experimental source: kidney, strain cornell N

Query Match 36.7%; Score 18; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 SNP 8
DB 5 SNPS 8

RESULT 6

S71919
alcohol dehydrogenase (EC 1.1.1.1) - grass carp (fragment)
C:Species: Ctenopharyngodon idella (grass carp)
C>Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999
C:Accession: S71919
R:Tsuji, H.T.; Mock, W.Y.; Lau, K.K.; Fong, W.P.
Biochim. Biophys. Acta 1296, 41-46, 1996
A:Title: Proteolytic activation of grass carp (Ctenopharyngodon idella) liver alcohol
A:Reference number: S71919; MID:96350418; PMID:8765227
A:Accession: S71919
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <TSU>
A>Note: the source is designated Ctenopharyngodon idella
C:Keywords: NAD; oxidoreductase

Query Match 34.7%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 SNPT 9
DB 1 SDPT 5

RESULT 7
149404
prenalbumin - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: 149404
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau,
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: 148934; MID:94319082; PMID:8043945
A:Accession: 149404
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <RES>
A:Cross-references: EMBL:U05689; NID:9497008; PID:AA860461.1; PID:9642825

Query Match 34.7%; Score 17; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SNP 7
DB 4 SNP 6

RESULT 8
S66608
quinoline 2-oxidoreductase gamma chain - Comamonas testosteroni (fragment)
C:Species: Comamonas testosteroni
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S66608
R:Schach, S.; Tshisuka, B.; Fetzner, S.; Lingsens, F.
Eur. J. Biochem. 232, 536-544, 1995
A:Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase fr
A:Reference number: S66606; MID:96035889; PMID:7556204
A:Accession: S66608
A:Molecule type: protein
A:Residues: 1-9 <SCH>
A:Experimental source: strain 63

Query Match 34.7%; Score 17; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 LQRTSNP 7
DB 2 IQAKNP 8

RESULT 9
PT0299
Ig heavy chain CRD3 region (clone 5-103B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0299
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0299
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 34.7%; Score 17; DB 2; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSN 6
|||
Db 6 YSN 8

RESULT 10
JP0073
ribosomal protein L32 - leuconostoc mesenteroides (fragment)
C:Species: Leuconostoc mesenteroides
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
C:Accession: JP0073
R:Ochi, K.
submitted to JIPID, February 1994
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pr
A:Reference number: JP0042
A:Accession: JP0073
A:Molecule type: protein
A:Residues: 1-9 <OCH>
C:Keywords: protein biosynthesis; ribosome

Query Match
Best Local Similarity 32.7%; Score 16; DB 2; Length 9;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 SNPT 9
|||
Db 4 SNKNS 8

RESULT 11
G56978
collagen alpha 1(I) chain - bovine (fragment)
N:Alternate names: collagen alpha 3(XI) chain
C:Species: Bos primigenius taurus (cattle)
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995
C:Accession: G56978
R:Wu, J.J.; Eyre, D.R.
J. Biol. Chem. 270, 18865-18870, 1995
A:Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Ins
A:Reference number: A56978; MUID:95370194; PMID:7642541
A:Accession: G56978
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <WDA>
A>Note: the residue designated 'X' is modified lysine in collagen 3(XI) some cross-link

Query Match
Best Local Similarity 32.7%; Score 16; DB 2; Length 9;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 QRYSNPN 8
|||
Db 1

Db 2 QREXGPD 8

RESULT 12
PD0443
3-oxoacid CoA-transferase (EC 2.8.3.5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999
C:Accession: PD0443
R:Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.
submitted to JIPID, August 1998
A:Description: Proteome analysis of mouse brain.
A:Reference number: PD0441
A:Accession: PD0443
A:Contents: Striatum
A:Molecule type: protein
A:Residues: 1-9 <KAW>
C:Keywords: CoA-transferase

Query Match
Best Local Similarity 32.7%; Score 16; DB 2; Length 9;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSNP 7
||:|
Db 4 YTD P 7

RESULT 13
A44916
mosquitocidal toxin 21 - Bacillus sphaericus (fragment)
C:Species: Bacillus sphaericus
C:Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: A44916
R:Thanabalu, T.; Hindley, J.; Berry, C.
J. Bacteriol. 174, 5051-5056, 1992
A:Title: Proteolytic processing of the mosquitocidal toxin from Bacillus sphaericus S
A:Reference number: A44916; MUID:92332441; PMID:1352768
A:Accession: A44916
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-6 <THA>
A:Experimental source: SSII-1
A>Note: sequence extracted from NCBI backbone (NCBIP:108973)

Query Match
Best Local Similarity 30.6%; Score 15; DB 2; Length 6;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 SNPN 8
:|||
Db 3 ASPN 6

RESULT 14
PH0921
T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0921
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0921
A:Molecule type: mRNA
A:Residues: 1-9 <GOL>
A:Experimental source: concanavalin A-activated lymphoblast
C:Keywords: T-cell receptor

Query Match
Best Local Similarity 30.6%; Score 15; DB 2; Length 9;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 SNPNT 9
1: 11
Db 3 SSENT 7

RESULT 15

139964
ribosomal protein S4 - Bacillus circulans (fragment)
C:Species: Bacillus circulans
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: 139964
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: 139963; MUID:93015735; PMID:1400226
A:Accession: 139964
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99041; NID:g143471
C:Genetics:
A:Gene: rpsD

Query Match 28.6%; Score 14; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQRY 5
1: 11
Db 1 MARYT 5

Search completed: February 25, 2003, 11:23:08
Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:09:48 ; Search time 131 seconds
(without alignments)

34.451 Million cell updates/sec

Title: US-09-743-482A-4

Sequence: 1 SATSLAD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 174137

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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27: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	7	US-09-743-482A-4	Sequence 4, Appl1
2	27	87.1	7	US-08-053-451A-69	Sequence 69, Appl1
3	27	87.1	7	US-08-053-451A-77	Sequence 77, Appl1
4	27	87.1	7	US-08-336-525-69	Sequence 69, Appl1
5	27	87.1	7	US-08-336-525-77	Sequence 77, Appl1
6	27	87.1	7	US-08-336-525A-69	Sequence 69, Appl1

7	27	87.1	7	US-08-336-525A-77	Sequence 77, Appl1
8	27	87.1	7	US-08-480-120-9	Sequence 9, Appl1
9	27	87.1	7	US-09-647-468-137	Sequence 137, Appl1
10	25	80.6	7	PCT-US98-04644-6	Sequence 6, Appl1
11	25	80.6	7	US-09-293-854-6	Sequence 6, Appl1
12	25	80.6	7	US-09-990-586-6	Sequence 6, Appl1
13	23	74.2	7	US-08-802-083-11	Sequence 11, Appl1
14	22	71.0	7	US-08-553-501-63	Sequence 63, Appl1
15	21	67.7	7	US-09-954-385-232	Sequence 232, Appl1
16	19	61.3	7	US-08-996-140-17	Sequence 17, Appl1
17	19	61.3	7	US-09-649-063-17	Sequence 17, Appl1
18	19	61.3	7	US-09-730-857-82	Sequence 82, Appl1
19	18	58.1	5	PCT-US98-04368-24	Sequence 24, Appl1
20	18	58.1	5	US-09-390-896A-25	Sequence 25, Appl1
21	18	58.1	5	US-09-535-832A-25	Sequence 25, Appl1
22	18	58.1	5	US-09-859-214-62	Sequence 62, Appl1
23	18	58.1	6	US-08-984-098-69	Sequence 69, Appl1
24	18	58.1	7	PCT-US00-06588-38	Sequence 38, Appl1
25	18	58.1	7	PCT-US01-44807-126	Sequence 126, Appl1
26	18	58.1	7	PCT-US97-04696-5	Sequence 5, Appl1
27	18	58.1	7	PCT-US97-04696A-5	Sequence 5, Appl1
28	18	58.1	7	US-08-295-161-21	Sequence 21, Appl1
29	18	58.1	7	US-08-460-383-25	Sequence 25, Appl1
30	18	58.1	7	US-09-155-106-5	Sequence 5, Appl1
31	18	58.1	7	US-09-549-676A-2	Sequence 2, Appl1
32	18	58.1	7	US-09-724-396-120	Sequence 120, Appl1
33	18	58.1	7	US-09-724-531-120	Sequence 120, Appl1
34	18	58.1	7	US-09-731-242A-35	Sequence 35, Appl1
35	18	58.1	7	US-09-996-265-126	Sequence 126, Appl1
36	18	58.1	7	US-09-996-288-126	Sequence 126, Appl1
37	17	54.8	5	US-08-859-214-41	Sequence 41, Appl1
38	17	54.8	6	US-08-166-038-54	Sequence 54, Appl1
39	17	54.8	6	US-08-757-425-29	Sequence 29, Appl1
40	17	54.8	6	US-08-757-425A-29	Sequence 29, Appl1
41	17	54.8	6	US-08-757-425B-29	Sequence 29, Appl1
42	17	54.8	6	US-08-978-607-29	Sequence 29, Appl1
43	17	54.8	6	US-08-978-607A-29	Sequence 29, Appl1
44	17	54.8	7	PCT-US95-01210-18	Sequence 8, Appl1
45	17	54.8	7	US-07-703-422-16	Sequence 16, Appl1

ALIGNMENTS

```
US-09-743-482A-4
; Sequence 4, Application US/09743482A
; GENERAL INFORMATION:
; APPLICANT: Connex GmbH
; TITLE OF INVENTION: Immunological reagent specifically interacting with the
; TITLE OF INVENTION: extracellular domain of the human zeta chain
; FILE REFERENCE: C1368PCT
; CURRENT APPLICATION NUMBER: US/09/743,482A
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: EP 98 11 2867.1
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-743-482A-4
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Query Match 100.0% Score 31; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
DB 1 SATSLAD 7

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RESULT 2
US-08-053-451A-69
; Sequence 69, Application US/08053451A
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Dittow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White - Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451A
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 2716/26869-J
; TELEPHONE: (212) 278 0400
; TELEFAX: (212) 391 0525
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-053-451A-69

Query Match      87.1%; Score 27; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ATSLAD 7      111111
DB      2 ATSLAD 7

RESULT 3
US-08-053-451A-77
; Sequence 77, Application US/08053451A
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Dittow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White - Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451A
FILING DATE: 26-APR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 2716/26869-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278 0400
TELEFAX: (212) 391 0525
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451A-77
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Query Match      87.1%; Score 27; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 ATSLAD 7      111111
DB      2 ATSLAD 7
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```
RESULT 4
US-08-336-525-69
; Sequence 69, Application US/08336525
; GENERAL INFORMATION:
; APPLICANT: Charles C. Dittow, et al.
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White - Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,525
; FILING DATE: Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 2976/26869L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278 0400
; TELEFAX: (212) 391 0525
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
```

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-336-525-69

Query Match
Best Local Similarity 87.1%; Score 27; DB 7; Length 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSLAD 7
DB 2 ATSLAD 7

RESULT 5
US-08-336-525-77
Sequence 77, Application US/08336525
GENERAL INFORMATION:

APPLICANT: Charles C. Dittow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White - Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,525
FILING DATE: Herewith

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 2976/26869L
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278 0400
TELEFAX: (212) 391 0525

INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-336-525-77

Query Match
Best Local Similarity 87.1%; Score 27; DB 7; Length 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSLAD 7
DB 2 ATSLAD 7

RESULT 6
US-08-336-525A-69

Sequence 69, Application US/08336525A
GENERAL INFORMATION:
APPLICANT: Charles C. Dittow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF

NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White - Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,525A
FILING DATE: 09-Nov-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 2976/26869L

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278 0400
TELEFAX: (212) 391 0525

INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-336-525A-69

Query Match
Best Local Similarity 87.1%; Score 27; DB 7; Length 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSLAD 7
DB 2 ATSLAD 7

RESULT 7
US-08-336-525A-77

Sequence 77, Application US/08336525A
GENERAL INFORMATION:
APPLICANT: Charles C. Dittow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White - Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,525A
FILING DATE: 09-Nov-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 2976/26869L

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278 0400
TELEFAX: (212) 391 0525
TELEFAX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-336-525A-77

Query Match 87.1%; Score 27; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSLAD 7
DB 2 ATSLAD 7

RESULT 8
US-08-480-120-9
Sequence 9, Application US/08480120
GENERAL INFORMATION:
APPLICANT: Jolliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Pulito, Virginia L.
TITLE OF INVENTION: CDR-GRAFTED ANTI-TISSUE FACTOR
TITLE OF INVENTION: ANTIBODIES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,120
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9598
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-480-120-9

Query Match 87.1%; Score 27; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 ATSLAD 7

DB 2 ATSLAD 7

RESULT 9
US-09-647-468-137
Sequence 137, Application US/09647468
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOTIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
FILE REFERENCE: 053466/0289
CURRENT FILING DATE: 2000-09-29
CURRENT APPLICATION NUMBER: US/09/647,468
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 137
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
US-09-647-468-137

Query Match 87.1%; Score 27; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSLAD 7
DB 2 ATSLAD 7

RESULT 10
PCT-US98-04644-6
Sequence 6, Application PC/TUS9804644
GENERAL INFORMATION:
APPLICANT: Wong, Hing C.
APPLICANT: Jiao, Jin-an
APPLICANT: Esperanza, Nieves
TITLE OF INVENTION: Lawrence, Luersch
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/04644
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Corleiss, Peter F.
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943-PCT
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
PCT-US98-04644-6

Query Match
Best Local Similarity 80.6%; Score 25; DB 1; Length 7;
71.4%; Pred. No. 4.2e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
:|||||
DB 1 AATNLAD 7

RESULT 11
US-09-293-854-6
Sequence 6, Application US/09293854
GENERAL INFORMATION:
APPLICANT: Wong, Hing C.
Jiao, Jinan
Esperanza, Nieves
Lawrence, Lupepschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIke, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,854
FILING DATE: 16-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/814,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F.
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-293-854-6

Query Match
Best Local Similarity 80.6%; Score 25; DB 16; Length 7;
71.4%; Pred. No. 4.2e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
:|||||
DB 1 AATNLAD 7

RESULT 12
US-09-990-586-6
Sequence 6, Application US/0990586
GENERAL INFORMATION:
APPLICANT: JIAO, JIN-AN
APPLICANT: WONG, HING C.
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
OF USE THEREOF
FILE REFERENCE: 71758/46943-CIP2
CURRENT APPLICATION NUMBER: US/09/990,586
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/293,854
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-990-586-6

Query Match
Best Local Similarity 80.6%; Score 25; DB 23; Length 7;
71.4%; Pred. No. 4.2e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
:|||||
DB 1 AATNLAD 7

RESULT 13
US-09-802-083-11
Sequence 11, Application US/09802083
GENERAL INFORMATION:
APPLICANT: Kirchofer, Daniel K.
APPLICANT: Lowe, David G.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Anti-tissue Factor Antibodies with Enhanced
File Reference: PI736R1
CURRENT APPLICATION NUMBER: US/09/802,083
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 60/189,775
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 11
LENGTH: 7
TYPE: PRT
ORGANISM: Mus musculus
US-09-802-083-11

Query Match
Best Local Similarity 74.2%; Score 23; DB 22; Length 7;
83.3%; Pred. No. 4.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATSLAD 7
:|||||
DB 2 ATSLAE 7

```

RESULT 14
US-08-553-501-63
: Sequence 63, Application US/08553501
: GENERAL INFORMATION:
: APPLICANT: TSUCHIYA, Masayuki
: APPLICANT: SATO, Koh
: APPLICANT: HIRATA, Yuichi
: TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
: TITLE OF INVENTION: INTERLEUKIN-6
: NUMBER OF SEQUENCES: 91
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 3000 K Street, N.W., Suite 500
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/553,501
: FILING DATE: 20-FEB-1996
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/JP94/00859
: FILING DATE: 30-MAY-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 5-129787
: FILING DATE: 31-MAY-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: WEGNER, Harold C.
: REGISTRATION NUMBER: 25,258
: REFERENCE/DOCKET NUMBER: 53466/177/AOK
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)672-5300
: TELEFAX: (202)672-5399
: TELEX: 904136
: INFORMATION FOR SEQ ID NO: 63:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
US-08-553-501-63
:
Query Match 71.0%; Score 22; DB 9; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 SATSLAD 7
: 11111
DB 1 AATYLLAD 7

```

```

: NUMBER OF SEQ ID NOS: 433
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 232
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: binding peptide
US-09-954-385-232
:
Query Match 67.7%; Score 21; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSL 5
: 11111
DB 2 SATSL 6

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Search completed: February 25, 2003, 11:14:22
 Job time : 132 secs

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RESULT 15
US-09-954-385-232
: Sequence 232, Application US/09954385
: GENERAL INFORMATION:
: APPLICANT: Aehle, Wolfgang
: APPLICANT: Baldwin, Toby L.
: APPLICANT: Van Gestel, Franciscus J.C.
: APPLICANT: Janssen, Giselle G.
: APPLICANT: Murray, Christopher J.
: APPLICANT: Wang, Huang
: APPLICANT: Winetzkyl, Deborah S.
: TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
: TITLE OF INVENTION: Complexes
: FILE REFERENCE: GC690
: CURRENT APPLICATION NUMBER: US/09/954,385
: CURRENT FILING DATE: 2001-09-12

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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:10:39 : Search time 12 Seconds
(without alignments)
18.124 Million cell updates/sec

Title: US-09-743-482A-4
Perfect score: 31
Sequence: 1 SATSLAD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues
Total number of hits satisfying chosen parameters: 12797

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	80.6	7	9	US-09-293-854-6
2	19	61.3	7	10	US-09-730-857-82
3	18	58.1	5	10	US-09-859-214-62
4	18	58.1	7	9	US-09-996-288-126
5	18	58.1	7	10	US-09-731-242A-95
6	17	54.8	5	10	US-09-859-214-41
7	17	54.8	7	10	US-09-832-723-59
8	16	51.6	7	9	US-09-884-767A-92
9	16	51.6	7	10	US-09-924-099-4
10	15	48.4	4	10	US-09-740-026A-11
11	15	48.4	6	9	US-10-014-162-70
12	15	48.4	7	9	US-10-014-162-69
13	15	48.4	7	10	US-09-933-497B-34
14	14	45.2	4	9	US-10-254-577-12
15	14	45.2	4	9	US-09-799-250-717
16	14	45.2	4	10	US-09-741-148A-12
17	14	45.2	4	10	US-09-818-656A-7
18	14	45.2	5	10	US-09-898-461-3
19	14	45.2	7	9	US-09-968-561A-17

20	14	45.2	7	9	US-09-968-561A-41	Sequence 41, Appl
21	14	45.2	7	9	US-09-968-561A-71	Sequence 71, Appl
22	14	45.2	7	9	US-09-968-561A-77	Sequence 77, Appl
23	14	45.2	7	9	US-09-968-561A-83	Sequence 83, Appl
24	14	45.2	7	9	US-09-968-561A-89	Sequence 89, Appl
25	14	45.2	7	9	US-09-968-561A-95	Sequence 95, Appl
26	14	45.2	7	9	US-09-968-561A-125	Sequence 125, Appl
27	14	45.2	7	9	US-09-968-561A-131	Sequence 131, Appl
28	14	45.2	7	9	US-09-968-561A-137	Sequence 137, Appl
29	14	45.2	7	9	US-09-968-561A-143	Sequence 143, Appl
30	14	45.2	7	9	US-09-968-561A-149	Sequence 149, Appl
31	14	45.2	7	9	US-09-968-561A-191	Sequence 191, Appl
32	14	45.2	7	9	US-09-968-561A-197	Sequence 197, Appl
33	14	45.2	7	9	US-09-968-561A-215	Sequence 215, Appl
34	14	45.2	7	9	US-09-968-561A-221	Sequence 221, Appl
35	14	45.2	7	9	US-09-968-561A-239	Sequence 239, Appl
36	14	45.2	7	9	US-09-968-561A-263	Sequence 263, Appl
37	14	45.2	7	9	US-09-968-561A-269	Sequence 269, Appl
38	14	45.2	7	9	US-09-968-561A-275	Sequence 275, Appl
39	14	45.2	7	9	US-09-968-561A-287	Sequence 287, Appl
40	14	45.2	7	9	US-09-968-561A-299	Sequence 299, Appl
41	14	45.2	7	9	US-09-968-561A-311	Sequence 311, Appl
42	14	45.2	7	9	US-09-968-561A-317	Sequence 317, Appl
43	14	45.2	7	9	US-09-996-288-77	Sequence 77, Appl
44	14	45.2	7	9	US-09-185-908-121	Sequence 121, Appl
45	14	45.2	7	10	US-09-765-086-131	Sequence 131, Appl

ALIGNMENTS

RESULT 1
US-09-293-854-6
Sequence 6, Application US/09293854
Patent No. US20020168357A1
GENERAL INFORMATION:
APPLICANT: Wong, Hing C.
Jiao, Jin-an
Esperanza, Nieves
Lawrence, Luopshen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronsteijn, Roberts & Cushman, LLP
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293, 854
FILING DATE: 16-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/814, 806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F.
REGISTRATION NUMBER: 33, 860
REFERENCE/DOCKET NUMBER: 46943
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-293-854-6

Query Match 80.6%; Score 25; DB 9; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.3e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
DB 1 AATNLAD 7

RESULT 2
US-09-730-857-82

Sequence 82, Application US/09730857
Patent No. US20020082396A1

GENERAL INFORMATION:

APPLICANT: Matsushita, Kouji

Matsushita, Yoshitiro

Yamada, Yoshiki

Sato, Koh

Tsushita, Masayuki

Yamazaki, Tatsumi

TITLE OF INVENTION: Reshaped Human Antibody to

Interleukin-8

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORISON & FOERSTER

STREET: 2000 Pennsylvania Avenue, NW, suite 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/730,857

FILING DATE: 07-Dec-2000

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/416,557

FILING DATE: 1999-10-12

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 35029-20001.10

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-887-1500

TELEFAX: 202-822-0168

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 82:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 82:

US-09-730-857-82

Query Match 61.3%; Score 19; DB 10; Length 7;

Best Local Similarity 57.1%; Pred. No. 1.3e+05;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SATSLAD 7
DB 1 NAKTLAD 7

RESULT 3
US-09-859-214-62

Sequence 62, Application US/09859214
Patent No. US20020103111A1

GENERAL INFORMATION:

APPLICANT: Schwoef, Charles F.

Schwoef, Hitesh N.

TITLE OF INVENTION: INHIBITORS OF MDCAM-1-MEDIATED

INTERACTIONS AND METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: USA

ZIP: 02421

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/859,214

FILING DATE: 16-May-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/109,879

FILING DATE: <unknown>

APPLICATION NUMBER: US 08/582,740

FILING DATE: 04-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: LKS95-12A2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 861-9540

TELEFAX: (781) 861-9540

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: <unknown>

TOPOLOGY: circular

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 62:

US-09-859-214-62

Query Match 58.1%; Score 18; DB 10; Length 5;

Best Local Similarity 80.0%; Pred. No. 1.3e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 TSLAD 7
DB 1 TSLAD 5

RESULT 4
US-09-996-288-126

Sequence 126, Application US/09996288
Patent No. US2002017126A1

GENERAL INFORMATION:

APPLICANT: Young, James

APPLICANT: Scott, Koenig

APPLICANT: Leslie, Johnson

TITLE OF INVENTION: Methods of Administering/Dosing Anti-NSV Antibodies for Prophyl

and Treatment

FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 126
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-288-126

Query Match
Best Local Similarity 58.1%; Score 18; DB 9; Length 7;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TSLAD 7
DB 2 TSLAD 6

RESULT 5
US-09-731-242A-35
Sequence 35, Application US/09731242A
Patent No. US20020058253A1
GENERAL INFORMATION:
APPLICANT: KRANZ, DAVID
APPLICANT: WITTRUP, K. DANE
APPLICANT: HOLLER, PHILIP
TITLE OF INVENTION: HIGH AFFINITY TCR PROTEINS AND METHODS
FILE REFERENCE: 89-99
CURRENT APPLICATION NUMBER: US/09/731,242A
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US 60/169,179
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/009,388
PRIOR FILING DATE: 1998-01-20
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 35
LENGTH: 7
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1..1)
OTHER INFORMATION: CDR3alpha sequence
US-09-731-242A-35

Query Match
Best Local Similarity 58.1%; Score 18; DB 10; Length 7;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SATSLA 6
DB 1 SATSPA 6

RESULT 6
US-09-859-214-41
Sequence 41, Application US/09859214
Patent No. US20020103111A1
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
APPLICANT: Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MADCAM-1-MEDIATED
INTERACTIONS AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA

ZIP: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/859,214
FILING DATE: 16-May-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/109,879
FILING DATE: <unknown>
APPLICATION NUMBER: US 08/582,740
FILING DATE: 04-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-12A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= modified aa
/note= "Pda - Leucine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label= modified aa
/note= "Leucine - NH2"
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-859-214-41

Query Match
Best Local Similarity 54.8%; Score 17; DB 10; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATSL 5
DB 2 ATSL 5

RESULT 7
US-09-832-723-59
Sequence 59, Application US/09832723
Patent No. US20020098524A1
GENERAL INFORMATION:
APPLICANT: Estell, David A.
APPLICANT: Chen, Yiyou
APPLICANT: Murray, Christopher J.
APPLICANT: Tijerina, Pilar
TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
FILE REFERENCE: GC617-2
CURRENT APPLICATION NUMBER: US/09/832,723
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/197,259
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 117
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 59
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: peptides screened from a phage display random
OTHER INFORMATION: peptide library
US-09-832-723-59

Query Match 54.8%; Score 17; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSL 5
DB 4 ATSL 7

RESULT 8
US-09-884-767A-92
Sequence 92, Application US/09884767A
Publication No. US20020192789A1
GENERAL INFORMATION:

APPLICANT: DYAX CORP.
APPLICANT: Ley, Arthur C.
APPLICANT: Luneau, Christopher J.
APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
FILE REFERENCE: DXX-012.1 US, DXX-012.1 PCT
CURRENT APPLICATION NUMBER: US/09/884,767A
CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 09/597,321
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
SEQ ID NO 92
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-92

Query Match 51.6%; Score 16; DB 9; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 SLAD 7
DB 2 SMAD 5

RESULT 9
US-09-924-099-4
Sequence 4, Application US/09924099
Patent No. US20020128450A1
GENERAL INFORMATION:
APPLICANT: NISHIDA, Yoshihiro
APPLICANT: OKURA, Takanori
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PEPTIDE
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 4
LENGTH: 7
TYPE: PRT
ORGANISM: Mus musculus
US-09-924-099-4

Query Match 51.6%; Score 16; DB 10; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ATSLAD 7
DB 1 ATSLAD 6

RESULT 10
US-09-740-026A-11
Sequence 11, Application US/09740026A
Patent No. US20020081678A1
GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady V. et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: CL001012
CURRENT APPLICATION NUMBER: US/09/740,026A
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
US-09-740-026A-11

Query Match 48.4%; Score 15; DB 10; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 SLAD 7
DB 1 SVAD 4

RESULT 11
US-10-014-162-70
Sequence 70, Application US/10014162
Publication No. US20030032096A1
GENERAL INFORMATION:
APPLICANT: Usdin, Ted B.
APPLICANT: Hoare, Samuel R.J.
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
FILE REFERENCE: NIH175.001C1
CURRENT APPLICATION NUMBER: US/10/014,162
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: PCT/US00/1677
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/139335
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 70
LENGTH: 6
TYPE: PRT
ORGANISM: Bos taurus
US-10-014-162-70

Query Match 48.4%; Score 15; DB 9; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 SLAD 7
DB 3 ALAD 6

RESULT 12
US-10-014-162-69
Sequence 69, Application US/10014162

Publication No. US20030032096A1
GENERAL INFORMATION:
APPLICANT: usdin, Ted B.
APPLICANT: Hoare, Samuel R.J.
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
FILE REFERENCE: NIH175.001C1
CURRENT APPLICATION NUMBER: US/10/014.162
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: PCT/US00/1677
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/139335
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 69
LENGTH: 7
TYPE: PRT
ORGANISM: Bos taurus
US-10-014-162-69

Query Match 48.4%; Score 15; DB 9; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 SLAD 7
DB 3 ALAD 6

RESULT 13
US-09-933-497B-34
Sequence 34, Application US/09933497B
Patent No. US20020098193A1
GENERAL INFORMATION:
APPLICANT: Ward, Elizabeth S.
TITLE OF INVENTION: IMMUNOGLOBULIN-LIKE DOMAINS WITH INCREASED HALF LIVES
FILE REFERENCE: UTSD:483
CURRENT APPLICATION NUMBER: US/09/933.497B
CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/013.563
PRIOR FILING DATE: 1996-03-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-933-497B-34

Query Match 48.4%; Score 15; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATSLA 6
DB 2 AISLA 6

RESULT 14
US-10-254-577-12
Sequence 12, Application US/10254577
Publication No. US20030027746A1
GENERAL INFORMATION:
APPLICANT: Chunhua YAN et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: CL000566 CON
CURRENT APPLICATION NUMBER: US/10/254.577
CURRENT FILING DATE: 2002-09-26

PRIOR APPLICATION NUMBER: 09/741.148
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/206.982
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
US-10-254-577-12

Query Match 45.2%; Score 14; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

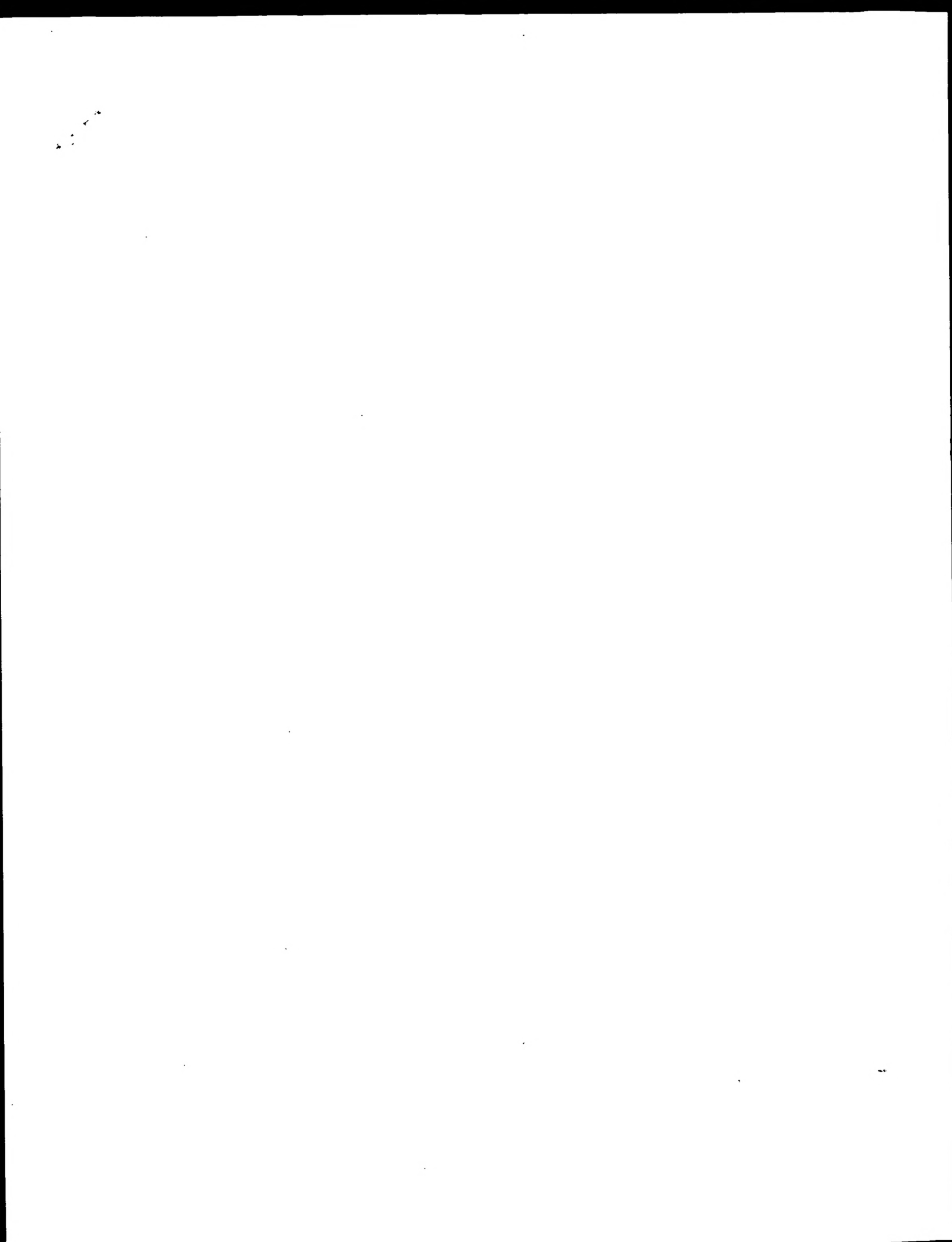
QY 4 SLAD 7
DB 1 SLCD 4

RESULT 15
US-09-799-250-717
Sequence 717, Application US/09799250
Publication No. US20030032087A1
GENERAL INFORMATION:
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Faris
APPLICANT: Daniel E.H. Afar
TITLE OF INVENTION: 121PFL: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129.34US01
CURRENT APPLICATION NUMBER: US/09/799.250
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 719
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 717
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250-717

Query Match 45.2%; Score 14; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 SLAD 7
DB 1 SLVD 4

Search completed: February 25, 2003, 11:15:09
Job time : 13 secs



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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:00:18 ; Search time 82 Seconds
(Without alignments)
11.375 Million cell updates/sec

Title: US-09-743-482a-4
Perfect score: 31
Sequence: 1 SATSLAD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 64668

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	27	87.1	7	15	AAV78320
3	27	87.1	7	18	AAV78320
4	27	87.1	7	18	AAV78320
5	25	80.6	7	18	AAV78320
6	25	80.6	7	18	AAV78320
7	23	74.2	7	22	AAV78320
8	22	71.0	7	16	AAV78320
9	22	71.0	7	16	AAV78320
10	20	64.5	7	15	AAV78320

11	20	64.5	7	22	AAU07504
12	19	61.3	7	23	AAV63826
13	19	61.3	7	19	AAU72828
14	18	58.1	5	18	AAV02011
15	18	58.1	5	21	AAV03692
16	18	58.1	6	13	AAV20423
17	18	58.1	6	13	AAV23451
18	18	58.1	7	18	AAV23434
19	18	58.1	7	21	AAV85596
20	18	58.1	7	21	AAV23216
21	18	58.1	7	22	AAV62821
22	17	54.8	5	18	AAV02047
23	17	54.8	5	19	AAV66695
24	17	54.8	6	19	AAV63828
25	17	54.8	6	19	AAV66694
26	17	54.8	7	16	AAV85849
27	17	54.8	7	20	AAV06697
28	17	54.8	7	22	AAV99166
29	17	54.8	7	22	AAV5763
30	17	54.8	7	22	AAV57595
31	17	54.8	7	22	AAV58005
32	17	54.8	7	23	AAV05325
33	16	51.6	5	23	AAV07322
34	16	51.6	6	16	AAV83515
35	16	51.6	6	16	AAV83524
36	16	51.6	6	18	AAV30477
37	16	51.6	6	20	AAV84412
38	16	51.6	6	20	AAV84421
39	16	51.6	7	15	AAV6809
40	16	51.6	7	15	AAV63536
41	16	51.6	7	19	AAV64501
42	16	51.6	7	19	AAV70945
43	16	51.6	7	20	AAV40722
44	16	51.6	7	20	AAV40725
45	16	51.6	7	21	AAV30061

ALIGNMENTS

RESULT 1
AAV78320 standard; Protein: 7 AA.
AAV78320:
04-MAY-2000 (first entry)
Anti-zeta-chain antibody 2-B-5 VL-region CDR2 protein sequence.
Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; Immunisation; complementing determining region; CDR; autoimmunity; cytotoxic; immune deficiency; T-cell malignancy; infectious disease; antiviral; immunosuppressive; antimicrobial; immune response modulator; NK-cell.
Rattus norvegicus.
W0200003016-A1.
20-JAN-2000.
09-JUL-1999; 99W0-EP04838.
10-JUL-1998; 98EP-0112867.
(CONN-) CONNEX GMBH.
Reiter C;
WPI: 2000-160926/14.
N-PSDB: AA288316.
New oligonucleotide, polypeptide, antibody useful for treating

Synthetic peptide
Human Mab #117-10C
Anti-NKG2D hybrid
peptide used to pr
heparin-beta fragm
Anti-b-endorphin m
V beta 6 clone fou
CDR-2 of rW12 ligh
IGG glycosylation
Hsp47-binding phag
Amino acid sequenc
peptide used to pr
peptide partial se
peptide specific a
peptide partial se
peptide rVII deriv
Ab2 variable light
Human scfv clone 2
B cell surface rec
BLR-1 C-terminal c
Bgg-soil and not s
Mortine/rat tryptop
zif268 zinc finger
zif268 zinc finger
Major outer membra
HTV-1 nucleic acid
HIV-1 nucleic acid
Phytase derived pe
HT-LCP internal pe
Neurotoxic beta-am
CDR2 of the light
S3 derivative #19
S3 derivative #22
Scarfoid protein S

PT autoimmune disease, immune deficiencies, T-cell malignancies and
 PT Infectious diseases -
 XX
 XX
 PS Claim 10; Fig 7; 79pp; English.
 CC
 CC The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is
 CC encoded by (I), is obtained by immunising a rat with jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,
 CC infectious diseases and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC or viral infections. The antibody, and fragments of it, can be useful for
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC treatment of NK-cell derived malignancies. It can also be useful for the
 CC determination of zeta-chain or eta-chain expression on NK-cells,
 CC T-lymphocytes or their precursors. The present sequence represents the
 CC CDR2 of the VL-region of the anti-zeta-chain antibody 2-B-5, produced
 CC by rats from the present invention.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SATSLAD 7
 Db 1 SATSLAD 7
 ID AAR62886 standard; peptide: 7 AA.
 AAR62886
 AC AAR62886;
 XX
 XX 18-JUL-1995 (first entry)
 DT
 DE Murine anti-human atherosclerotic plaque MAb 22D3 VK CDR2.
 XX
 XX Atherosclerosis; atherosclerotic plaque; anti-hydroxysteroid antibody;
 KM murine monoclonal antibody; Kappa light chain variable region; CDR2;
 KM complementarily determining region; imaging; plaque ablation.
 XX
 OS Mus musculus.
 XX
 XX Key Location/Qualifiers
 FH Region 1.7
 FT Label= CDR2
 FT
 XX WO9425053-A.
 PN 10-NOV-1994.
 PD
 XX 26-APR-1994; 94WO-US04641.
 PF
 XX 26-APR-1993; 93US-0053451.
 PR
 XX (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
 PA
 PI Calenoff E, Chen FW, Dillow CC;
 XX
 XX WPI; 1994-357904/44.
 DR N-PSDB; AAQ78742.
 XX
 XX New antigen comprising hydroxy:steroid and quat. ammonium salt -
 PT and related antibodies, useful e.g. for imaging, ablating or
 PT treating atherosclerotic plaque, and detecting plaque specific

PT antibodies
 XX
 XX Claim 201; Page 165; 288pp; English.
 PS
 CC Mice were immunised with an extract of human atherosclerotic plaque,
 CC then spleen cells were fused with SP2/01-Ag-14 myeloma cells.
 CC Hybridomas were screened by ELISA for reactivity with the immunogen
 CC and clone 22D3 was isolated. The 22D3 antibody reacts specifically
 CC with atherosclerotic tissue; it recognises a non-protein antigen
 CC containing cholesterol (or similar steroid that is a substrate for
 CC cholesterol oxidase) and a quaternary ammonium salt (pref. a
 CC phosphatidylcholine or related compound that is a substrate for
 CC phospholipase C). The CDR sequences for the heavy and light chains
 CC of 22D3 were determined; peptides comprising the CDRs are claimed,
 CC including chimeric (CDR-grafted) murine-human antibodies.
 XX
 SQ Sequence 7 AA;
 Query Match 87.1%; Score 27; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ATSLAD 7
 Db 2 ATSLAD 7
 ID AAW10226 standard; Peptide: 7 AA.
 AAW10226
 AC AAW10226;
 XX
 XX 01-APR-1997 (first entry)
 DT
 DE CDR-grafted antibody light chain CDR2.
 XX
 XX Tissue factor; complementarily determining region; CDR;
 KM humanised antibody; monoclonal antibody; TF8-5G9; coagulation;
 KM thrombosis; restenosis; arteriosclerosis; therapy.
 XX
 OS Mus sp.
 XX
 XX WO9640921-A1.
 PN 19-DEC-1996.
 PD
 XX 06-JUN-1996; 96WO-US09287.
 PF
 XX 07-JUN-1995; 95US-0480120.
 PR
 XX (JOHN J) JOHNSON & JOHNSON.
 PA
 PI Jolliffe LK, Pulito VL, Zivin RA;
 XX
 XX WPI; 1997-099935/09.
 DR
 XX CDR-grafted antibody capable of inhibiting human tissue factor -
 PT used in the treatment of thrombotic disorders, e.g. intravascular
 PT coagulation, arterial restenosis etc.
 PT
 XX Claim 4; Page 90; 142pp; English.
 PS
 CC Heavy chain CDRs 1-3 (AAW10222-24) and light chain CDRs 1-3 (AAW10225-
 CC 27) from the murine anti-tissue factor monoclonal antibody TF8-5G9
 CC can be grafted into framework and constant regions derived from
 CC human antibodies to generate CDR-grafted antibodies (see also
 CC W1022-33) capable of inhibiting human tissue factor. Such
 CC antibodies can be used to treat or prevent thrombotic disorders
 CC such as intravascular coagulation, arterial restenosis or
 CC arteriosclerosis.
 CC
 XX Sequence 7 AA;
 SQ

Query Match 87.1%; Score 27; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSLAD 7
 DB 2 ATSLAD 7

RESULT 4
 AA52753
 ID AAV52753 standard; Peptide: 7 AA.

XX AC AAV52753;

XX DT 26-JAN-2000 (first entry)

XX DE Humanised ATR-5 L chain V region CDR2.

XX KM Human tissue factor; TF: humanised; antibody: mouse monoclonal antibody;

XX KM ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;

XX KM disseminated intravascular coagulation; immunogenicity; chimeric.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO951743-A1.

XX PD 14-OCT-1999.

XX PF 02-APR-1999; 99MO-JP01768.

XX PR 03-APR-1998; 98JP-0091850.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Sato K, Adachi H, Yabuta N;

XX DR WPI; 1999-620204/53.

PT Humanised antibody recognizing human tissue factor, used for treatment
 of disseminated intravascular coagulation

PS Claim 16; Page 273; 291pp; Japanese.

CC The present invention describes chimeric antibody (Ab) heavy (H) chains
 containing the variable region of the H chain of a mouse monoclonal Ab
 recognizing human tissue factor (hrf) and the constant region of the H
 chain of a human Ab. The variable region is one of six specified
 sequences (which are the H chain variable regions from mouse monoclonal
 CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)
 chains containing the variable region of the L chain of a mouse
 monoclonal Ab recognizing human tissue factor (hrf) and the constant
 region of the L chain of a human Ab, the variable region being one of six
 specified sequences (which are the L chain variable regions from mouse
 CC monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for
 CC the treatment and prevention of thrombotic disease, especially of
 CC disseminated intravascular coagulation (DIC). The humanised antibody has
 CC the high hrf binding activity of the mouse monoclonal antibody but
 CC greatly reduced immunogenicity. AA233001 to AA233091 and Y527007 to
 CC AA52767 represent sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 7 AA;

Query Match 87.1%; Score 27; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSLAD 7
 DB 2 ATSLAD 7

RESULT 5
 AAW27351
 ID AAW27351 standard; peptide: 7 AA.

XX AC AAW27351;

XX DT 12-DEC-1997 (first entry)

XX DE CDR2 from murine anti-human IgE receptor antibody light chain.

XX XX Complementarity determining region; CDR2; murine; mouse; human;

XX KW high affinity; immunoglobulin E; receptor; monoclonal antibody;

XX KW IgE; Mab; light chain; variable region; humanised; semi-chimeric;

XX KW chimeric; treatment; prevention; disease; allergy.

XX OS Mus spp.

XX OS JP09191886-A.

XX PD 29-JUL-1997.

XX PF 19-JAN-1996; 96JP-0024816.

XX PR 19-JAN-1996; 96JP-0024816.

XX PA (ASAK) ASAKI BREWERIES LTD.

XX PA (NIKK-) NIKKA WHISKEY KK.

XX PA (TORI) TORII YAKUHIN KK.

XX PA (TSUR/) TSURA T.

XX DR WPI; 1997-429186/40.

XX XX Humanised, semi-chimeric and chimeric antibodies against human

XX PT high-affinity IgE receptor - useful medicinally and have low

XX PT antigenicity in humans

XX PS Claim 1; Page 13; 26pp; Japanese.

CC The present complementarity determining region 2 (CDR2), which is

CC from a murine, anti-human high affinity immunoglobulin E (IgE)

CC receptor, monoclonal antibody (Mab) light chain variable region,

CC can be used in the preparation of humanised or semi-chimeric

CC anti-human high affinity IgE receptor Mab. The Mab can be used to

CC treat or prevent diseases, specifically allergies, associated with

CC the receptor. The humanised, semi-chimeric or chimeric Mab have

CC very low antigenicity in humans.

XX SQ Sequence 7 AA;

Query Match 80.6%; Score 25; DB 18; Length 7;
 Best Local Similarity 71.4%; Pred. No. 7.8e+05;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
 DB 1 AATNLAD 7
 RESULT 6
 AAW71856
 ID AAW71856 standard; peptide: 7 AA.
 XX AC AAW71856;
 XX DT 10-DEC-1998 (first entry)
 XX DE Human anti-tissue factor antibody hypervariable region #2.
 XX KW Human; anti-tissue factor light chain variable region; H36.D2.B7;
 KW anti-tissue factor heavy chain variable region; inhibition; antibody;
 KW blood coagulation; thrombosis; restenosis; thromboembolic condition;

PR 30-MAR-1994: 94JP-0082693.
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX
 XX Atsushi O, Hirofumi Y, Ikunoshin K, Takashi T, Yoshinobu O;
 XX WPI: 1995-338286/44.
 DR
 XX
 PT Gene encoding variable region of anti-human influenza A type virus
 PT antibody - useful for prodn. of artificial antibodies
 XX
 PS Claim 6; Page 22; 42pp; English.
 CC
 CC AA82830-R82832 represent the three complementarity determining regions
 CC (CDR's) of the variable light chain region of an anti-human influenza A
 CC type virus antibody. The antibody recognises the stem region of the
 CC haemagglutinin (HA) molecule of the H1N1 and H2N2 subtypes of human
 CC influenza A type virus, and shows neutralisation activity against these
 CC two subtypes. The antibody shows no recognition of the H3N2 subtype.
 CC The DNA encoding the variable heavy chain sequence (see AAT04159) and
 CC the variable light chain coding sequence (see AAT04160) are useful in
 CC the production of artificial antibodies and antigen-binding
 CC polypeptides. These artificial antibodies and polypeptides are useful in
 CC the diagnosis and treatment of human influenza. As the antibodies
 CC recognise the stem region of the HA molecule, the influenza virus will be
 CC recognised even if the HA molecule changes. This provides an advantage
 CC over current vaccines, as the virus periodically alters it's HA
 CC molecule.
 CC
 CC Sequence 6 AA:
 SQ
 Query Match 71.0%; Score 22; DB 16; Length 6;
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SATSLA 6
 Db 1 AATSLA 6
 RESULT 9
 AAR77202
 ID AAR77202 standard; Peptide: 7 AA.
 XX
 AC AAR77202;
 XX
 DT 23-AUG-1995 (first entry)
 XX
 DE Mouse anti-human IL-6 Ab L chain V region CDR2.
 XX
 KW Primer: PCR; amplify; kappa; light chain; variable region; mouse; human;
 KW Interleukin; antibody; hydridoma; CDR; framework; constant region;
 KW heavy chain; disorder; antigenicity.
 XX
 OS Synthetic.
 XX
 PN W09428159-A.
 XX
 PD 08-DEC-1994.
 XX
 PF 30-MAY-1994: 94WO-JP00859.
 XX
 PR 31-MAY-1993: 93JP-0129787.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 PA (CHUS) CHUGAI PHARM CO LTD.
 XX
 PI Hirata Y, Sato K, Tsuchiya M;
 XX
 DR WPI: 1995-022828/03.
 XX
 PT Antibody against IL-6 - useful for the therapy and treatment of
 PT IL-6 related disorders.

XX
 PS Claim 1; Page 64; 82pp; Japanese.
 XX
 CC The sequence of the mouse anti-human interleukin-6 (IL-6) antibody light
 CC chain variable region complementarily determining region (CDR) 2. This
 CC sequence and that of CDR1 and 3 (AAR77201+3) were used in conjunction
 CC with the framework regions 1-4 (AAR77204-7) to construct a chimeric
 CC antibody against human interleukin-6 (IL-6). The vectors AAQ75914-7
 CC express constructs encoding fragments of a chimeric antibody to the
 CC human IL-6 comprising (a) a light chain with (i) a variable region
 CC containing 3 CDR (AAR77201-3) inserted into several framework regions
 CC (FR) (AAR77204-7) and (ii) a human light chain constant region and (b) a
 CC heavy chain with (i) a variable region containing 3 CDR (AAR77212-4)
 CC inserted into an FR (AAR77215-8) and (ii) a human light chain constant
 CC region. The FR of the light chain may be mouse derived (AAQ75888) or
 CC from the human antibody REI. The heavy chain FR may also be mouse derived
 CC (AAQ75889) or from the human antibody DAW. The antibodies can be used in
 CC the treatment of IL-6 related disorders. The antibodies are useful as
 CC they have low antigenicity due to the use of human derived sequences and
 CC low antigenicity mouse derived sequences.
 CC
 CC Sequence 7 AA:
 SQ
 Query Match 71.0%; Score 22; DB 16; Length 7;
 Best Local Similarity 71.4%; Pred. No. 7.8e+05;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SATSLAD 7
 Db 1 AATYLAD 7
 RESULT 10
 AAR52528
 ID AAR52528 standard; Peptide: 7 AA.
 XX
 AC AAR52528;
 XX
 DT 10-OCT-1996 (first entry)
 XX
 DE D1.3 light chain complementarity determining region 2.
 XX
 KW antibody; humanised; murine; human; heavy chain; light; variable;
 KW framework region; complementarity determining region; resipling;
 KW modelling; surface residue; modify; anti-phenylarsenate antibody.
 XX
 OS Synthetic.
 XX
 PN EP592106-A1.
 XX
 PD 13-APR-1994.
 XX
 PF 07-SEP-1993: 93EP-0307051.
 XX
 PR 09-SEP-1992: 92US-0942245.
 XX
 PA (PEDE/) PEDERSEN J T.
 PA (IMMU-) IMMUNOGEN INC.
 XX
 PI Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
 XX
 DR WPI: 1994-120230/15.
 XX
 PT Method of resurfacing of rodent antibodies to produce humanised
 PT antibody forms - for producing non-human antibodies with improved
 PT therapeutic efficiency by presenting human surface on V-region
 XX
 PS Example 2; Page 31; 230pp; English.
 XX
 CC The predicted structures of 4 different antibody (Gloop-2 and D1.3
 CC anti-Lysozyme Abs: 36-71, an anti-phenylarsenate Ab; and 3D6, an anti-
 CC protein (GP41 of HIV) Ab) Fv regions were analysed. This information
 CC can be used in a method to determine how to modify a rodent antibody or

CC fragment by resurfacing in order to produce a humanised rodent antibody.
 CC Global fits give a more realistic measure of the accuracy of the model.
 CC than a local least-squares fit over the loops since they account for
 CC the overall positioning of the loops in the context of the Fv structure.
 CC Differences between local and global Root Mean Square deviations arise
 CC from differences in VH/VL domain packing and differences in loop "take
 CC off" angles and positions. AAR52523-46 are the peptide sequences of the
 CC 24 CDRs.

XX Sequence 7 AA:

Query Match 64.5%; Score 20; DB 15; Length 7;
 Best Local Similarity 80.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TSLAD 7
 1:111
 Db 3 TTLAD 7

RESULT 11
 AAU07504 standard; Peptide; 7 AA.

XX AAU07504;

XX 24-OCT-2001 (first entry)

XX Synthetic peptide L-CDR2-LYS/P5.

XX L-CDR2-LYS/P5; antimicrobial; antiviral; cytostatic; immunomodulatory;
 KM antibody; gene therapy; HIV; human immunodeficiency virus; tumour;
 KW metabolic disorder; immune disorder; auto-immune disorder; lysosome.

XX Synthetic.

XX WO200149713-A2.

XX 12-JUL-2001.

XX 29-DEC-2000; 2000WO-TT00554.

XX 30-DEC-1999; 99IT-RM00803.

XX (CENEN) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.

XX (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.

XX Benvenuto E, Franconi R, Desiderio A, Tavladoraki P;

XX WPI: 2001-502555/55.

XX Peptides which are able to confer stability and solubility to an
 PT antibody comprising these peptides, useful for treating pathologies
 PT (e.g. tumour) associated with accumulation of a molecule inside or
 PT outside a human, or animal cell -

XX Disclosure; Page 101; 109pp; English.

XX The invention relates to peptides which are able to confer stability and
 CC solubility to an antibody comprising these peptides. The peptides
 CC are especially H-FR1, H-FR2, H-FR3, HFR4, L-FR1, L-FR2, L-FR3 or L-FR4
 CC present within a variable region of an antibody which makes the antibody
 CC soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to
 CC H-FR4 are present within the variable region of the heavy chain of an
 CC antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order
 CC (H-FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and
 CC peptides having the sequences of L-FR1 to L-FR4 are present within
 CC the variable region of the light chain of an antibody, covalently
 CC linked to the L-CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(
 CC L-FR2)-(L-CDR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and
 CC polynucleotides (e.g. by gene therapy) are useful for the manufacture
 CC of a medicament for the treatment of pathologies associated with
 CC accumulation of a molecule inside or outside a human, animal cell

CC or plant cell. The pathologies are infectious (e.g. viral infections such
 CC as HIV, human immunodeficiency virus, infections), tumour, metabolic and
 CC immune (especially auto-immune) pathologies. The present sequence
 CC represents the peptide L-CDR2-LYS/P5 which, when included in an
 CC antibody molecule, gives specificity for lysosome.

XX Sequence 7 AA:

Query Match 64.5%; Score 20; DB 22; Length 7;
 Best Local Similarity 80.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TSLAD 7
 1:111
 Db 3 TTLAD 7

RESULT 12
 AAM63826 standard; Peptide; 7 AA.

XX AAM63826;

XX 28-SEP-1998 (first entry)

XX Human Mab #117-10C light chain CDR2 peptide fragment.

XX Interleukin-18; IL-18; human; treatment; autoimmune disease; Mab;
 KM immunosuppressant; inhibitor; receptor protein; detection; light chain;
 KW monoclonal antibody; Mab; complementarity determining region; CDR2.

XX Homo sapiens.

XX EP850952-A1.

XX 01-JUL-1998.

XX 23-DEC-1997; 97EP-0310555.

XX 28-JUL-1997; 97JP-0215490.

XX 26-DEC-1996; 96JP-0356426.

XX 21-FEB-1997; 97JP-0052526.

XX 06-JUN-1997; 97JP-0163490.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Kunikata T, Kurimoto M, Torigoe K, Ushio S;

XX WPI: 1998-335317/30.

XX New interleukin-18 receptor protein used to inhibit interleukin-18,
 PT to treat autoimmune disease and as immunosuppressant - and new
 PT monoclonal antibody and hybridoma used to detect interleukin -18
 PT receptor protein

XX Claim 14; Page 19; 35pp; English.

XX This sequence represents the human monoclonal antibody (Mab) #117-10C
 CC light chain complementarity determining region, CDR2 which is used in a
 CC method involved in neutralising IL-18 or to treat autoimmune diseases or
 CC as an immunosuppressant using anti-IL-18 antibodies which can inhibit
 CC IL-18. Such antibodies can also be used to detect the IL-18 receptor
 CC protein (labelled with an enzyme or a radioactive or fluorescent
 CC substance). The protein is used to treat e.g. graft rejection, periclitous
 CC anaemia, atrophic gastritis, insulin-resistant diabetes, Wegener
 CC granulomatosis, discoid lupus erythematosus, ulcerative colitis,
 CC cold-agglutinin-relating diseases, Goodpasture's syndrome, primary
 CC biliary cirrhosis, sympathetic ophthalmitis, hyperthyroidism, juvenile
 CC onset type diabetes, Sjogren syndrome, autoimmune hepatitis, autoimmune
 CC haemolytic anaemia, myasthenia gravis, systemic scleroderma, systemic
 CC lupus erythematosus, polytypic cold haemaglobinuria, polymyositis,
 CC periarthritis nodosa, multiple sclerosis, Addison's disease, purpura
 CC haemorrhagica, Basedow's disease, leucopenia, Behcet's disease,

CC *climacterium praecox*, rheumatoid arthritis, rheumatopyra, chronic
 CC thyroiditis, Hodgkin's disease, HIV, aschma, atopic dermatitis, allergic
 CC nasitis, pollinosis, apitoxin-allergy and septic shock resulting from
 CC production or administration of excessive gamma interferon (IFN-gamma).
 XX

SO Sequence 7 AA:

Query Match 61.3%; Score 19; DB 19; Length 7;
 Best Local Similarity 57.1%; Pred. No. 7.8e+05;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SATSLAD 7
 : : : : : : :
 Db 1 NAKTLAD 7

RESULT 13

AAU72828
 ID AAU72828 standard; Peptide: 7 AA.

AAU72828:

26-FEB-2002 (first entry)

Anti-NKG2D hybridoma 11B2D10 variable light chain CDR3.

Human: NKG2D receptor complex; cancer; infectious disease; tumour;
 autoimmunity disease; head; neck; stomach; oesophagus; colon; liver; ovary;
 intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
 prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; EV;
 sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI0;
 nematode; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
 8G/C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
 P4-15; P5-2; P5-3; P5-9; P5-11; P5-23; 3B10XP4-3; 3B10XP4-14;
 P53 tetramerisation domain; 3B10XP5-2; 3B10XP5-23.

Homosapiens.

WO200171005-A2.

27-SEP-2001.

26-MAR-2001; 2001WO-EP03414.

24-MAR-2000; 2000EP-0106467.

(KUFE/) KUFER P.

Kuifer P, Riettmueller G, Lutterbuese R, Borschert K, Kischel R;
 Mayer M, Hofmeister R.

WPI: 2002-055119/07.

Multi-functional polypeptides comprising binding sites that specifically
 recognise extracellular groups of the NKG2D receptor complex and
 domains which function as receptors or ligands, useful for treating
 cancers and infectious diseases -

Example 3; Fig 16; 114pp: English.

The invention relates to a multi-functional polypeptide comprising a
 domain with a binding site that specifically recognises an extracellular
 group of the NKG2D receptor complex and a second domain which functions
 as a receptor or ligand. The polypeptide and its associated
 polynucleotide are used for the preparation of a pharmaceutical
 composition for the treatment of cancer, infections and/or autoimmune
 conditions. The cancer may be a tumour of the head and neck, stomach,
 oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
 larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
 bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
 The infectious diseases can be caused by viruses, bacteria, fungi,
 protozoa or helminths. The autoimmune diseases include multiple
 sclerosis, Grave's disease, ankylosing spondylitis, acute anterior

CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
 CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
 CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
 CC receptor and the polypeptides of the invention.
 XX

SO Sequence 7 AA:

Query Match 61.3%; Score 19; DB 23; Length 7;
 Best Local Similarity 57.1%; Pred. No. 7.8e+05;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SATSLAD 7
 : : : : : : :
 Db 1 NAKTLAD 7

RESULT 14

AAV02011
 ID AAV02011 standard; peptide: 5 AA.

AAV02011:

02-JUL-1999 (first entry)

Peptide used to produce MadCAM-1 mediated interaction inhibitors.

Mucosal addressing cell adhesion molecule-1; MadCAM-1; inhibitor;
 leukocyte infiltration; disease; inflammatory bowel disease;
 insulin-dependent diabetes mellitus; inflammatory bowel disease;
 ulcerative colitis; Crohn's disease; ileitis; coeliac disease;
 noninfectious enteropathy; seronegative arthropathy; colitis;
 eosinophilic gastroenteritis; pouchitis; proctocolitis;
 ileoanal anastomosis; alpha4-beta1 integrin.

Synthetic.

WO9725351-A2.

17-JUL-1997.

03-JAN-1997; 97WO-US00291.

04-JAN-1996; 96US-0582740.

(LEUK-) LEUKOSTITE INC.

Schwender CF, Shroff HN.

WPI: 1997-384978/35.

New polypeptide(s) for inhibiting MadCAM-1-mediated interactions -
 useful for treatment of diseases associated with leukocyte
 infiltration of tissues, especially inflammatory bowel disease and
 insulin-dependent diabetes mellitus

Claim 10; Page 78; 108pp: English.

The specification describes inhibitors of mucosal addressing cell
 adhesion molecule-1 (MadCAM-1) mediated interactions. These inhibitors
 comprise peptides which mimic the conserved amino acid motif LPTSL of
 MadCAM-1, and which have groups bonded to the N and C terminals.
 The inhibitors can be used for the treatment of a disease associated
 with leukocyte infiltration of tissues expressing the MadCAM-1,
 especially inflammatory bowel disease and insulin-dependent diabetes
 mellitus. Inflammatory bowel diseases which can be treated include
 ulcerative colitis, Crohn's disease, ileitis, coeliac disease,
 noninfectious enteropathy associated with seronegative
 arthropathies, microscopic or collagenous colitis, eosinophilic
 gastroenteritis, or pouchitis resulting after proctocolectomy, and
 ileoanal anastomosis. The inhibitors can also be used to inhibit the
 binding of a cell expressing a ligand for MadCAM-1 on the cell surface to
 MadCAM-1. They are also useful in diagnostic and research applications,
 e.g. as immunogens (when conjugated to a suitable carrier) to induce the

CC formation of antibodies which selectively bind MACAM-1. These antibodies
 CC can in turn be used to identify cells expressing MACAM-1 on their cell
 CC surface or to detect MACAM-1 in a sample. The compounds can also be
 CC labelled and used to detect alpha-beta-integrin and/or to quantitate
 CC expression of this the surface of cells. The present sequence is
 CC used to produce the inhibitors of the invention.

XX
 SQ Sequence 5 AA:

Query Match 58.1%; Score 18; DB 18; Length 5;
 Best Local Similarity 80.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TSLAD 7
 1 1 1
 1 1 1
 Db 1 TSLD 5

RESULT 15

AAB03692
 ID AAB03692 standard; peptide; 5 AA.

XX
 AC AAB03692;

XX
 DT 04-OCT-2000 (first entry)

XX
 DE heparin-beta fragment amino acid sequence.

XX
 KM Aortic aneurysm-associated antigen protein; AAP; microfibrillar protein;
 KM abdominal aortic aneurysm disease; treatment; detect; tolerance; human;

XX
 KM heparin-beta.

XX
 OS homo sapiens.

XX
 PN US6048704-A.

XX
 PD 11-APR-2000.

XX
 PF 07-MAR-1997; 97US-0812586.

XX
 PR 07-MAR-1996; 96US-0012976.

XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.

XX
 PI TILSON MD;

XX
 DR WPI; 2000-316895/27.

XX
 PT Isolated microfibrillar protein for alleviating abdominal aortic
 PT aneurysm disease is purified from human aortic tissue and binds
 PT immunoreactively with immunoglobulin

XX
 PS Example 2; Column 23; 70pp; English.

XX
 CC The present invention relates to an isolated microfibrillar protein of
 CC approximately 40KD. The protein is isolated from human aortic tissue and
 CC binds immunoreactively with immunoglobulin purified from human abdominal
 CC aortic aneurysm (AAA) tissue. The protein is referred to as aortic
 CC aneurysm-associated antigenic protein (AAP). The protein is capable of
 CC forming a disulphide bonded dimer. The protein is immunoreactive with
 CC human kappa immunoglobulin. Also included in the invention are
 CC recombinantly produced human AAA proteins. AAP shows regions of homology
 CC with the bovine microfibrillar associated glycoprotein MFAP-4 and also with
 CC fibrinogen and vitronectin. The isolated microfibrillar protein is useful
 CC for alleviating abdominal aortic aneurysm (AAA) disease and detecting the
 CC presence of AAA-associated immunoglobulin bound to the human aortic
 CC tissue. Antibodies directed against AAP can be used to detect AAA
 CC disease. The recombinant protein can be used to induce tolerance to
 CC antigenic AAA protein in the subject e.g. human. This sequence represents
 CC a heparin-beta fragment amino acid sequence. The fragment is used in the
 CC identification and characterisation of the aortic aneurysm-associated
 CC antigenic protein of the invention.

SQ Sequence 5 AA:

Query Match 58.1%; Score 18; DB 21; Length 5;
 Best Local Similarity 80.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TSLAD 7
 1 1 1
 1 1 1
 Db 1 TSLD 5

Search completed: February 25, 2003, 11:09:42
 Job time : 84 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:06:33 ; Search time 28 Seconds
(Without alignments)
51.512 Million cell updates/sec

Title: US-09-743-482A-4
Perfect score: 31
Sequence: 1 SATSLAD 7

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 58

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL-21:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriophage:*
17: sp-archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	32.3	7	2 P70804	P70804 azotobacter
2	10	32.3	7	2 O54248	O54248 streptomyces
3	10	32.3	7	2 P72081	P72081 nocardia la
4	8	25.8	6	10 P82181	P82181 spinacia ol
5	8	25.8	6	10 P82541	P82541 spinacia ol
6	8	25.8	6	10 P82182	P82182 spinacia ol
7	7	22.6	5	2 P83073	P83073 bacillus ce
8	7	22.6	5	10 Q99007	Q99007 hordeum vul
9	7	22.6	7	2 Q47505	Q47505 escherichia
10	7	19.4	7	2 O07354	O07354 synechococ
11	6	19.4	7	2 Q47029	Q47029 enterobacte
12	6	19.4	7	2 Q47477	Q47477 escherichia
13	6	19.4	7	4 O15897	O15897 homo sapien
14	6	19.4	7	5 P83274	P83274 macrobrachi
15	6	19.4	7	6 Q28742	Q28742 oryctolagus
16	6	19.4	7	10 O49223	O49223 glycine max

17	6	19.4	7	10 Q9C583	Q9C583 arabidopsis
18	6	19.4	7	11 O63480	O63480 rattus norv
19	6	19.4	7	11 O55184	O55184 rattus norv
20	6	19.4	7	12 O65578	O65578 bovine herp
21	6	19.4	7	15 Q07624	Q07624 rous sarcom
22	5	16.1	7	2 O34028	O34028 sphingomona
23	5	16.1	7	8 Q95945	Q95945 saccharomyc
24	5	16.1	7	10 P93233	P93233 lycopersico
25	5	16.1	7	10 P82445	P82445 nicotiana t
26	5	16.1	7	13 O42564	O42564 funy rubrip
27	4	12.9	4	11 Q08433	Q08433 rattus norv
28	4	12.9	5	13 P83308	P83308 gallus gall
29	4	12.9	7	2 O50556	O50556 actinobacill
30	4	12.9	7	4 O15903	O15903 homo sapien
31	4	12.9	7	8 P92372	P92372 haynaldia v
32	4	12.9	7	8 P92403	P92403 lophopyrum
33	4	12.9	7	8 P92425	P92425 pseudotrogon
34	4	12.9	7	8 P92387	P92387 henaridla p
35	4	12.9	7	8 P92427	P92427 peridictyon
36	4	12.9	7	8 P92390	P92390 heteranthel
37	4	12.9	7	8 P92226	P92226 crithepsis
38	4	12.9	7	8 P92214	P92214 amblyopyrum
39	4	12.9	7	8 P92430	P92430 aegilops ta
40	4	12.9	7	8 P92221	P92221 bromus iner
41	4	12.9	7	8 P92442	P92442 taenialatheru
42	4	12.9	7	8 P92381	P92381 hordeum bra
43	4	12.9	7	8 P92393	P92393 hordeum vul
44	4	12.9	7	8 P92218	P92218 australopyr
45	4	12.9	7	8 P92440	P92440 thnopyrum

ALIGNMENTS

RESULT 1

ID P70804 PRELIMINARY; PRT; 7 AA.

AC P70804; 01-FEB-1997 (TREMUREL.02, Created)
DT 01-FEB-1997 (TREMUREL.02, Last sequence update)
DT 01-DEC-2001 (TREMUREL.19, Last annotation update)

DE ALG1 protein (Fragment).
GN ALG1.
OS Acetobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Acetobacter.
OX NCBI_TaxID=354;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=E;
RX MEDLINE=6427318; PubMed=8830682;

RA Rehm B.H.A., Ertesvag H., Valla S.;

RT "A new Acetobacter vinelandii mannuronan C-5-epimerase gene (alg5) is part of an alg gene cluster physically organized in a manner similar to that in Pseudomonas aeruginosa.";

RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL: X87973; CAA61230.1; -

FT NON_TER 1
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;

Query Match 32.3%; Score 10; DB 2; Length 7;
Best local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SAT 3
1:1
DB 5 SST 7

RESULT 2

ID O54248 PRELIMINARY; PRT; 7 AA.
AC O54248;

DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE RplO protein (Fragment).
 GN RplO.
 OS Streptomyces griseus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2-3-11;
 RX MEDLINE=20011291; PubMed=10542330;
 RA Poehling S., Piepersberg W., Wehmeler U.F.;
 RT "Analysis and regulation of the sec Y gene from Streptomyces griseus
 N2-3-11 and interaction of the Sec Y protein with the SecA protein.";
 RL Blochim. Biophys. Acta 1447:298-302(1999).
 DR EMBL: X95915; CAA65160.1; -;
 FT NON_TER
 SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

Query Match 32.3%; Score 10; DB 2; Length 7;
 Best Local Similarity 40.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SATSL 5
 DB 2 TVTEL 6

RESULT 3
 P72081 PRELIMINARY; PRT; 7 AA.
 AC P72081;
 DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE 3'-methylcephem hydroxylase (Fragment).
 GN CEF.
 OS Nocardi lactamdurans.
 OC Bacteria; Firmicutes; Actinobacteridae; Actinobacteriales;
 OC Actinomycetales; Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.
 OX NCBI_TaxID=1913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6009872; PubMed=7557411;
 RA Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
 RA Liras P.;
 RT "Characterization of the cmh genes of Nocardi lactamdurans and
 RT Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem
 RT O-carbamoyltransferase for cephamycin biosynthesis.";
 RL Gene 162:21-27(1995).
 DR EMBL: Z21682; CAA9797.1; -;
 FT NON_TER
 SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;

Query Match 32.3%; Score 10; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 SATS 4
 DB 4 AVTS 7

RESULT 4
 P82181 PRELIMINARY; PRT; 6 AA.
 AC P82181;
 DT 01-JUN-2000 (TREMblrel. 14, Created)
 DT 01-JUN-2000 (TREMblrel. 14, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 beta (Fragment).

OS Spinacia oleracea (Spinach)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. ALMARO; TISSUE=LEAF.
 RX MEDLINE=20435798; PubMed=10674046;
 RA Yamaguchi K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR002363; Ribosomal_L10.
 DR InterPro: IPR002363; Ribosomal_L10eub.
 DR Pfam: PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 25.8%; Score 8; DB 10; Length 6;
 Best Local Similarity 66.7%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SAT 3
 DB 3 SRT 5

RESULT 5
 P82541 PRELIMINARY; PRT; 6 AA.
 AC P82541;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC STRAIN=CV. ALMARO; TISSUE=LEAF.
 RX MEDLINE=20435797; PubMed=10874039;
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the small subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28455-28465(2000).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -1- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
 CC -1- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
 CC -1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN P.I. S19 BETA
 CC FORM IS THE MINOR BASIC FORM.
 CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR002222; Ribosomal_S19.
 DR Pfam: PF00203; Ribosomal_S19; PARTIAL.
 DR PRINTS: PR00975; RIBOSOMALS19; PARTIAL.
 DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER
 SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 25.8%; Score 8; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

OY 4 SL 5
 11
 DB 3 SL 4

RESULT 6

P82182 PRELIMINARY; PRT; 6 AA.
 ID P82182;
 AC P82182;
 DT 01-JUN-2000 (TREMBlrel. 14, Created)
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
 OS Spinacia oleracea (Spinach).
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 NCBI_TaxID=3562;
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. ALVARO; TISSUE=LEAF;
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR001790; Ribosomal_L10.
 DR Pfam: PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 25.8%; Score 8; DB 10; Length 6;
 Best Local Similarity 66.7%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SAT 3
 11
 DB 3 SRT 5

RESULT 7

P83073 PRELIMINARY; PRT; 5 AA.
 ID P83073;
 AC P83073;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE 88 kDa protein (Fragment).
 OS Bacillus cereus.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 CC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dows B.C.A.;
 RT Submitted (Jul-2001) to the SWISS-PROT data bank.
 FT NON_TER
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 22.6%; Score 7; DB 2; Length 5;
 Best Local Similarity 33.3%; Pred. No. 6.7e+05;
 Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 LAD 7
 11
 DB 1 MKD 3

RESULT 8

O99007 PRELIMINARY; PRT; 5 AA.
 ID O99007;
 AC O99007;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE Alpha-amylase (EC 3.2.1.1) (Fragment).
 GN AMY1.
 OS Hordeum vulgare (Barley).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 CC Triticeae; Hordeum.
 NCBI_TaxID=4513;
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
 RX MEDLINE=91329704; PubMed=1831055;
 RA Jacobsen J.V., Close T.D.;
 RT "Control of transient expression of chimeric genes by gibberellin
 acid and abscisic acid in protoplasts prepared from mature barley
 aleurone layers.";
 RL Plant Mol. Biol. 16:713-721(1991).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
 CC BARLEY.
 DR EMBL: X54643; CAA38455.1; -
 KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family.
 FT NON_TER
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 22.6%; Score 7; DB 10; Length 5;
 Best Local Similarity 33.3%; Pred. No. 6.7e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 LAD 7
 11
 DB 1 MAN 3

RESULT 9

O47505 PRELIMINARY; PRT; 7 AA.
 ID O47505;
 AC O47505;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Mcca protein.
 GN MCCA.
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96099297; PubMed=8522520;
 RA Gonzalez-Pastor J.E., San Millan J.L., Castilla M.A., Moreno F.;
 RT "Structure and organization of plasmid genes required to produce the
 translation inhibitor microcin C7.";
 RL J. Bacteriol. 177:7131-7140(1995).

DR EMBL: X57583; CAA40808.1; -
 KW Plasmid.
 SO SEQUENCE 7 AA; 763 MW; 644DD4481B406F0 CRC64;

Query Match 22.6%; Score 7; DB 2; Length 7;
 Best Local Similarity 40.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 TSLAD 7
 1 1;
 DB 3 TGNAN 7

RESULT 10

007354 PRELIMINARY; PRT: 7 AA.

AC 007354;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE NifK (Fragment).
 GN NifK.
 OS *Synechococcus* sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
 CC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
 OX NCBI_TaxID=41431;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=RF-1;
 RX MEDLINE=98231861; PubMed=10217509;

RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
 RT "Organization and expression of nitrogen-fixation genes in the aerobic
 RT nitrogen-fixing unicellular cyanobacterium *Synechococcus* sp. strain
 RF-1."
 RL Microbiology 145:743-753(1999).
 DR EMBL: AF003700; AAC35193.1; -
 FT NON_TER 1 1
 SO SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;

Query Match 19.4%; Score 6; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 D 7
 1 1
 DB 4 D 4

RESULT 11

047029 PRELIMINARY; PRT: 7 AA.

AC 047029;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE Aad A1 protein (Fragment).
 GN Aad A1.
 OS *Enterobacter cloacae*.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter
 OX NCBI_TaxID=550;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94079349; PubMed=8257126;
 RA Rather P.N., Mann P.A., Mierza R., Hare R.S., Miller G.H., Shaw K.J.;
 RT "Analysis of the aac(3)-Via gene encoding a novel 3-N-
 RT acetyltransferase."
 RL Antimicrob. Agents Chemother. 37:2074-2079(1993).
 DR EMBL: M88012; AAA16193.1; -
 FT NON_TER 1 1
 SO SEQUENCE 7 AA; 744 MW; 633862D2C321A030 CRC64;

Query Match 19.4%; Score 6; DB 2; Length 7;
 Best Local Similarity 33.3%; Pred. No. 6.7e+05;

Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 TSL 5
 1 1;
 DB 2 TKV 4

RESULT 12

047477 PRELIMINARY; PRT: 7 AA.

AC 047477;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE Tpi protein (Fragment).
 GN tpi.
 OS *Escherichia coli*.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN 11
 RP SEQUENCE OF 7-7 FROM N.A.
 RX MEDLINE=85203917; PubMed=3158524;
 RA Hellinga H.W., Evans P.R.;
 RT "Nucleotide sequence and high-level expression of the major
 RT *Escherichia coli* phosphofructokinase."
 RL Eur. J. Biochem. 149:363-373(1985).
 RN 12
 RP SEQUENCE FROM N.A.
 RA Evans P.;
 RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X02519; CAA26359.1; -
 FT NON_TER 1 1
 SO SEQUENCE 7 AA; 773 MW; 7416D33DDDB1DB0 CRC64;

Query Match 19.4%; Score 6; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 AD 7
 1 1;
 DB 1 AE 2

RESULT 13

015897 PRELIMINARY; PRT: 7 AA.

AC 015897;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE (clone XP6A11A) (Fragment).
 OS *Homo sapiens* (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries."
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL: L32077; AAA73887.1; -
 FT NON_TER 1 1
 SO SEQUENCE 7 AA; 814 MW; 672B1DD372046B0 CRC64;

Query Match 19.4%; Score 6; DB 4; Length 7;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 AD 7
1:
DB 5 AE 6

DB 5 D 5

Search completed: February 25, 2003, 11:10:34
Job time : 30 secs

RESULT 14

P83274 PRELIMINARY: PRT: 7 AA.
AC P83274:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE FMRamide-like neuropeptide FLP1 (DRNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota: Metazoa: Arthropoda: Crustacea: Malacostraca:
OC Eumalacostraca: Eucarida: Decapoda: Pleocyemata: Caridea:
OC Palaemonoidea: Palaemonidae: Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-EYESTALK;
RA Sitthigorngul P., Saraithongkum W., Jaidechchoy S., Longyant S.,
RT Sitthigorngul W.;
RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -1- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KM Neuropeptide: Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA: 967 MW: 69D40729CA540AC0 CRC64;

Query Match 19.4%; Score 6; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

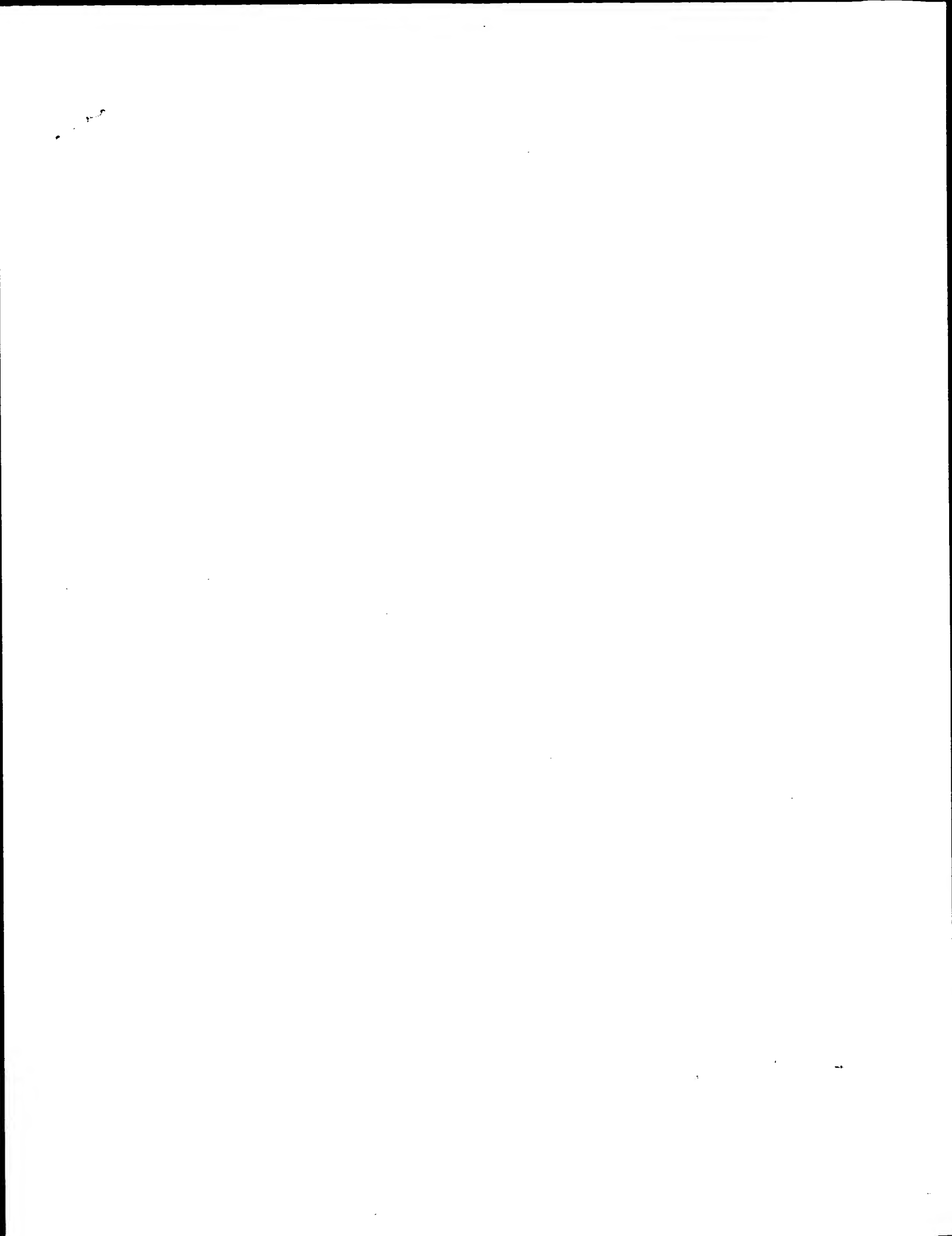
OY 7 D 7
1:
DB 1 D 1

RESULT 15

Q28742 PRELIMINARY: PRT: 7 AA.
AC Q28742:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Lagomorpha: Leporidae: Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL: K01698; AAA31415.1; -;
FT NON_TER 1
SQ SEQUENCE 7 AA: 916 MW: 6B1B1A1E69326B0 CRC64;

Query Match 19.4%; Score 6; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 D 7
1:



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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:06:13 : Search time 11 Seconds
(without alignments)
26.394 Million cell updates/sec

Title: US-09-743-482A-4

Perfect score: 31
Sequence: 1 SATSLAD 7

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 85

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	11	35.5	7 1 UC24_MAIZE	P80630 zea mays (m
2	10	32.3	4 1 ACH1_ACHFU	P35904 achalina fu
3	10	32.3	4 1 TMOF_SARBU	P41495 sarcophaga
4	9	29.0	4 1 RM01_YEAST	P36515 saccharomyc
5	8	25.8	7 1 CIA_ENTFA	P11932 enterococcu
6	8	25.8	7 1 PAR3_HAECC	P81298 haemophilu
7	8	25.8	7 1 PAR3_PANRE	P41874 panagrellus
8	8	25.8	7 1 MNP1_LEPDE	P42984 leptinotars
9	8	25.8	7 1 UH11_RAT	P56576 rattus norv
10	7	22.6	3 1 LUXE_VIBRI	P24272 vibrio fisc
11	7	22.6	5 1 UXA4_CHLTR	P38005 chlamydia t
12	6	19.4	4 1 DCMS_PSECH	P19918 pseudomonas
13	6	19.4	4 1 OCP3_OCTMI	P56648 octopus min
14	6	19.4	4 1 OCP3_OCTMI	P56648 octopus min
15	6	19.4	5 1 BIOA_CITFR	P13071 citrobacter
16	6	19.4	5 1 BIOB_CITFR	P12997 citrobacter
17	6	19.4	5 1 RE11_LITRU	P82070 litorea rub
18	6	19.4	5 1 TRM3_ECOLI	P13973 escherichia
19	6	19.4	6 1 ASP2_LACSN	P82655 lactobacill
20	6	19.4	6 1 LOK1_LOCM1	P41491 locusta mig
21	6	19.4	6 1 OVA_LEPDE	P42985 leptinotars
22	6	19.4	6 1 TRP1_PSEPU	P36414 pseudomonas
23	6	19.4	6 1 UNO6_CLOPA	P81351 clostridium
24	6	19.4	6 1 VP19_HSVIK	P23210 herpes slmp
25	6	19.4	7 1 ALI2_CARMA	P81805 carcinos ma
26	6	19.4	7 1 ALI3_CARMA	P81806 carcinos ma
27	6	19.4	7 1 ALI4_CARMA	P81807 carcinos ma
28	6	19.4	7 1 ALI5_CARMA	P81808 carcinos ma
29	6	19.4	7 1 ALI7_CYDPO	P82158 cydia pomon
30	6	19.4	7 1 CHOX_ALCSP	P16101 alcaligenes
31	6	19.4	7 1 EI05_LITRU	P82101 litorea rub
32	6	19.4	7 1 FAR1_HELTI	P41871 heliosoma tr
33	6	19.4	7 1 FAR2_PROCL	P38498 procambatus

34	6	19.4	7 1 FAR6_CALVO	P41866 calliphora
35	6	19.4	7 1 GFRP_MOUSE	P99025 mus musculu
36	6	19.4	7 1 UPO3_MOUSE	P38641 mus musculu
37	6	19.4	7 1 UPO4_MOUSE	P38642 mus musculu
38	5	16.1	4 1 TUPT_HUMAN	P01858 homo sapien
39	5	16.1	5 1 EI04_LITRU	P82100 litorea rub
40	5	16.1	5 1 PRCT_PERAM	P01373 periplaneta
41	5	16.1	5 1 PSK_DAVCA	P58261 daucus caro
42	5	16.1	5 1 RE31_LITRU	P82072 litorea rub
43	5	16.1	5 1 RE32_LITRU	P82073 litorea rub
44	5	16.1	5 1 SUCA_ACHDO	P19991 acheta dome
45	5	16.1	7 1 CCF1_ENTFA	P20104 enterococcu

ALIGNMENTS

RESULT 1
UC24_MAIZE STANDARD; PRT; 7 AA.
AC P80630:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 447)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=coleoptile;
RA Touret P., Ricciardi F., Morin C., Damerlat C., Huet J.-C.,
RT Permollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -I- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 30.0 kDa.
CC Maize-2DPAGE; P80630; COLEOPTILE.
DR MaizeDB; 123956; -.
DT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA: 665 MW: 6DC1B5B33DC1B5D0 CRC64;
Query Match 35.5%; Score 11; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 SATSLA 6
DB 2 TAKSTA 7
RESULT 2
ACH1_ACHFU STANDARD; PRT; 4 AA.
AC P35904:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Achalin-I.
OS Achalina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Stylomatophora;
OC Achatinacea; Achatinidae; Achalina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC STRAIN=Perussac; TISSUE=Ganglion;
RX MEDLINE=89273551; PubMed=2597281;
Kamataki Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,

RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.,
 RT "Achatin-I, an endogenous neuroexcitatory retropeptide from Achatina
 RT fulica Ferrussac containing a D-amino acid residue.",
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN-FERUSSAC; TISSUE-Heart atrium;
 RX MEDLINE=91264856; PubMed=1675568;
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.,
 RT "Purification of achatin-I from the atria of the African giant snail,
 RT Achatina fulica, and its possible function.",
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=93014529; PubMed=1399265;
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA "Crystal structure and molecular conformation of achatin-I
 RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 RT D-amino acid residue.",
 RL Int. J. Pept. Protein Res. 39:258-264(1992).
 CC -1- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
 CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
 CC NEURON (DON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
 CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
 DR PIR: A32480; A32480.
 KW Hormone: D-amino acid.
 FT MOD_RES 2 2 D-PHENYALANINE.
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C81000000 CRC64;

Query Match
 Best Local Similarity 32.3%; Score 10; DB 1; Length 4;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AD 7
 DB 3 AD 4

RESULT 3
 ID TMOF_SARBU STANDARD; PRT; 6 AA.
 AC P41495;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Trypsin-modulating oostatic factor (TMOF).
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Oestroidea; Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Ovary;
 RX MEDLINE=94211930; PubMed=8159807;
 RA Bytemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
 RA de Loof A.,
 RT "Sequencing and characterization of trypsin modulating oostatic
 RT factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
 RT (Sarcophaga) bullata.",
 RL Regul. Pept. 50:61-72(1994).
 CC -1- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
 CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
 CC CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
 CC DEVELOPMENT.
 CC -1- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
 CC EPITHELIUM AFTER A BLOOD MEAL.
 KW Hormone.
 SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match
 Best Local Similarity 32.3%; Score 10; DB 1; Length 6;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 TSL 5
 DB 3 TNL 5

RESULT 4
 ID RM01_YEAST STANDARD; PRT; 4 AA.
 AC P36515;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Mitochondrial 60S ribosomal protein L1 (tmL1) (Fragment).
 GN MRPL1.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91285106; PubMed=2060626;
 RA Grohmann L., Graack H.-R., Kruff V., Choi T., Goldschmidt-Reisin S.,
 RA Kitakawa M.;
 RT "Extended N-terminal sequencing of proteins of the large ribosomal
 RT subunit from yeast mitochondria.",
 RL FEBS Lett. 284:51-56(1991).
 DR PIR: S17255; S17255.
 DR SGD: L0002681; MRPL1.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D00000000 CRC64;

Query Match
 Best Local Similarity 29.0%; Score 9; DB 1; Length 4;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SAT 3
 DB 1 SVT 3

RESULT 5
 ID CIA_ENTFA STANDARD; PRT; 7 AA.
 AC P11932;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
 OS Enterococcus faecalis (Clumping-inducing agent) (CIA).
 CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87005252; PubMed=3093276;
 RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
 RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
 RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
 RT CAM373.",
 RL FEBS Lett. 206:69-72(1986).
 CC -1- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS.
 CC HARBORING PAM373.
 CC -1- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
 CC SPECIFICITY OF PHEROMONES TO PLASMIDS.
 CC -1- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
 DR PIR: A25269; A25269.
 KW Pheromone.
 SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;

Query Match 25.8%; Score 8; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LA 6
 11
 DB 5 LA 6

RESULT 6
 FAR3_HAECO STANDARD; PRT; 7 AA.

ID FAR3_HAECO
 AC P81298;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide PF3 (KSAVMRF-amide).
 OS Haemochus contortus (Barber pole worm).
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
 CC NCBI_TaxID=6289;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Neuron;
 RX MEDLINE=99318264; PubMed=10391380;
 RA Marks N.J., Sangster N.C., Maule A.G., Halton D.W., Thompson D.P.,
 RA Geary T.G., Shaw C.;
 RT "Structural characterisation and pharmacology of KHELFamide (AF2)
 and KSAVMRFamide (PF3/AF8) from Haemonchus contortus.";
 RL Mol. Biochem. Parasitol. 100:185-194(1999).
 CC -1- FUNCTION: ACTIVE ON NEUROMUSCULATURE.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY

KW Neuropeptide; Amidation.
 FT MOD.RES 7
 SQ SEQUENCE 7 AA; 902 MW; 69D406B5DC5B350 CRC64;

Query Match 25.8%; Score 8; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SA 2
 11
 DB 2 SA 3

RESULT 7
 FAR3_PANRE STANDARD; PRT; 7 AA.

ID FAR3_PANRE
 AC P41874;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRamide-like neuropeptide PF3 (KSAVMRF-amide).
 OS Panagrellus redivivus.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrellidae; Panagrellidae; Panagrellus.
 CC NCBI_TaxID=6233;
 RN [1]

RN SEQUENCE AND SYNTHESIS.
 RX MEDLINE=94235053; PubMed=8179635;
 RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
 RA Geary T.G., Thim L.;
 RT "KSAVMRFamide: a novel FMRamide-related heptapeptide from the free-
 living nematode, Panagrellus redivivus, which is myoactive in the
 parasitic nematode, Ascaris suum.";
 RL Biochem. Biophys. Res. Commun. 200:973-980(1994).
 CC -1- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT
 CC MUSCLE TENSION INCREASE.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY

CC PTR: PC2132; PC2132.
 KW Neuropeptide; Amidation.

FT MOD.RES 7
 SQ SEQUENCE 7 AA; 902 MW; 69D406B5DC5B350 CRC64;

Query Match 25.8%; Score 8; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SA 2
 11
 DB 2 SA 3

RESULT 8
 MNPL_LEPDE STANDARD; PRT; 7 AA.

ID MNPL_LEPDE
 AC P42984;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Myotropic neuropeptide 1 (led-MNP-1).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pseryota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 CC Cucujiformia; Phytophaga; Chrysomeloidea; Chrysomelidae;
 CC Chrysomelinae; Leptinotarsa.
 CC NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.

RC TISSUE=Head;
 RX MEDLINE=95380343; PubMed=7651886;
 RA Spilthals K., Vankesterden A., Schoofs L., Torrekens S.,
 RA Grauwels L., van Leuven F., de Loof A.;
 RT "Identification, characterization, and immunological localization of
 a novel myotropic neuropeptide in the Colorado potato beetle,
 Leptinotarsa decemlineata.";
 RT Peptides 16:365-374(1995).

CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC OVIDUCT.
 KW Neuropeptide; Amidation.
 FT MOD.RES 7
 SQ SEQUENCE 7 AA; 705 MW; 6DD7376874555D80 CRC64;

Query Match 25.8%; Score 8; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LA 6
 11
 DB 6 LA 7

RESULT 9
 UH11_RAT STANDARD; PRT; 7 AA.

ID UH11_RAT
 AC P56576;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]

RN SEQUENCE.
 RC SPRAIN-Mistar; TISSUE=Heart;
 RA Li X.-P., Pleissner K.-P., Scheeler C., Regitz-Zagrosek V., Salkov J.,
 RA Jungblut P.R.;
 RL Submitted (SEP-1998) ON THE SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 8.5, ITS MW IS: 42 KDa.
 CC FT UNSURE 2
 OR A.

FT NON_TER 7 7

SQ SEQUENCE 7 AA: 775 MW: 6866DB04D0C5A6B0 CRC64;
 Query Match 25.8%; Score 8; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SA 2
 11
 DB 2 SA 3
 RESULT 10
 LUXE_VIBRI
 ID LUXE_VIBRI STANDARD: PRT; 3 AA.
 AC P24272;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-
 protein synthetase) (Fragment).
 GN LUXE.
 OS Vibrio fischeri.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91072226; PubMed=2254256;
 RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
 RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
 site for the lux operon."
 RL J. Bacteriol. 172:6797-6802(1990).
 CC -1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
 CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
 CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
 CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
 CC -1- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
 CC an acyl-protein thioester.
 CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 DR EMBL; M62812; ; NOT_ANNOTATED_CDS.
 KW Luminescence; Ligase.
 FT NON_TER 1
 SQ SEQUENCE 3 AA: 374 MW: 6AA3303000000000 CRC64;
 Query Match 22.6%; Score 7; DB 1; Length 3;
 Best Local Similarity 33.3%; Pred. No. 1.1e+05;
 Matches 1: Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 5 LAD 7
 11
 DB 1 IKD 3
 RESULT 11
 UXAA_CHLTR
 ID UXAA_CHLTR STANDARD: PRT; 5 AA.
 AC P38005;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Unknown protein from 2D-page from elementary body (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]

RP SEQUENCE.
 RC STRAIN=L2/434/Bu;
 RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
 RA Comanducci M., Christlanen G., Birkelund S., Vitreton E., Ratli G.,
 RA Ballini V.;
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
 DR Siena-2DPAGE; P38005; -;
 FT NON_TER 5
 SQ SEQUENCE 5 AA: 474 MW: 75BA865A800000 CRC64;
 Query Match 22.6%; Score 7; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 2: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 SATS 4
 11
 DB 2 SDDS 5
 RESULT 12
 DCMS_PSECH
 ID DCMS_PSECH STANDARD: PRT; 4 AA.
 AC P19918;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit S) (CO-DH S) (Fragment).
 GN CUTS.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Bradyrhizobium group.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxyotrophic bacteria."
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -1- COFACTOR: BINDS TWO 2FE-2S CLUSTERS.
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR: P10146; P10146.
 KW Oxidoreductase; Iron-sulfur.
 FT NON_TER 4
 SQ SEQUENCE 4 AA: 420 MW: 6DD33DD6F0000000 CRC64;
 Query Match 19.4%; Score 6; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 1: Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 5 LA 6
 11
 DB 1 MA 2
 RESULT 13
 OCP1_OCTMI
 ID OCP1_OCTMI STANDARD: PRT; 4 AA.
 AC P58648;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cardioactive peptides Ocp-1/Ocp-2.
 OS Octopus minor (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;

```

OC Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RX TISSUE=Brain;
MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RL Octopus minor.";
Peptides 21:623-630(2000).
CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-2 is a 1000 time less
CC active than Ocp-1.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
FT MOD_RES 2 2 D-PHENYALANINE.
SQ SEQUENCE 4 AA: 394 MW: 6AA879C810000000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 D 7
DB 4 D 4

RESULT 14
OCP3_OCTMT STANDARD: PRT; 4 AA.
AC P58649;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RX TISSUE=Brain;
MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RL Octopus minor.";
Peptides 21:623-630(2000).
CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-4 is a 1000 time less
CC active than Ocp-3.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
FT MOD_RES 2 2 D-SERINE (IN OCP-4).
SQ SEQUENCE 4 AA: 463 MW: 6AB365B810000000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 D 7
DB 4 D 4

RESULT 15
BIOA_CITFR STANDARD: PRT; 5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)

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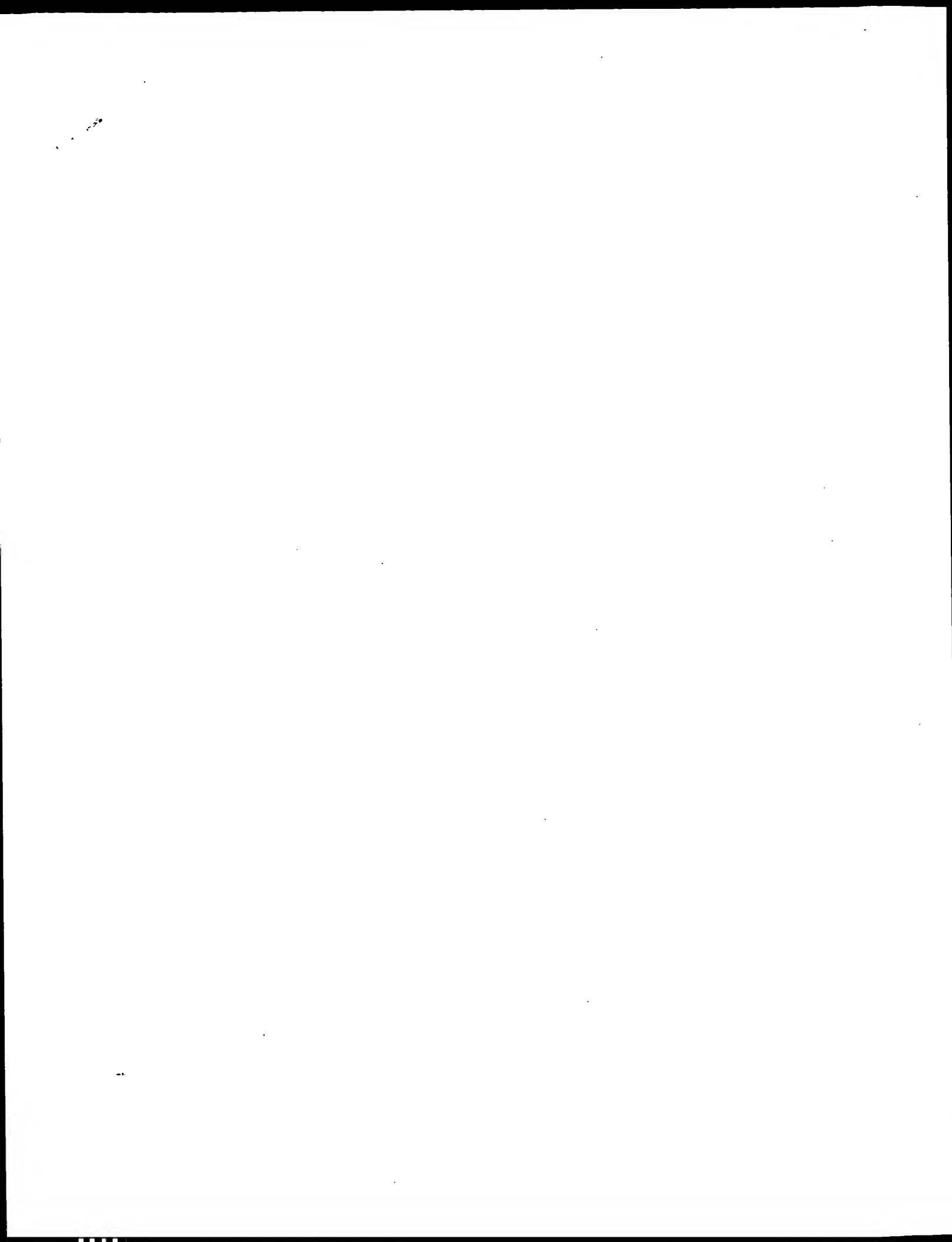
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (NAPA
DE aminotransferase) (Fragment).
GN BIOA.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminononanoate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: Biotin biosynthesis.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: M21922; NOT_ANNOTATED_CDS.
CC InterPro: IPR000954; AminoTran_3.
CC PROSITE: PS00600; AA_TRANSFR_CLASS_3; PARTIAL.
KW Biotin biosynthesis; Transferase; Aminotransferase;
KW Pyridoxal phosphate.
FT NON_TER 5 5
SQ SEQUENCE 5 AA: 582 MW: 6AAAB1BA6F00000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TS 4
DB 2 TT 3

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Search completed: February 25, 2003, 11:09:59
 Job time : 13 secs



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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:58:03 : Search time 14 Seconds
(Without alignments)
23.118 Million cell updates/sec

Title: US-09-743-482A-2
Perfect score: 59
Sequence: 1 QASQDIGNMLA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 83753

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	62.7	11	1	US-07-942-245-518
2	36	61.0	11	2	US-08-480-434-76
3	36	61.0	11	2	US-08-053-451B-76
4	36	61.0	11	3	US-08-649-100-11
5	36	61.0	11	3	US-08-649-100-27
6	35	59.3	11	1	US-07-942-245-496
7	31	52.5	11	1	US-08-137-117D-117
8	31	52.5	11	2	US-08-436-717-117
9	31	52.5	11	2	US-08-318-157B-20
10	31	52.5	11	3	US-08-599-226-7
11	31	52.5	11	4	US-09-125-098-7
12	31	52.5	11	4	US-08-918-148-20
13	30	50.8	11	1	US-07-942-245-497
14	30	50.8	11	2	US-08-480-434-66
15	30	50.8	11	2	US-08-480-434-75
16	30	50.8	11	2	US-08-053-451B-66
17	30	50.8	11	2	US-08-053-451B-75
18	30	50.8	11	2	US-08-182-067-4
19	30	50.8	11	2	US-08-465-313-4
20	27	45.8	6	2	US-08-482-228-162
21	27	45.8	6	3	US-08-482-528-162
22	27	45.8	8	4	US-09-082-279B-1486
23	27	45.8	8	4	US-09-315-304B-1640
24	27	45.8	11	1	US-07-942-245-494
25	26	44.1	8	1	US-08-249-371-7
26	26	44.1	8	1	US-08-497-134A-28
27	26	44.1	8	5	PCT-US95-06451-7

28	26	44.1	9	1	US-08-186-266-15	Sequence 15, App1
29	26	44.1	9	2	US-08-350-260A-534	Sequence 534, App
30	26	44.1	9	3	US-08-159-339A-582	Sequence 582, App
31	26	44.1	9	4	US-08-197-484-58	Sequence 58, App1
32	26	44.1	9	4	US-08-197-484-137	Sequence 137, App
33	26	44.1	9	5	PCT-US95-02121-58	Sequence 58, App1
34	26	44.1	9	5	PCT-US95-02121-137	Sequence 137, App
35	26	44.1	10	1	US-08-186-266-19	Sequence 19, App1
36	26	44.1	11	1	US-07-942-245-495	Sequence 495, App
37	26	44.1	11	1	US-08-649-272A-1	Sequence 1, App1
38	26	44.1	11	1	US-08-024-253-16	Sequence 16, App1
39	26	44.1	11	3	US-09-105-799-1	Sequence 1, App1
40	26	44.1	11	4	US-09-406-535-8	Sequence 8, App1
41	25	42.4	6	1	US-08-401-908-8	Sequence 279, App1
42	25	42.4	7	4	US-09-258-754-279	Sequence 279, App
43	25	42.4	7	4	US-09-042-107-279	Sequence 279, App
44	25	42.4	7	4	US-09-400-208B-9	Sequence 9, App1
45	25	42.4	8	1	US-08-798-897-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
US-07-942-245-518
: Sequence 518, Application US/07942245
: Patent No. 5639641
: GENERAL INFORMATION:
: APPLICANT: PEDERSEN, Jan T.
: APPLICANT: SEARLE, Stephen M.J.
: APPLICANT: REES, Anthony R.
: APPLICANT: ROGUSKA, Michael A.
: APPLICANT: GUIDI, Braydon C.
: TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
: NUMBER OF SEQUENCES: 522
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
: STREET: 2100 Pennsylvania Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: United States
: ZIP: 20037-3202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: HP 9000/700 Workstation
: OPERATING SYSTEM: UNIX
: SOFTWARE: In house
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/942,245
: FILING DATE: 09-SEP-1992
: CLASSIFICATION: 530
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 293-7060
: TELEFAX: (202) 293-7860
: TELEX: 6491103
: INFORMATION FOR SEQ ID NO: 518:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-07-942-245-518

Query Match Score 37; DB 1; Length 11;
Best Local Similarity 63.6%; Pred. No. 1.8;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QASQDIGNMLA 11
DB 1 RASQISRMMLA 11

RESULT 2
US-08-480-434-76
Sequence 76, Application US/08480434
Patent No. 5811248
GENERAL INFORMATION:
APPLICANT: Charles C. Dittow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-480-434-76

Query Match
Best Local Similarity 61.0%; Score 36; DB 2; Length 11;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNWL 10
:|||||1:1
DB 1 RASQDISNYL 10

RESULT 3
US-08-053-451B-76
Sequence 76, Application US/08053451B
Patent No. 5953584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Dittow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-76

Query Match
Best Local Similarity 61.0%; Score 36; DB 2; Length 11;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNWL 10
:|||||1:1
DB 1 RASQDISNYL 10

RESULT 4
US-08-649-100-11
Sequence 11, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGERAZU
APPLICANT: CO, MAN SONG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-100-11

Query Match 61.0%; Score 36; DB 3; Length 11;
Best Local Similarity 70.0%; Pred. No. 2.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QASODIGNWL 10
:|||||:|
Db 1 RASODISNYL 10

RESULT 5
US-08-649-100-27
Sequence 27, Application US/08649100
Patent No. 6114507

GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KANON
APPLICANT: MATSUDA, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SONG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-100-27

Query Match 61.0%; Score 36; DB 3; Length 11;
Best Local Similarity 70.0%; Pred. No. 2.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QASODIGNWL 10
:|||||:|
Db 1 RASODISNYL 10

RESULT 6
US-07-942-245-496
Sequence 496, Application US/07942245

Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 496:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-496

Query Match 59.3%; Score 35; DB 1; Length 11;
Best Local Similarity 70.0%; Pred. No. 4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QASODIGNWL 10
:|||||:|
Db 1 RASODINNFL 10

RESULT 7
US-08-137-117D-117
Sequence 117, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-137-117D-117

Query Match 52.5%; Score 31; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNML 10
Db 1 RASODISSYL 10

RESULT 8
US-08-436-717-117
Sequence 117, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-436-717-117

Query Match 52.5%; Score 31; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNML 10
Db 1 RASODISSYL 10

RESULT 9
US-08-318-157B-20
Sequence 20, Application US/08318157B
Patent No. 5874540
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
APPLICANT: ARMOUR, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,157B
FILING DATE: 05-OCT-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-157B-20

Query Match 52.5%; Score 31; DB 2; Length 11;

Best Local Similarity 54.5%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 QASODIGNWLA 11
Db 1 KASQDVGTSA 11

RESULT 10

US-08-599-226-7
Sequence 7, Application US/08599226
Patent No. 6090382

GENERAL INFORMATION:

APPLICANT: Salfeld, Jochen G.
APPLICANT: Allen, Deborah J.
APPLICANT: Hoogenboom, Hendricus R.J.M.
APPLICANT: Kaymakalan, Zehra
APPLICANT: Labkovsky, Boris
APPLICANT: Mankovich, John A.
APPLICANT: McGuinness, Brian T.
APPLICANT: Roberts, Andrew J.
APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Tristian J.
APPLICANT: White, Michael
TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
NUMBER OF SEQUENCES: 37
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,226
FILING DATE: 08-FEB-1996
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-599-226-7

Query Match 52.5%; Score 31; DB 3; Length 11;
Best Local Similarity 63.6%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 QASODIGNWLA 11
Db 1 KASQDVGTSA 11

RESULT 11

US-09-125-098-7
Sequence 7, Application US/09125098
Patent No. 6238562

GENERAL INFORMATION:

APPLICANT: Salfeld, Jochen G.
APPLICANT: Allen, Deborah J.
APPLICANT: Hoogenboom, Hendricus R.J.M.
APPLICANT: Kaymakalan, Zehra
APPLICANT: Labkovsky, Boris
APPLICANT: Mankovich, John A.
APPLICANT: McGuinness, Brian T.
APPLICANT: Roberts, Andrew J.
APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Tristian J.
APPLICANT: White, Michael
TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
NUMBER OF SEQUENCES: 37
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,098
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,226
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-125-098-7

Query Match 52.5%; Score 31; DB 4; Length 11;
Best Local Similarity 63.6%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 QASODIGNWLA 11
Db 1 KASQDVGTSA 11

RESULT 12

US-08-918-148-20
Sequence 20, Application US/08918148A
Patent No. 6142220

GENERAL INFORMATION:

APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A

```

: CURRENT FILING DATE: 1997-08-25
: NUMBER OF SEQ ID NOS: 79
: SEQ ID NO 20
: LENGTH: 11
: TYPE: PRT
: ORGANISM: artificial
: FEATURE:
: NAME/KEY: SE5scFv, 10D10scFv, 12D5scFv VL CDR1
: LOCATION: 1-11
: OTHER INFORMATION: also 12B5scFv VL CDR1
US-08-918-148-20

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Query Match	52.5%	Score 31	DB 4	Length 11
Best local Similarity	54.5%	Pred. No. 19		
Matches	6	Conservative	3	Mismatches 2; Indels 0; Gaps 0

RESULT 13
 US-07-942-245-497
 : Sequence 497, Application US/07942245
 : Patent No. 5639641
 : GENERAL INFORMATION:
 : APPLICANT: PEDERSEN, Jan T.
 : APPLICANT: SEARLE, Stephen M.J.
 : APPLICANT: REES, Anthony R.
 : APPLICANT: ROGUSKA, Michael A.
 : APPLICANT: GUILD, Bradley C.
 : TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
 : ANTI-BODIES
 : TITLE OF INVENTION: 522
 : NUMBER OF SEQUENCES: 522
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Sudhree, Mion, Zinn, Macpeak & Seas
 : STREET: 2100 Pennsylvania Avenue, N.W.
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: United States
 : ZIP: 20037-3202
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: HP 9000/700 workstation
 : OPERATING SYSTEM: UNIX
 : SOFTWARE: in house
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/07/942,245
 : FILING DATE: 09-SEP-1992
 : CLASSIFICATION: 530
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (202) 293-7060
 : TELEFAX: (202) 293-7860
 : TELEX: 6491103
 : INFORMATION FOR SEQ ID NO: 497:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 11 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 US-07-942-245-497

Query Match	50.8%;	Score 30;	DB 1;	Length 11;
Best Local Similarity	75.0%;	Pred. No. 28;		
Matches	6;	Conservative	1;	Mismatches 1;

RESULT 14
US-08-480-434-66

Sequence 66, Application US/08480434
Patent No. 5811248
GENERAL INFORMATION:
APPLICANT: Charles C. Dittow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 11.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N

```

50.8%; Score 30; DB 2; Length 11;
Best Local Similarity 54.5%;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 QASDPICGNWLA 11
      :|||||::|:
db 1 KASDPDKSYLS 11

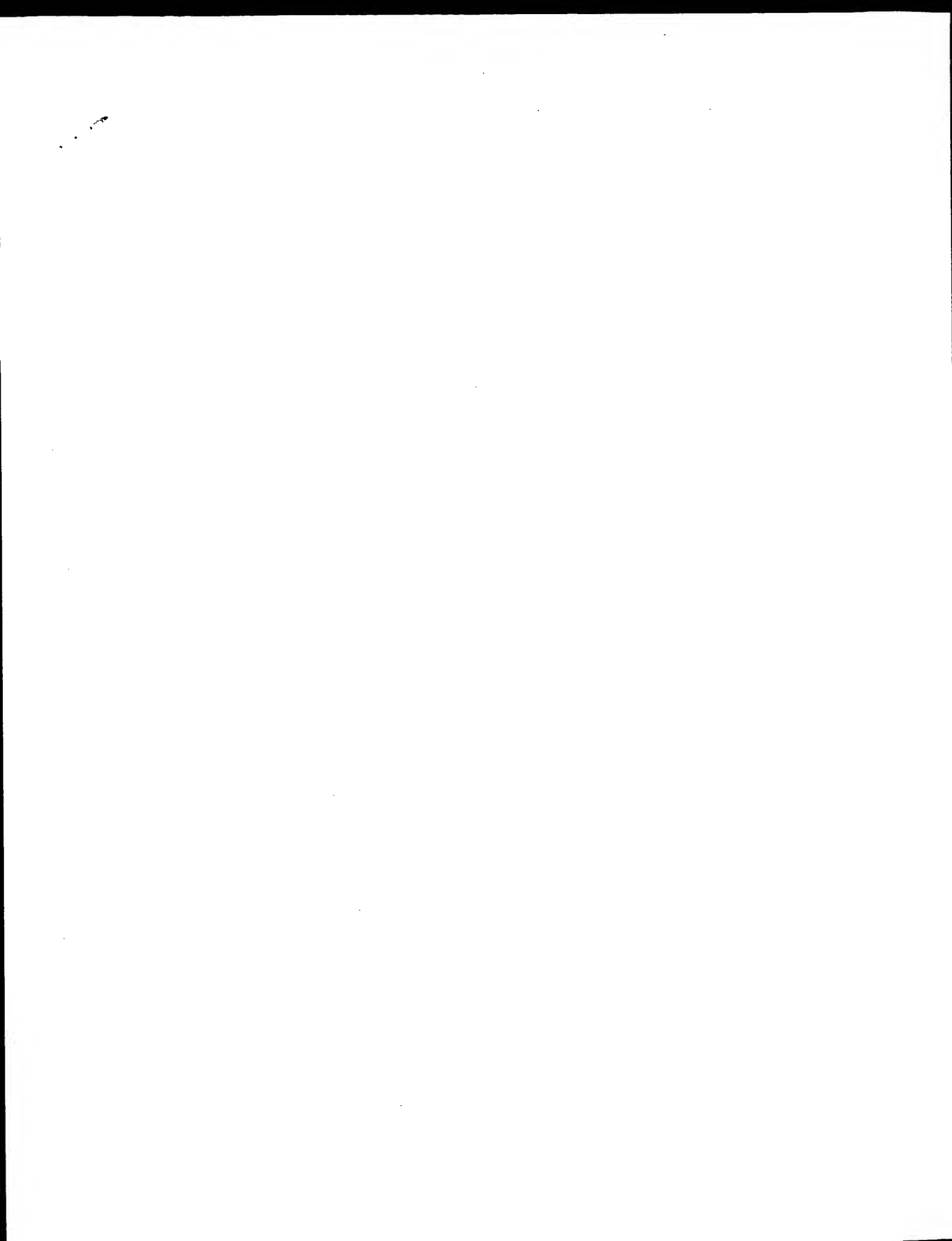
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RESULT 15 434-75
 US-08-480-434-75
 Sequence 75, Application US/08480434
 Patent No. 5811248
 GENERAL INFORMATION:
 APPLICANT: Charles C. Dillow, et al.
 TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS.
 NUMBER OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
 NUMBER OF SEQUENCES: 88
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennile & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.24
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-480-434-75

Query Match 50.8%; Score 30; DB 2; Length 11;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 QASODIGNMMLA 11
:|||||:|:
Db 1 KASODIKSYLS 11

Search completed: February 25, 2003, 11:06:29
Job time : 16 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 11:07:38 ; Search time 47 seconds
(without alignments)
14.318 Million cell updates/sec

Title: US-09-743-482A-4

Perfect score: 31

Sequence: 1 SATSLAD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 456

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	51.6	6	2	PT0519
2	14	45.2	4	2	I48126
3	13	41.9	6	2	PT0645
4	13	41.9	5	2	PT0624
5	13	41.9	5	2	PT0625
6	13	41.9	5	2	PT0713
7	13	41.9	5	2	H4817
8	13	41.9	5	2	F4817
9	13	41.9	5	2	B4817
10	13	41.9	5	2	D4817
11	13	41.9	6	2	I51317
12	13	41.9	6	2	PT0621
13	13	41.9	6	2	PT0730
14	13	41.9	6	4	S15596
15	13	41.9	7	2	S20446
16	13	41.9	7	2	PH1602
17	13	41.9	7	2	PT0579
18	13	41.9	7	2	PT0581
19	12	38.7	7	2	PC1316
20	11	35.5	4	2	PT0551
21	11	35.5	5	2	PT0597
22	11	35.5	6	2	PT0643
23	11	35.5	7	2	A34026
24	11	35.5	7	2	E48394
25	11	35.5	7	2	PT0665
26	11	35.5	7	2	PT0567
27	11	35.5	7	2	PT0688
28	11	35.5	7	2	PT0586
29	10	32.3	4	2	A32480

30	10	32.3	4	2	A26209	protein-glutamine
31	10	32.3	5	2	S11075	alcohol dehydrogen
32	10	32.3	5	2	PT0686	T-cell receptor be
33	10	32.3	5	2	PT0651	T-cell receptor be
34	10	32.3	6	2	A44916	mosquitoicidal toxi
35	10	32.3	6	2	A20186	fatty-acid synthas
36	10	32.3	7	4	PT0599	T-cell receptor be
37	10	32.3	7	4	A58725	virotaxin - destro
38	9	29.0	3	3	PT0636	T-cell receptor be
39	9	29.0	3	3	PT0622	T-cell receptor be
40	9	29.0	4	2	S18401	thyroglobulin - do
41	9	29.0	4	2	S17255	ribosomal protein
42	9	29.0	4	2	PT0696	T-cell receptor be
43	9	29.0	4	2	PT0712	T-cell receptor be
44	9	29.0	4	2	PT0698	T-cell receptor be
45	9	29.0	4	2	PT0566	T-cell receptor be

ALIGNMENTS

RESULT 1

PT0519 T-cell receptor beta chain V-D-J region (100-4c) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0519

R:Peeney, A.J. 174, 115-124, 1991

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0519

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FEF>

A:Experimental source: adult thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 51.6%; Score 16; DB 2; Length 6;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATSLAD 7

DB 1 ASSLMD 6

RESULT 2

I48126 alpha-tubulin - Chinese hamster (fragment)

C:Species: Cricetulus griseus (Chinese hamster)

C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999

C:Accession: I48126

R:Elliot, E.M.; Sarangi, F.; Henderson, G.; Ling, V.

Can. J. Biochem. Cell Biol. 63, 511-518, 1985

A:Title: Cloning of 11 alpha-tubulin gene sequences from the genome of Chinese hamster

A:Reference number: I48126; MUID:86001952; PMID:2931165

A:Accession: I48126

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6 <RBS>

A:Cross-references: GB:M25895; NID:9341417; PIDN:AAA74493.1; PID:9516601

C:Genetics:

A:introns: 3/3

Query Match 45.2%; Score 14; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LAD 7

DB 3 LAD 5

```
RESULT 3
PT0645
T-cell receptor beta chain V-D-J region (111-1A1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0645
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE2>
A:Experimental source: newborn thymus, strain BALB/c, 111-1A1
A:Accession: PT0626
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE2>
A:Experimental source: newborn thymus, strain BALB/c, 120-2CJ
C:Keywords: T-cell receptor

Query Match
Best Local Similarity 41.9%; Score 13; DB 2; Length 4;
Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSL 5
DB 1 ASSL 4

RESULT 4
PT0624
T-cell receptor beta chain V-D-J region (120-1K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0624
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match
Best Local Similarity 41.9%; Score 13; DB 2; Length 5;
Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSL 5
DB 1 ASSL 4

RESULT 5
PT0625
T-cell receptor beta chain V-D-J region (120-2S) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0625
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>
A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match
Best Local Similarity 41.9%; Score 13; DB 2; Length 5;
Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSL 5
DB 1 ASSL 4

RESULT 6
PT0713
T-cell receptor beta chain V-D-J region (165-3C) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0713
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE2>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match
Best Local Similarity 41.9%; Score 13; DB 2; Length 5;
Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSL 5
DB 1 ASSL 4

RESULT 7
H44817
34.5K structural protein - Leuconostoc oenos phage P32 (fragment)
C:Species: Leuconostoc oenos phage P32
C>Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: H44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NCBI backbone (NCBI:70332)

Query Match
Best Local Similarity 41.9%; Score 13; DB 2; Length 5;
Pred. No. 100.0%;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSL 4
DB 2 ATSL 4

RESULT 8
F44817
34.5K structural protein - Leuconostoc oenos phage P54 (fragment)
C:Species: Leuconostoc oenos phage P54
C>Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: F44817
A:Molecule type: protein
```

A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NCBI backbone (NCBIP:70335)

Query Match
Best Local Similarity 100.0%; Score 13; DB 2; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATS 4
Db 2 ATS 4

RESULT 9

B44817
34.5K structural protein - Leuconostoc oenos phage Pztl1-15 (fragment)

C:Species: Leuconostoc oenos phage Pztl1-15
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998

C:Accession: B44817

R:Arndt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A:Title: Lysogeny in Leuconostoc oenos.

A:Reference number: A44817; MUID:92085033; PMID:1748868

A:Accession: B44817

A:Molecule type: protein

A:Residues: 1-5 <ARE>

A:Note: sequence extracted from NCBI backbone (NCBIP:70342)

Query Match
Best Local Similarity 100.0%; Score 13; DB 2; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

OY 2 ATS 4
Db 2 ATS 4

RESULT 10

D44817
35K structural protein - Leuconostoc oenos phage Pat5-12 (fragment)

C:Species: Leuconostoc oenos phage Pat5-12
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998

C:Accession: D44817

R:Arndt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A:Title: Lysogeny in Leuconostoc oenos.

A:Reference number: A44817; MUID:92085033; PMID:1748868

A:Accession: D44817

A:Molecule type: protein

A:Residues: 1-5 <ARE>

A:Note: sequence extracted from NCBI backbone (NCBIP:70340)

Query Match
Best Local Similarity 100.0%; Score 13; DB 2; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATS 4
Db 2 ATS 4

RESULT 11

I51317

bHLH transcription factor inhibitor - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: I51317

R:Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G.

Mech. Dev. 50, 119-130, 1995

A:Title: Id gene activity during Xenopus embryogenesis.

A:Reference number: I51316; MUID:95344988; PMID:7619724

A:Accession: I51317

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-6 <ZHA>
A:Cross-references: GB:S79038; MUID:q1042006; PIDN:AA014294.1; PID:q4261994

C:Genetics:
A:Gene: Xidib
Query Match
Best Local Similarity 100.0%; Score 13; DB 2; Length 6;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SAT 3
Db 1 SAT 3

RESULT 12

PT0621
T-cell receptor beta chain V-D-J region (111-1M) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0621

R:Reaney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0621

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FEZ>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match
Best Local Similarity 75.0%; Score 13; DB 2; Length 6;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSL 5
Db 1 ATSL 4

RESULT 13

PT0730
T-cell receptor beta chain V-D-J region - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0730; PT0594; PT0731

R:Reaney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0730

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-6 <FEZ>

A:Experimental source: newborn thymus, strain BALB/c (clone 163-2C)

C:Keywords: T-cell receptor

Query Match
Best Local Similarity 75.0%; Score 13; DB 2; Length 6;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSL 5
Db 1 ATSL 4

Db 1 ASL 4

RESULT 14

S15596
orf 3 rara 5'-region - human
C:Species: Homo sapiens (man)
C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
C:Accession: S15596
R:Brand, N.J.; Petkovich, M.; Chambon, P.
Nucleic Acids Res. 18, 6799-6806, 1990
A:Title: Characterization of a functional promoter for the human retinoic acid receptor-
A:Reference number: S15594; MUID:91088249; PMID:2175878
A:Accession: S15596
A:Molecule type: DNA
A:Residues: 1-6

A:Cross-references: EMBL:X56058; NID:935876
A:Note: This ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0
C:Comment: This sequence is not thought to be translated.
C:Genetics:
A:Gene: GDB:RARA
A:Cross-references: GDB:120337; OMIM:180240
A:Map position: 17q12-17q12

Query Match 41.9%; Score 13; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

OY 1 SAT 3
|||
Db 4 SAT 6

RESULT 15

S20446
elastase - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C:Accession: S20446
R:Kessler, E.; Saffin, M.; Peretz, M.; Burstein, Y.
FEBS Lett. 299, 291-293, 1992
A:Title: Identification of cleavage sites involved in proteolytic processing of Pseudomc
A:Reference number: S20446; MUID:92183956; PMID:1544509
A:Accession: S20446
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <RES>

Query Match 41.9%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0;

OY 2 ATSLAD 7
| | |
Db 1 ANDLID 6

Search completed: February 25, 2003, 11:11:26
Job time : 47 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:59:58 ; Search time 31 Seconds
(without alignments)
11.025 Million cell updates/sec

Title: US-09-743-482a-2
Perfect score: 59
Sequence: 1 QASQDIGNMLA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 27392

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 100%
Maximum Match 0%

Listing first 45 summaries

Database :

Published Applications-AA:*

- 1: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubppa/PC1_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	74.6	11	US-09-798-058-8	Sequence 8, Appli
2	36	61.0	11	US-10-140-555-8	Sequence 8, Appli
3	35	59.3	11	US-09-056-1608-4	Sequence 46, Appli
4	33	55.9	11	US-09-974-449-6	Sequence 3, Appli
5	32	54.2	11	US-09-924-099-3	Sequence 20, Appli
6	31	52.5	11	US-09-253-794-20	Sequence 4, Appli
7	30	50.8	11	US-10-091-236-4	Sequence 6, Appli
8	30	50.8	11	US-09-861-294-6	Sequence 22, Appli
9	30	50.8	11	US-09-861-294-22	Sequence 2, Appli
10	30	50.8	11	US-09-809-739-2	Sequence 88, Appli
11	28	47.5	11	US-09-968-561A-88	Sequence 56, Appli
12	28	47.5	11	US-09-192-854-56	Sequence 37, Appli
13	28	47.5	11	US-09-828-708-37	Sequence 298, App
14	27	45.8	11	US-09-968-561A-298	Sequence 170, App
15	27	45.8	11	US-09-192-854-170	Sequence 316, App
16	26	44.1	11	US-09-968-561A-316	Sequence 178, App
17	26	44.1	11	US-09-192-854-178	Sequence 224, App
18	25	42.4	7	US-09-765-086-224	Sequence 19, Appli
19	25	42.4	8	US-09-738-396-19	

20	25	42.4	8	10	US-09-738-396-26	Sequence 26, Appli
21	25	42.4	11	9	US-09-423-800-59	Sequence 59, Appli
22	25	42.4	11	9	US-09-968-561A-10	Sequence 10, Appli
23	25	42.4	11	9	US-09-968-561A-16	Sequence 16, Appli
24	25	42.4	11	9	US-09-968-561A-22	Sequence 22, Appli
25	25	42.4	11	9	US-09-968-561A-28	Sequence 28, Appli
26	25	42.4	11	9	US-09-968-561A-34	Sequence 34, Appli
27	25	42.4	11	9	US-09-968-561A-40	Sequence 40, Appli
28	25	42.4	11	9	US-09-968-561A-46	Sequence 46, Appli
29	25	42.4	11	9	US-09-968-561A-52	Sequence 52, Appli
30	25	42.4	11	9	US-09-968-561A-64	Sequence 64, Appli
31	25	42.4	11	9	US-09-968-561A-100	Sequence 100, App
32	25	42.4	11	9	US-09-968-561A-106	Sequence 106, App
33	25	42.4	11	9	US-09-968-561A-112	Sequence 112, App
34	25	42.4	11	9	US-09-968-561A-118	Sequence 118, App
35	25	42.4	11	9	US-09-968-561A-124	Sequence 124, App
36	25	42.4	11	9	US-09-968-561A-136	Sequence 136, App
37	25	42.4	11	9	US-09-968-561A-154	Sequence 154, App
38	25	42.4	11	9	US-09-968-561A-160	Sequence 160, App
39	25	42.4	11	9	US-09-968-561A-166	Sequence 166, App
40	25	42.4	11	9	US-09-968-561A-172	Sequence 172, App
41	25	42.4	11	9	US-09-968-561A-178	Sequence 178, App
42	25	42.4	11	9	US-09-968-561A-202	Sequence 202, App
43	25	42.4	11	9	US-09-968-561A-208	Sequence 208, App
44	25	42.4	11	9	US-09-968-561A-226	Sequence 226, App
45	25	42.4	11	9	US-09-968-561A-232	Sequence 232, App

ALIGNMENTS

RESULT 1
US-09-798-058-8
Sequence 8, Application US/09798058
Patent No. US2002009852A1
GENERAL INFORMATION:
APPLICANT: Vaughan, Tristan John
APPLICANT: Wilton, Alison Jane
APPLICANT: Smith, Stephen
APPLICANT: Main, Sarah Helen
TITLE OF INVENTION: Human antibodies against ectoxin and their use
FILE REFERENCE: 84632-000100
CURRENT APPLICATION NUMBER: US/09/798,058
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 60/187,246
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-798-058-8

Query Match 74.6%; Score 44; DB 10; Length 11;
Best Local Similarity 72.7%;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQDIGNMLA 11
DB 1 RASQDISWLA 11

RESULT 2
US-10-140-555-8
Sequence 8, Application US/10140555
Patent No. US2002012727A1
GENERAL INFORMATION:
APPLICANT: Julie A. Abrahamson
APPLICANT: Stephen D. Holmes
APPLICANT: Jeffrey R. Jackson
TITLE OF INVENTION: RHAMM Antagonist Antibodies
FILE REFERENCE: P50857

;; CURRENT APPLICATION NUMBER: US/10/140,555
;; CURRENT FILING DATE: 2002-05-07
;; PRIOR APPLICATION NUMBER: US/09/443,790
;; PRIOR FILING DATE: 1999-11-19
;; PRIOR APPLICATION NUMBER: 60/109,041
;; PRIOR FILING DATE: 1998-11-19
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 8
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Mus musculus
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (1)...(11)
;; OTHER INFORMATION: light chain CDR 1
US-10-140-555-8

Query Match 61.0%; Score 36; DB 12; Length 11;
Best Local Similarity 70.0%; Pred. No. 1.9;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWL 10
Db 1 RASODISNVL 10

RESULT 3
US-09-056-160B-4
;; Sequence 4, Application US/09056160B
;; Patent No. US20020032315A1
;; GENERAL INFORMATION:
;; APPLICANT: Baca, Manuel
;; APPLICANT: Wells, James A.
;; APPLICANT: Presta, Leonard G.
;; APPLICANT: Lowman, Henry B.
;; APPLICANT: Chen, Yvonne M.
;; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
;; NUMBER OF SEQUENCES: 131
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/056,160B
;; FILING DATE: 06-Apr-1998
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/054,856
;; FILING DATE: 06-AUG-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hasak, Janet E.
;; REGISTRATION NUMBER: 28,616
;; REFERENCE/DOCKET NUMBER: P1093R2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1896
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: Amino acid
;; TOPOLOGY: Linear
US-09-056-160B-4

Query Match 59.3%; Score 35; DB 10; Length 11;

Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 ASODIGNWL 10
Db 2 ASODISNVL 10

RESULT 4
US-09-974-449-46
;; Sequence 46, Application US/09974449
;; Patent No. US20020141989A1
;; GENERAL INFORMATION:
;; APPLICANT: Kricek, Franz
;; APPLICANT: Stadler, Beda
;; APPLICANT: Vogel, Monique
;; TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODIES AGAINST
;; TITLE OF INVENTION: ANTIBODIES WHICH INHIBIT THE BINDING OF IMMUNOGLOBULIN E TO
;; FILE REFERENCE: 4-30888A
;; CURRENT APPLICATION NUMBER: US/09/974,449
;; CURRENT FILING DATE: 2001-10-10
;; PRIOR APPLICATION NUMBER: PCT/EP00/03288
;; PRIOR FILING DATE: 2000-04-12
;; NUMBER OF SEQ ID NOS: 62
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 46
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-974-449-46

Query Match 55.9%; Score 33; DB 10; Length 11;
Best Local Similarity 63.6%; Pred. No. 6.2;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 QASODIGNWLA 11
Db 1 RASODIGNWLA 11

RESULT 5
US-09-924-099-3
;; Sequence 3, Application US/09924099
;; Patent No. US20020128450A1
;; GENERAL INFORMATION:
;; APPLICANT: NISHIDA, Yoshihiro
;; APPLICANT: OKURA, Takao
;; APPLICANT: TANIMOTO, Tadao
;; APPLICANT: KURIMOTO, Masashi
;; TITLE OF INVENTION: PEPTIDE
;; FILE REFERENCE:
;; CURRENT APPLICATION NUMBER: US/09/924,099
;; CURRENT FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
;; NUMBER OF SEQ ID NOS: 33
;; SEQ ID NO 3
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-924-099-3

Query Match 54.2%; Score 32; DB 10; Length 11;
Best Local Similarity 70.0%; Pred. No. 9.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWNL 10
Db 1 RASODIGNWNL 10

Db 1 RASODIGSKL 10

RESULT 6

US-09-253-794-20

Sequence 20, Application US/09253794

Patent No. US20020018750A1

GENERAL INFORMATION:

APPLICANT: HANSEN, Hans J.

ARMOUR, Kathryn L.

TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED

MOUSE MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/253,794

FILING DATE: 22-Feb-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/318,157

FILING DATE: 05-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: SAXE, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 18733/464

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-253-794-20

Query Match 52.5%; Score 31; DB 10; Length 11;

Best Local Similarity 54.5%; Pred. No. 14;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASODIGMNL 11

Db 1 KASODVGTVA 11

RESULT 7

US-10-091-236-4

Sequence 4, Application US/10091236

Patent No. US20020168360A1

GENERAL INFORMATION:

APPLICANT: DINGLIAN, CHRISTINE A.

TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING INFLAMMATORY OR AUTOIMMUNE

DISORDERS BY ADMINISTERING INTEGRIN ALPHA-V-BETA-3 ANTAGONISTS

TITLE OF INVENTION: COMBINATION WITH OTHER PROPHYLACTIC OR THERAPEUTIC AGENTS

FILE REFERENCE: 10271-033-999

CURRENT APPLICATION NUMBER: US/10/091,236

CURRENT FILING DATE: 2002-03-04

PRIOR APPLICATION NUMBER: US 60/273,098

PRIOR FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: US 60/316,321

PRIOR FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.1

SEQ ID NO: 4

LENGTH: 11

TYPE: PRT

ORGANISM: Mus sp.

US-10-091-236-4

Query Match 50.8%; Score 30; DB 9; Length 11;

Best Local Similarity 70.0%; Pred. No. 20;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QASODIGMNL 10

Db 1 QASODISNHL 10

RESULT 8

US-09-861-294-6

Sequence 6, Application US/09861294

Patent No. US20020098190A1

GENERAL INFORMATION:

APPLICANT: MALAYA CHATTERJEE

APPLICANT: Kenneth A. POON

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

TUMORS BEARING HMG AND CEA ANTIGENS

FILE REFERENCE: 304142000620

CURRENT APPLICATION NUMBER: US/09/861,294

CURRENT FILING DATE: 2001-05-17

PRIOR APPLICATION NUMBER: 60/049,540

PRIOR FILING DATE: 1997-06-13

PRIOR APPLICATION NUMBER: 09/096,244

PRIOR FILING DATE: 1998-06-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO: 6

LENGTH: 11

TYPE: PRT

ORGANISM: Mus musculus

US-09-861-294-6

Query Match 50.8%; Score 30; DB 10; Length 11;

Best Local Similarity 85.7%; Pred. No. 20;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASODIG 7

Db 1 RASODIG 7

RESULT 9

US-09-861-294-22

Sequence 22, Application US/09861294

Patent No. US20020098190A1

GENERAL INFORMATION:

APPLICANT: MALAYA CHATTERJEE

APPLICANT: Kenneth A. POON

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

TUMORS BEARING HMG AND CEA ANTIGENS

FILE REFERENCE: 304142000620

CURRENT APPLICATION NUMBER: US/09/861,294

CURRENT FILING DATE: 2001-05-17

PRIOR APPLICATION NUMBER: 60/049,540

PRIOR FILING DATE: 1997-06-13

PRIOR APPLICATION NUMBER: 09/096,244

PRIOR FILING DATE: 1998-06-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO: 22

LENGTH: 11

TYPE: PRT

ORGANISM: Mus musculus
US-09-861-294-22

Query Match 50.8%; Score 30; DB 10; Length 11;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASODIGNML 10
:|||||:
DB 1 KASODINGTL 10

RESULT 10
US-09-809-739-2
Sequence 2, Application US/09809739
Patent No. US20020106369A1

GENERAL INFORMATION:
APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia E.
TITLE OF INVENTION: Method of inhibiting stenosis and
TITLE OF INVENTION: Restenosis
FILE REFERENCE: 1855.1069-003
CURRENT APPLICATION NUMBER: US/09/809,739
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 11
TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: SITE
LOCATION: (1)...(11)
OTHER INFORMATION: CDRL of YFCS1.1 light chain
OTHER INFORMATION: Rat
US-09-809-739-2

Query Match 50.8%; Score 30; DB 10; Length 11;
Best Local Similarity 54.5%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASODIGNML 11
:||| | |:
DB 1 KAKSISNYLA 11

RESULT 11
US-09-968-561A-88
Sequence 88, Application US/09968561A
Patent No. US20020164642A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/10738
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 88
LENGTH: 11

TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-88

Query Match 47.5%; Score 28; DB 9; Length 11;
Best Local Similarity 54.5%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASODIGNML 11
:|||||:
DB 1 RASOSIGPFLS 11

RESULT 12
US-09-192-854-56
Sequence 56, Application US/09192854
Patent No. US20020068276A1
GENERAL INFORMATION:
APPLICANT: Winter, Greg
APPLICANT: Tomlinson, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-192-854-56

Query Match 47.5%; Score 28; DB 10; Length 11;
Best Local Similarity 54.5%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASODIGNML 11
:|||||:
DB 1 RASOSIGPFLS 11

RESULT 13
US-09-828-708-37
Sequence 37, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their part
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-37

Query Match 47.5%; Score 28; DB 10; Length 11;
Best Local Similarity 54.5%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASODIGNML 11
:|||||:
DB 1 RASOSIGPFLS 11

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RESULT 34
US-09-968-561A-298
; Sequence 298, Application US/09968561A
; Patent No. US2002016462A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 298
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-298

Query Match
Best Local Similarity 45.8%; Score 27; DB 9; Length 11;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

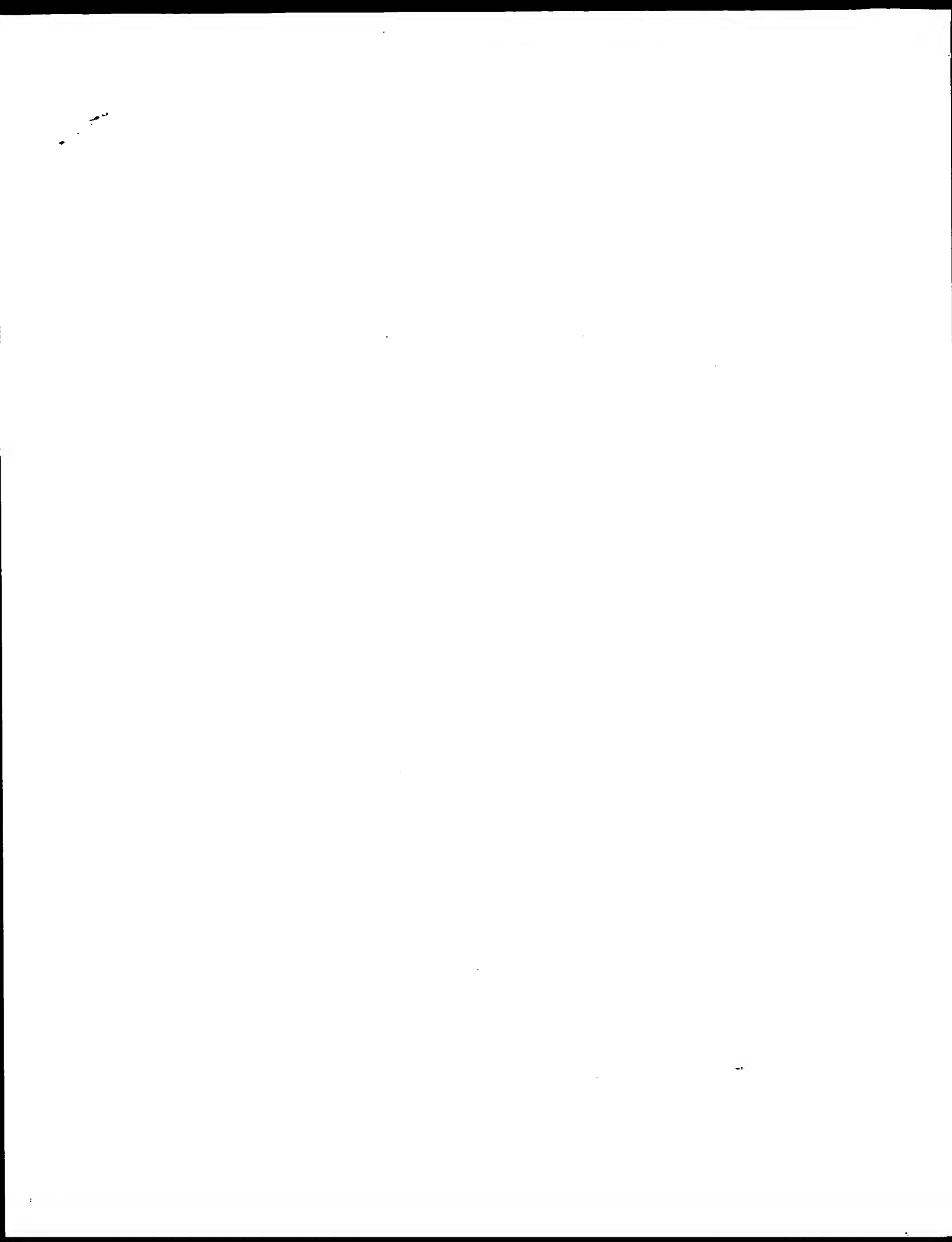
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:|||||:
Db 1 RASOSIGSSLS 11

RESULT 15
US-09-192-854-170
; Sequence 170, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 170
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-170

Query Match
Best Local Similarity 45.8%; Score 27; DB 10; Length 11;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASODIGNMLA 11
:|||||:
Db 1 RASOSIGSSLS 11
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Search completed: February 25, 2003, 11:08:10
Job time : 31 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:37:42 ; Search time 34 seconds

(without alignments)
43.110 Million cell updates/sec

Title: US-09-743-482a-2

Perfect score: 59

Sequence: 1 QASQDIGNWLA 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues 190898

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID2/gcgdata/geneseq/genesep-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	11	21	AAV78319
2	44	74.6	11	22	AAE10819
3	43	72.9	11	22	AAE63617
4	42	71.2	9	20	AAV10298
5	42	71.2	11	18	AAW23433
6	41	69.5	10	22	ABP12844
7	41	69.5	10	22	ABP17875
8	41	69.5	11	22	ABP12950
9	41	69.5	11	22	ABP12953
10	41	69.5	11	22	ABP18790

11	40	67.8	10	22	ABP12843	HIV A02 super moti
12	40	67.8	10	22	ABP17826	HIV B58 super moti
13	40	67.8	10	22	AAW99241	Vaccine related MH
14	40	67.8	11	20	AAV05008	Tumour antigen ant
15	40	67.8	11	22	ABP12949	HIV A02 super moti
16	40	67.8	11	22	ABP12952	HIV A02 super moti
17	40	67.8	11	22	ABP18748	HIV B62 super moti
18	40	67.8	11	22	AAE63614	Complementarity de
19	39	66.1	9	22	ABP17871	HIV B58 super moti
20	38	64.4	10	20	ABP18786	HIV B62 super moti
21	38	64.4	9	20	AAV10315	T cell epitope/MHC
22	38	64.4	9	20	AAV10297	T cell epitope/MHC
23	38	64.4	9	22	ABP17872	HIV B58 super moti
24	38	64.4	9	22	AAW99240	Vaccine related MH
25	38	64.4	10	22	ABP18743	HIV B62 super moti
26	37	62.7	10	22	ABP12845	HIV A02 super moti
27	37	62.7	10	22	ABP17898	HIV B58 super moti
28	37	62.7	11	20	AAW95265	Anti-progesterone
29	37	62.7	11	22	ABP12951	HIV A02 super moti
30	37	62.7	11	22	ABP12954	HIV A02 super moti
31	37	62.7	11	22	ABP18809	HIV B62 super moti
32	37	62.7	11	22	AAE67504	Human light chain
33	37	62.7	11	22	AAE82894	Anti-human CD154 a
34	37	62.7	11	23	AAW51161	Anti-tumour necros
35	37	62.7	11	23	AAU76518	Anti-interleukin-1
36	36	61.0	9	22	ABP12729	HIV A02 super moti
37	36	61.0	9	22	ABP15622	HIV A24 super moti
38	36	61.0	9	22	ABP17872	HIV B58 super moti
39	36	61.0	10	22	ABP12846	HIV A02 super moti
40	36	61.0	11	20	AAW95263	Anti-progesterone
41	36	61.0	11	21	AAV94220	Murine 16E10 light
42	35	59.3	9	20	AAV53518	HIV-1 P24 protein
43	35	59.3	9	20	AAV40367	Amino acid sequenc
44	35	59.3	9	20	AAV26859	HIV-derived lipope
45	35	59.3	9	22	ABP17823	HIV B58 super moti

ALIGNMENTS

RESULT 1

AAV78319

ID AAV78319 standard; Protein; 11 AA.

XX AAV78319;

XX

DT 04-MAY-2000 (first entry)

XX

XX Anti-zeta-chain antibody 2-B-5 VL-region CDRL protein sequence.

DE

XX Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;

KW complementary determining region; CDR; autoimmune disease; cytotoxic;

KW immune deficiency; T-cell malignancy; infectious disease; antiviral;

KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.

XX

XX Rattus norvegicus.

OS

XX

PN WO200003016-A1.

XX

PD 20-JAN-2000.

XX

PF 09-JUL-1999; 99WO-EP04838.

XX

PR 10-JUL-1998; 98EP-0112867.

XX

PA (CONN-) CONNEX GMBH.

XX

PI Reiter C;

XX

DR WPI: 2000-160926/14.

XX N-PSDB: AA88317.

XX

PT New oligonucleotide, polypeptide, antibody useful for treating

PT autoimmune disease, immune deficiencies, T-cell malignancies and
 PT infectious diseases -
 PS Claim 10; Fig 7; 79pp; English.
 XX
 CC The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is
 CC encoded by (I), is obtained by immunising a rat with jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,
 CC infectious diseases and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC or viral infections. The antibody, and fragments of it, can be useful for
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC treatment of NK-cell derived malignancies. It can also be useful for the
 CC determination of zeta-chain or eta-chain expression on NK-cells,
 CC T-lymphocytes or their precursors. The present sequence represents the
 CC CDR1 of the V_H-region of the anti-zeta-chain antibody 2-B-5, produced
 CC by rats from the present invention.
 CC
 SQ Sequence 11 AA:
 Query Match 100.0%; Score 59; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 QASODIGNWLA 11
 Db 1 QASODIGNWLA 11
 ID AAE10819 standard; peptide; 11 AA.
 AC AAE10819:
 XX 18-DEC-2001 (first entry)
 DT
 DE Human antibody CAT-212 VL complementarity determining region-1 (CDR-1).
 XX Human; ecotaxin; CAT-212; antibody; light chain variable region; VL;
 KW eczema; asthma; atopic disease; dermatological; rhinitis; food allergy;
 KW vasculitic; conjunctivitis; allergic colitis; psoriasis; pemphigoid;
 KW eosinophil-mediated disease; cellulitis; drug eruption; vasculitis;
 KW inflammatory bowel disease; complementarity determining region-1; CDR-1;
 KW gastroenteritis.
 XX Homo sapiens.
 OS
 XX WO200166754-A1.
 PN
 XX 13-SEP-2001.
 PD
 XX 02-MAR-2001; 2001WO-GB00927.
 PF
 XX 03-MAR-2000; 2000US-187246P.
 PR
 XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA
 XX Vaughan TJ, Wilton AJ, Smith S;
 PI
 XX WPI; 2001-589944/66.
 DR
 XX Human antibodies against ecotaxin useful for treating asthma, eczema and
 PT other atopic diseases, comprises an antibody variable heavy or variable
 PT light domain from CAT-212 or from complementary determining regions -
 XX
 PS Claim 1; Page 102; 107pp; English.

XX The invention relates to a specific binding member which binds to human
 CC ecotaxin. The binding member comprises an antibody variable heavy
 CC (VH)/variable light (VL) domain from CAT-212 VH/VL domain and a VH/VL
 CC domain comprising one or more VH/VL complementary determining regions
 CC (CDRs). Ecotaxin is a chemottractant protein that binds to a specific
 CC receptor which is expressed predominantly on eosinophils. The binding
 CC member is useful for neutralising ecotaxin, which is useful in treating
 CC asthma, eczema and other atopic diseases such as rhinitis, food allergy,
 CC conjunctivitis, allergic colitis which are recognised as eosinophil-
 CC mediated diseases; for treating skin and other atopic conditions such as
 CC psoriasis, pemphigoid, welts' syndrome, cellulitis, drug eruptions;
 CC inflammatory bowel disease which includes eosinophilic colitis/enteritis/
 CC gastroenteritis/Shulman's syndrome; vasculitis including Hughes-Stovin
 CC syndrome, Churg-Strauss syndrome. The present sequence is human
 CC antibody CAT-212 light chain variable domain (VL) complementarity
 CC determining region (CDR).
 CC
 SQ Sequence 11 AA:
 Query Match 74.6%; Score 44; DB 22; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.22;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 1 QASODIGNWLA 11
 Db 1 RASODISSWLA 11
 ID AAG63617 standard; peptide; 11 AA.
 AC AAG63617:
 XX 29-OCT-2001 (first entry)
 DT
 DE Complementarity determining region (CDR) 1 of SCFV1.2 H chain.
 XX
 KW Complementarity determining region; CDR; single chain antibody; SCFV;
 KW hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
 KW envelope glycoprotein.
 XX
 OS Homo sapiens.
 XX WO200158459-A1.
 PN
 XX 16-AUG-2001.
 PD
 XX 13-FEB-2001; 2001WO-JP00967.
 PF
 XX 14-FEB-2000; 2000JP-0034906.
 PR
 XX (MITS-) MITSUBISHI-TOKYO PHARM INC.
 PA
 XX Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y,
 PI Miyamura T;
 XX WPI; 2001-496986/54.
 DR
 XX Remedies for hepatitis C containing substances with antiviral effects
 PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
 PT compounds, by inhibiting binding of hepatitis C virus envelope
 PT glycoprotein or CD81 -
 XX
 PS Claim 20; Page 74; 136pp; Japanese.
 CC The present sequence represents a complementarity determining region
 CC (CDR) of a single chain (ScFv) antibody of the invention. The
 CC specification describes a substance can inhibit the binding between
 CC hepatitis C virus (HCV) and cells with potential HCV infection, cells
 CC with expression of CD81, or CD81. This substance is especially an
 CC antibody with affinity towards HCV E2/NS1 protein, containing amino
 CC acid sequences based on the CDR1, CDR2 and CDR3 of the H and L chain

CC variable regions. The antibody inhibits the viral envelope glycoprotein.
 CC It is also a CD81 inhibitor. The antibodies and drugs are used for
 CC treatment and/or prevention of hepatitis C, or for diagnosis of
 CC hepatitis C.

XX Sequence 11 AA;

Query Match 72.9%; Score 43; DB 22; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.34;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QASODIGNMLA 11
 :|||||
 Db 1 RASODISTWLA 11

RESULT 4
 AAY10298
 ID AAY10298 standard; Peptide; 9 AA.

XX AAY10298;
 XX
 DT 12-MAY-1999 (first entry) -
 DE T cell epitope/MHC ligand SEQ ID NO:228.

KW Cytotoxic T-lymphocyte response; CTL; antigen; Lymphatic system;
 KW Immunisation; tumour; infectious disease; immunotherapy; cancer;
 KW malignant melanoma; viral disease; hepatitis; AIDS.

OS Synthetic.
 OS Human Immunodeficiency virus type 1.

PN WO9902183-AZ.

XX 21-JAN-1999.

PF 10-JUL-1998; 98WO-US14289.

PR 10-DEC-1997; 97US-0988320.

XX 10-JUL-1997; 97CA-2209815.

PA (CTL-) CTL IMMUNOTHERAPIES CORP.

PI Kuendig TM, Simard JTL;

DR WPI: 1999-120514/10.

XX Inducing a cytotoxic T lymphocyte response - by maintaining a level
 PT of antigen in the lymphatic system of a mammal so as to provide a
 PT sustained CTL response, used to treat, e.g. AIDS

PS Disclosure; Page 32; 199pp; English.

XX The present invention describes a method of inducing and/or sustaining
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
 CC method comprises: (a) delivering an antigen to the mammal at a level to
 CC induce an immunological CTL response in the mammal; and (b) maintaining
 CC the level of the antigen in the mammal's lymphatic system to maintain
 CC the immunologic CTL response. The method can be used for the delivery of
 CC e.g. a differentiation antigen, a tumour-specific multilineage antigen,
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
 CC gene antigen, or a viral antigen. They can be used for the treatment of
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
 CC to the lymphatic system provides for potent CTL stimulation that takes
 CC place in the milieu of the lymphoid organ, and it sustains stimulation
 CC that is necessary to keep CTL active, cytotoxic and recirculating
 CC through the body. AAY10071 to AAY10639 represent examples of peptide
 CC antigens given in the present invention.

XX Sequence 9 AA;

Query Match 71.2%; Score 42; DB 20; Length 9;
 Best Local Similarity 77.8%; Pred. No. 7.8e+05;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNW 9
 :|||||
 Db 1 QASODVKNW 9

RESULT 5
 AAW23433
 ID AAW23433 standard; peptide; 11 AA.

XX AAW23433;
 XX

DT 23-APR-1998 (first entry)
 DE CDR-1 of rW12 light chain.

KW Antibody; complementarity determining region; CDR; light chain; rat; CEA;
 KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.

OS Rattus sp.

PN WO9734636-A1.

PD 25-SEP-1997.

PF 19-MAR-1997; 97WO-US04696.

PR 20-MAR-1996; 96US-0013708.

PA (IMMU-) IMMUNOMEDICS INC.

PI Hansen H, Leung S, Losman MJ;

DR WPI: 1997-479997/44.

XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic
 PT antibodies - useful in detection of anti-CEA antibodies and as
 PT vaccine to stimulate immune response against cancer

PS Claim 4; Page 30; 46pp; English.

XX This sequence represents the complementarity determining region-1 (CDR-1)
 CC of the rW12 light chain. This sequence is used in an antibody of the
 CC invention. The antibody of the invention is a chimeric or humanised
 CC anti-idiotypic antibodies (cab and hab, respectively) or a fragment which
 CC specifically binds to the idiotype region of an anti-carcinoembryonic
 CC antigen (CEA), where: (i) cab comprises the rW12 light (L) and
 CC heavy (H) chain variable regions, or silent mutations; and (ii) hab
 CC comprises rW12 complementarity determining regions (CDR) and humanised
 CC framework (FR) regions. The hab is used as a vaccine to stimulate an
 CC immune response in a patient against cancers expressing CEA. The hab, can
 CC be used to clear non-targeted antibody in a method of diagnosis or
 CC treatment of a patient where a CEA antibody is used as a (pre-)targeting
 CC or therapy agent. The cab is used to detect the presence of an antibody
 CC that specifically binds to CEA in a sample.

XX Sequence 11 AA;

Query Match 71.2%; Score 42; DB 18; Length 11;
 Best Local Similarity 80.0%; Pred. No. 0.51;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 QASODIGNWL 10
 :|||||
 Db 1 RASODIGNWL 10

RESULT 6
 ABP12844

ID	ABP12844 standard; Peptide: 10 AA.
XX	
AC	ABP12844;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	HIV A02 super motif gag peptide #315.
XX	
KW	HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; Immunisation; virucide.
XX	
OS	Human immunodeficiency virus type 1.
XX	
PN	MOZ00124810-A1.
PD	12-Apr-2001.
XX	
PE	05-OCT-2000; 2000WO-US27766.
PR	05-OCT-1999; 99US-0412863.
XX	
PA	(EPIM-) EPIMUNE INC.
PI	Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI	Baker DM, Celis RT, Grey HM;
XX	
DR	WPI: 2001-354887/37.
PT	Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
PS	
XX	
XX	Claim 32; Page 132; 448bp; English.
CC	The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABR25337). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABR25412 represent peptide sequences used in the exemplification of the present invention.
SO	
Sequence	10 AA:
Query Match	69.5%; Score 41; DB 22; Length 10;
Best Local Similarity	60.0%; Pred. No. 0.69;
Matches	6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY	1 OASDIGNWL 10
DB	1 : : : 10
	1 QATQDYKNMM 10
RESULT 7	
ID	ABP17875
XX	
AC	ABP17875 standard; peptide: 10 AA.
ABP17875;	

XX		15-JUL-2002 (first entry)	
DT			
XX		HIV B58 super motif gag peptide #94.	
DE			
XX		HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;	
KW	vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;		
KW	antigen; vaccine; HIV infection; immunisation; virucide.		
OS			
XX		Human immunodeficiency virus type 1.	
PN			
PM	WO200124810-A1.		
PD			
XX	12-Apr-2001.		
PF			
XX	05-Oct-2000; 2000WO-US27766.		
PR			
XX	05-Oct-1999; 99US-0412863.		
PA			
XX	(EPIM-) EPIMUNE INC.		
Pt			
PI	Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;		
XX	Baker DM, Celis E, Kubo RT, Grey HM;		
DR			
XX	WPI: 2001-354887/37.		
PT			
XX	Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)		
PS	peptide groups, useful for vaccinating against HIV-1 -		
XX	Claim 32; Page 235; 44Bpp; English.		
CC			
CC	The present invention describes a composition (I) comprising a prepared		
CC	human immunodeficiency virus-1 (HIV-1) group comprising an amino acid		
CC	sequence selected from 51 defined amino acid sequences (AB25347 to		
CC	ABP25337). (I) has virucide activity and can be used in vaccines. (I)		
CC	may be used for immunising subjects against HIV-1 infections. The use of		
CC	group-based vaccines has several advantages over traditional vaccines,		
CC	particularly when compared to the use of whole antigens in vaccine		
CC	compositions. There is evidence that the immune response to whole		
CC	antigens is directed largely toward variable regions of the antigen,		
CC	allowing for immune escape due to mutations. The groups for inclusion in		
CC	an group-based vaccine may be selected from conserved regions of viral or		
CC	tumour-associated antigens, which therefore reduces the likelihood of		
CC	escape mutants. Furthermore, immunosuppressive groups that may be present		
CC	in whole antigens can be avoided with the use of group-based vaccines.		
CC	An additional advantage of an group-based vaccine approach is the ability		
CC	to combine selected groups (CTL and HTL), and further, to modify the		
CC	composition of the groups, achieving, for example, enhanced		
CC	immunogenicity. Accordingly, the immune response can be modulated, as		
CC	appropriate, for the target disease. Similar engineering of the response		
CC	is not possible with traditional approaches. ABP1501 to ABP25412		
CC	represent peptide sequences used in the exemplification of the present		
CC	invention.		
XX			
SO	Sequence 10 AA:		
QY			
DB			
1	QASODIGNWL 10		
11	::::: 11:		
1	OATQDVKNMM 10		
Query Match	69.5%;	Score 41;	DB 22; Length 10;
Best local Similarity	60.0%;	Pred. No. 0.69;	
Matches 6; Conservative	3;	Mismatches 1;	Indels 0; Gaps 0;
Result 8			
ABP12950			
ID	ABP12950 standard; Peptide; 11 AA.		
AC	ABP12950;		
XX			
DT	15-JUL-2002 (first entry)		
XX			

DE HIV A02 super motif gag peptide #421.
 XX
 KW HIV-1: human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpr; tat; cytoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27766.
 XX
 PR 05-OCT-1999; 99US-0412863.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Settle A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cells E, Kubo RT, Grey HM;
 DR WPI: 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX
 PS Claim 32: Page 134; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 CC
 SQ Sequence 11 AA;
 XX
 Query Match 69.5%; Score 41; DB 22; Length 11;
 Best Local Similarity 60.0%; Pred. No. 0.77;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASODIGNWL 10
 11:11:11:
 Db 2 QATQDVKNMM 11
 11:11:11:
 RESULT 9
 ABP12953
 ID ABP12953 standard; Peptide; 11 AA.
 XX
 AC ABP12953;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV A02 super motif gag peptide #424.
 XX
 KW HIV-1: human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW antigen; vaccine; HIV infection; immunisation; virucide.

KW vpr; tat; cytoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27766.
 XX
 PR 05-OCT-1999; 99US-0412863.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Settle A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cells E, Kubo RT, Grey HM;
 DR WPI: 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX
 PS Claim 32: Page 134; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 CC
 SQ Sequence 11 AA;
 XX
 Query Match 69.5%; Score 41; DB 22; Length 11;
 Best Local Similarity 60.0%; Pred. No. 0.77;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASODIGNWL 10
 11:11:11:
 Db 1 QATQDVKNMM 10
 11:11:11:
 RESULT 10
 ABP18790
 ID ABP18790 standard; Peptide; 11 AA.
 XX
 AC ABP18790;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV B62 super motif gag peptide #83.
 XX
 KW HIV-1: human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpr; tat; cytoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27766.
 XX
 PR 05-OCT-1999; 99US-0412863.
 XX
 PA (EPIIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cells E, Kubo RT, Grey HM;
 DR WPI: 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX
 PS Claim 32: Page 254; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 CC
 CC Sequence 11 AA;
 XX
 SO
 Query Match 69.5%; Score 41; DB 22; Length 11;
 Best Local Similarity 60.0%; Pred. No. 0.77; Indels 0; Gaps 0;
 Matches 6; Conservative 3; Mismatches 1;
 OY 1 QASODIGNWL 10
 1111111111
 Db 2 QATQDVKNMM 11
 RESULT 11
 ABP12843
 ID ABP12843 standard; Peptide: 10 AA.
 XX
 AC ABP12843;
 XX
 DT 15-JUL-2002 (first entry)
 DE
 XX HIV A02 super motif gag peptide #314.
 DE
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810-A1.

XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27766.
 XX
 PR 05-OCT-1999; 99US-0412863.
 XX
 PA (EPIIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cells E, Kubo RT, Grey HM;
 DR WPI: 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX
 PS Claim 32: Page 131; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 CC
 CC Sequence 10 AA;
 XX
 SO
 Query Match 67.8%; Score 40; DB 22; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 OY 1 QASODIGNWL 10
 1111111111
 Db 1 QASQEVKNMM 10
 RESULT 12
 ABP17826
 ID ABP17826 standard; Peptide: 10 AA.
 XX
 AC ABP17826;
 XX
 DT 15-JUL-2002 (first entry)
 DE
 XX HIV B58 super motif gag peptide #45.
 DE
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.


```

PR 04-AUG-1997: 97US-0905835.
PR 04-AUG-1997: 97US-1112222.
XX
XX (IXSY-) IXSYS INC.
XX
XX Huse WD, Watkins JD, Wu H;
XX
XX WPI: 1999-153951/13.
DR N-PSDB; AAX28185.
XX
XX Identifying binding molecules for ligands, particularly tumour
XX antigens - by selectively immobilising a population of binding
XX molecules to a solid support and screening for binding to two or
XX more ligands
XX
XX Claim 17; Page 57; 80pp; English.
XX
XX This sequence represents a light chain complementarity determining
XX region (CDR) from a tumour antigen specific antibody.
XX The invention relates to a method for identifying a binding molecule
XX having selective affinity for a ligand comprising: (a) selectively
XX immobilising a diverse population of binding molecules to a solid
XX support; (b) simultaneously contacting the diverse population immobilised
XX on the solid support with 2 or more ligands; and (c) determining at least
XX one binding molecule which selectively binds to one or more of the
XX ligands. The method allows for the rapid and efficient methods for the
XX identification of binding molecules which exhibit selective affinity for
XX one or more ligands of interest. They are used particularly for
XX identifying tumour-specific binding polypeptides which can be used as
XX targeting agents for cancer therapy that minimises impact on non-tumour
XX tissues.
XX
XX Sequence 11 AA:
XX
XX Query Match 67.8%; Score 40; DB 20; Length 11;
XX Best Local Similarity 63.6%; Pred. No. 1.2;
XX Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 QASODIGMWLA 11
XX :|:|:|:|:|
XX Db 1 RAKONIGRWLA 11
XX
XX RESULT 15
XX ABP12949
XX ID ABP12949 standard; peptide: 11 AA.
XX
XX AC ABP12949;
XX
XX DT 15-JUL-2002 (first entry)
XX
XX DE HIV A02 super motif gag peptide #420.
XX
XX XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX OS Human immunodeficiency virus type 1.
XX
XX PN WO200124810-A1.
XX
XX PD 12-APR-2001.
XX
XX PF 05-OCT-2000: 2000MO-US27766.
XX
XX PR 05-OCT-1999: 99US-0412863.
XX
XX (EPIIM-) EPIIMUNE INC.
XX
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Cells E, Kubo RT, Grey HM;
XX WPI: 2001-354887/37.

```

```

XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1 -
XX
XX Claim 32; Page 134; 448pp; English.
XX
XX The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABP25347 to
XX ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP11501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 11 AA:
XX
XX Query Match 67.8%; Score 40; DB 22; Length 11;
XX Best Local Similarity 60.0%; Pred. No. 1.2;
XX Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 QASODIGMWL 10
XX :|:|:|:|:|
XX Db 2 QASQEVKNWM 11

```

Search completed: February 25, 2003, 10:57:58
 Job time : 35 secs


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AC 08W854;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema mexicanum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
OC Diadema.
OX NCBI_TaxID=105358;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=GI25;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN 121
RP SEQUENCE FROM N.A.
RC STRAIN=GI25;
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012941; AAL33848.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 9 AA; 1151 MW; 2CED173B46DDC2D3 CRC64;

Query Match 37.3%; Score 22; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 NMLA 11
DB 1 NMLA 4

RESULT 3
08W8M6 PRELIMINARY; PRT; 9 AA.
ID 08W8M6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema antillarum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
OC Diadema.
OX NCBI_TaxID=105358;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=CN3, AND CNS;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN 121
RP SEQUENCE FROM N.A.
RC STRAIN=CN3, AND CNS;
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).

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DR EMBL; AY012853; AAL33827.1; -.
DR EMBL; AY012855; AAL33829.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 9 AA; 1151 MW; 2CED173B46DDC2D3 CRC64;

Query Match 37.3%; Score 22; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 NMLA 11
DB 1 NMLA 4

RESULT 4
08W8M5 PRELIMINARY; PRT; 9 AA.
ID 08W8M5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema setosum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
OC Diadema.
OX NCBI_TaxID=31175;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=DEL1, DEL2, DEL3, AND DEL5;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
DR EMBL; AY012890; AAL33833.1; -.
DR EMBL; AY012891; AAL33834.1; -.
DR EMBL; AY012892; AAL33835.1; -.
DR EMBL; AY012893; AAL33836.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 9 AA; 1151 MW; 2CED173B46DDC2D3 CRC64;

Query Match 37.3%; Score 22; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 NMLA 11
DB 1 NMLA 4

RESULT 5
09QVH3 PRELIMINARY; PRT; 11 AA.
ID 09QVH3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chromogranin-B, CGB-GLUCAGONOMA peptide (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN 11
RP SEQUENCE.
RX MEDLINE=92063871; PubMed=1954895;
RA Nielsen E., Wellinder B.S., Madsen O.D.;
RT "Chromogranin-B, a putative precursor of eight novel rat glucagonoma
RT peptides through processing at mono-, di-, or tribasic residues.";

```


RL Endocrinology 129:3147-3156(1991).
 DR InterPro: IPR001990: Granlin.
 DR Pfam: PF01271: Granlin; 1.

FT NON_TER 1 11
 FT NON_TER 1 11
 SQ SEQUENCE 11 AA: 1342 MW: 608203737452CAAB CRC64;

Query Match 36.4%; Score 21.5; DB 11; Length 11;
 Best Local Similarity 57.1%; Pred. No. 1.6e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

Qy 3 SODIGNW 9
 1: 1: 11
 Db 3 SEDV-NW 8

RESULT 6

09CLR7 09CLR7 PRELIMINARY; PRT: 11 AA.

AC 09CLR7;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE SsulP (Fragment).
 GN SSU1.

OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.

OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Perez-Ortin J.E.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF239758; AAK15080.1; -.
 FT NON_TER 11
 SQ SEQUENCE 11 AA: 1274 MW: 1256714D732D374 CRC64;

Query Match 35.6%; Score 21; DB 3; Length 11;
 Best Local Similarity 40.0%; Pred. No. 2e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 IGNNL 10
 1: 1: 11
 Db 2 VANWV 6

RESULT 7

09R5M1 09R5M1 PRELIMINARY; PRT: 9 AA.

AC 09R5M1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 66 kDa cell surface adhesin for heparan sulfate (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE.

RA Liang O.D., Ascencio F., Fransson L.A., Wadstrom T.;
 RT "Binding of heparan sulfate to Staphylococcus aureus."
 RL Infect. Immun. 60:899-906(1992).
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 9 AA: 990 MW: 2289DD7337861B3 CRC64;

Query Match 33.9%; Score 20; DB 2; Length 9;
 Best Local Similarity 57.1%; Pred. No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 DIGNNLA 11
 1: 1: 11
 Db 1 DWTGMLA 7

RESULT 8

09ZYS6 09ZYS6 PRELIMINARY; PRT: 10 AA.

AC 09ZYS6;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Stenocercus crassicaudatus.

OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Stenocercus.

OX NCBI_TaxID=81828;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99162288; PubMed=10051389;
 RA Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
 RT "Molecular tests of phylogenetic taxonomies: A general procedure and
 example using four subfamilies of the lizard family Iguanidae.";
 RL Mol. Phylogenet. Evol. 10:367-376(1998).
 DR EMBL: AF049866; AAD02541.1; -.
 KW Mitochondrion.
 FT NON_TER 10
 SQ SEQUENCE 10 AA: 1315 MW: 0A3480C733640440 CRC64;

Query Match 32.2%; Score 19; DB 8; Length 10;
 Best Local Similarity 60.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 IGNNL 10
 1: 1: 11
 Db 3 INRWL 7

RESULT 9

079888 079888 PRELIMINARY; PRT: 10 AA.

AC 079888;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Basiliiscus plumifrons.

OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Corytophaninae;
 OC Basiliiscus.
 OX NCBI_TaxID=52191;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Evolutionary shifts in three major structural features of the
 mitochondrial genome among Iguanian lizards.";
 RL J. Mol. Evol. 44:660-674(1997).
 DR EMBL: U82680; AAC62269.1; -.
 KW Mitochondrion.
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA: 1254 MW: 1A3580C733640440 CRC64;

Query Match 32.2%; Score 19; DB 8; Length 10;
 Best Local Similarity 60.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 IGNNL 10
 1: 1: 11

Db 3 INRWL 7

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RESULT 10
079897 ID 079897 PRELIMINARY: PRT: 10 AA.
AC 079897;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Hoplocercus spinosus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hopllocercinae;
OC Hoplocercus.
OX NCBI_TaxID=52193;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97315309; PubMed=9169559;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Evolutionary shifts in three major structural features of the
RT mitochondrial genome among iguanian lizards.";
RL Biol. J. Linn. Soc. 69:75-102(2000).
DR EMBL; U82683; AAC62284.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;
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Query Match 32.2% Score 19; DB 8; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Oy 6 IGWML 10
1 11
Db 3 INRWL 7

```
RESULT 11
0978X1 ID 0978X1 PRELIMINARY: PRT: 10 AA.
AC 0978X1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Liolaemus alticolor.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
OX NCBI_TaxID=109393;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SDSU3574;
RA Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
RT "Phylogenetic relationships in the Iguanid lizard Genus Liolaemus:
RT Multiple origins of viviparous reproduction and evidence for recurring
RT Andean vicariance and dispersal.";
RL Biol. J. Linn. Soc. 69:75-102(2000).
DR EMBL; AF099218; AAF18760.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 10 AA; 1315 MW; 0A3480C733640440 CRC64;
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Query Match 32.2% Score 19; DB 8; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Oy 6 IGWML 10
1 11
Db 3 INRWL 7

RESULT 12

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0978W5 ID 0978W5 PRELIMINARY: PRT: 10 AA.
AC 0978W5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Liolaemus robertmertensi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
OX NCBI_TaxID=109435;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SDSU3498;
RA Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
RT "Phylogenetic relationships in the Iguanid lizard Genus Liolaemus:
RT Multiple origins of viviparous reproduction and evidence for recurring
RT Andean vicariance and dispersal.";
RL Biol. J. Linn. Soc. 69:75-102(2000).
DR EMBL; AF099220; AAF18766.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 10 AA; 1254 MW; 1A3580C733640440 CRC64;
```

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Query Match 32.2% Score 19; DB 8; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Oy 6 IGWML 10
1 11
Db 3 INRWL 7

```
RESULT 13
0978P3 ID 0978P3 PRELIMINARY: PRT: 10 AA.
AC 0978P3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Liolaemus andinus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
OX NCBI_TaxID=109394;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
RT "Phylogenetic relationships in the Iguanid lizard Genus Liolaemus:
RT Multiple origins of viviparous reproduction and evidence for recurring
RT Andean vicariance and dispersal.";
RL Biol. J. Linn. Soc. 69:75-102(2000).
DR EMBL; AF099245; AAF18841.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 10 AA; 1254 MW; 1A3580C733640440 CRC64;
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Query Match 32.2% Score 19; DB 8; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Oy 6 IGWML 10
1 11
Db 3 INRWL 7

RESULT 14

Q9T8P0

ID Q9T8P0 PRELIMINARY: PRT: 10 AA.

AC Q9T8P0:

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN

OS Liolaemus famatinae.

OC Mitochondrion

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.

OX NCBI_TaxID=109411;

RN

RN [1]

RP SEQUENCE FROM N.A.

RA Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;

RT "Phylogenetic relationships in the Iguanid lizard Genus Liolaemus:

RT Multiple origins of viviparous reproduction and evidence for recurring

RT Andean vicariance and dispersal."

RL Biol. J. Linn. Soc. 69:75-102(2000).

DR EMBL; AF099246; AAF18844.1; -

KW Mitochondrion.

FT NON_TER

SQ SEQUENCE 10 AA: 1254 MW: 1A3580C733640440 CRC64;

Query Match

Best Local Similarity 32.2%; Score 19; DB 8; Length 10;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 IGNNL 10

DB 3 INRWL 7

RESULT 15

Q9T8N7

ID Q9T8N7 PRELIMINARY: PRT: 10 AA.

AC Q9T8N7:

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN

OS Liolaemus orientalis.

OC Mitochondrion

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.

OX NCBI_TaxID=109468;

RN

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SDSU3517;

RA Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;

RT "Phylogenetic relationships in the Iguanid lizard Genus Liolaemus:

RT Multiple origins of viviparous reproduction and evidence for recurring

RT Andean vicariance and dispersal."

RL Biol. J. Linn. Soc. 69:75-102(2000).

DR EMBL; AF099247; AAF18847.1; -

KW Mitochondrion.

FT NON_TER

SQ SEQUENCE 10 AA: 1254 MW: 1A3580C733640440 CRC64;

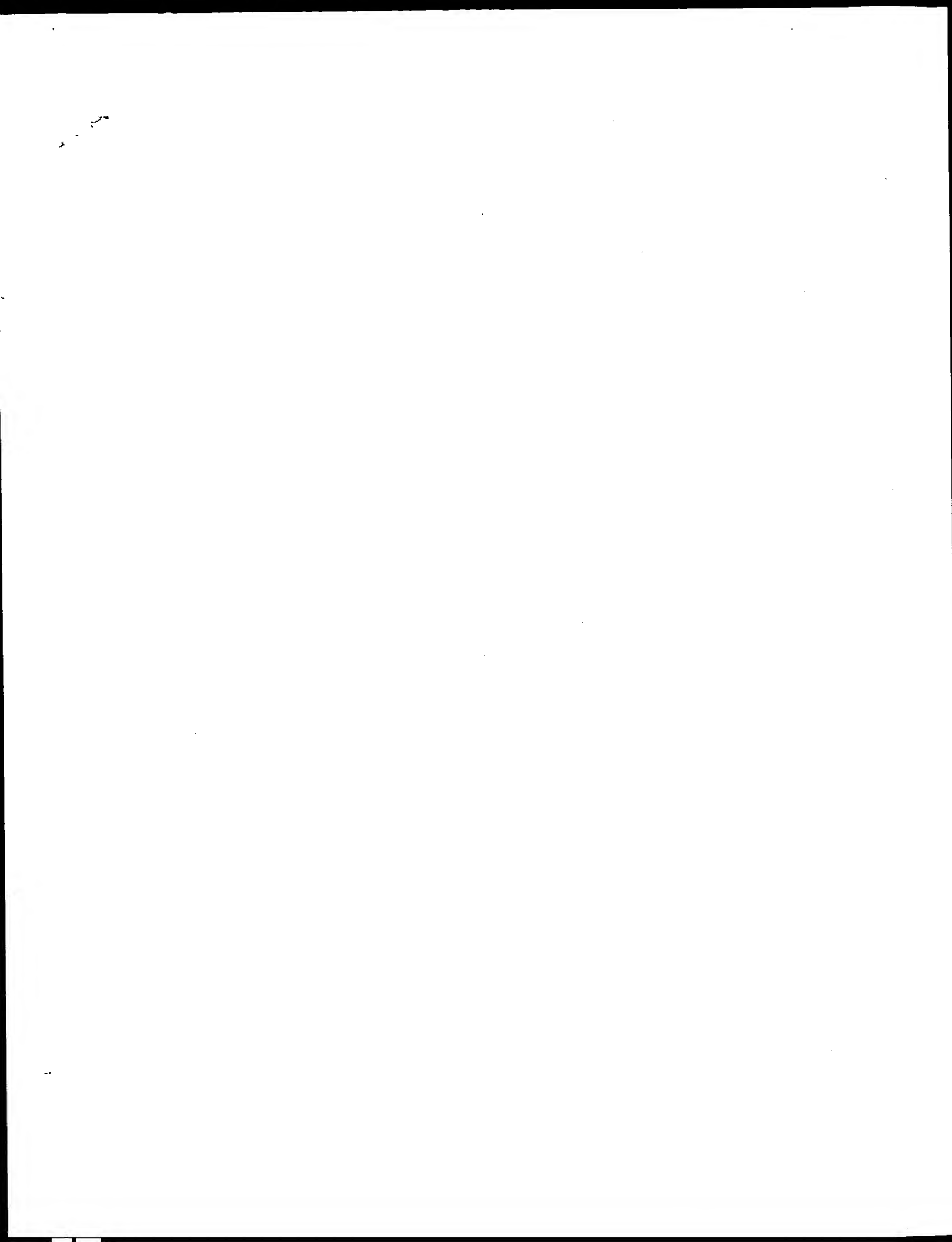
Query Match

Best Local Similarity 32.2%; Score 19; DB 8; Length 10;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 IGNNL 10

DB 3 INRWL 7



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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:38:52 : Search time 11 Seconds
(without alignments)
41.476 Million cell updates/sec

Title: US-09-743-482a-2
Perfect score: 59
Sequence: 1 QASQDIGNWLA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 411

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	39.0	10	1 TPIS_NICPL	P19118 nicotiana p
2	21	35.6	5	1 UF01_MOUSE	P38639 mus musculus
3	21	35.6	10	1 CAER_LITXA	P56264 litorea xan
4	19	32.2	10	1 CA12_LITCI	P82086 litorea cit
5	18.5	31.4	11	1 CA31_LITCI	P82089 litorea cit
6	18	30.5	4	1 OCP3_OCTMI	P58649 octopus min
7	17	28.8	8	1 HTF1_PERAM	P04548 periplaneta
8	17	28.8	8	1 HTF2_PERAM	P04549 periplaneta
9	17	28.8	9	1 HTF_TENMO	P25419 tenebrio mo
10	17	28.8	9	1 DL_NEPNO	P24816 nephris no
11	17	28.8	9	1 NEF_HY128	P12481 human immun
12	17	28.8	10	1 BPP2_BOTIN	P30422 bothrops in
13	17	28.8	10	1 BPP2_BOTJA	P10122 bothrops ja
14	17	28.8	10	1 HTF1_ROMMI	P18110 romalea mic
15	17	28.8	10	1 HTF2_CARMO	P13385 carausius m
16	16.5	28.0	11	1 CA32_LITCI	P82090 litorea cit
17	16	27.1	8	1 LCK3_LEUMA	P21142 leucophaea
18	16	27.1	10	1 LSK2_LEUMA	P09039 leucophaea
19	16	27.1	10	1 TKU1_UREUN	P40751 urechis uni
20	16	27.1	11	1 HS70_PINPS	P81672 pinus pinas
21	16	27.1	11	1 UN05_CLOPA	P81350 clostridium
22	15.5	26.3	9	1 PTSP_BOMMO	P82003 bombyx mori
23	15	25.4	5	1 TPIS_CANFA	P54714 canis fami
24	15	25.4	8	1 CCKN_MACEU	P30369 macropus eu
25	15	25.4	8	1 LCK8_LEUMA	P19990 leucophaea
26	15	25.4	9	1 FAR2_CALVO	P41857 calliphora
27	15	25.4	9	1 FAR3_CALVO	P41858 calliphora
28	15	25.4	9	1 FAR4_CALVO	P41859 calliphora
29	15	25.4	10	1 FAR5_CALVO	P41860 calliphora
30	15	25.4	10	1 GON3_ONCKE	P20267 oncorhynch
31	15	25.4	10	1 GON4_ONCKE	P27429 squallus aca
32	15	25.4	10	1 GSO9_BACSU	P80443 bacillus su
33	15	25.4	10	1 MP2_MITOC	P81533 micropylitis

34	15	25.4	11	1 TRN_ELEMO	P01293 eleone mos
35	14.5	24.6	9	1 LMIP_LOEMI	P31799 locusta mlg
36	14	23.7	9	1 ULAH_HUMAN	P31934 homo sapien
37	14	23.7	10	1 FARP_MANSE	P18523 manduca sex
38	14	23.7	10	1 LABA_JATNU	P13270 jatropa mu
39	14	23.7	10	1 LCKS_LEUMA	P21144 leucophaea
40	14	23.7	11	1 LSK1_LEUMA	P04428 leucophaea
41	14	23.7	11	1 TRK2_CALVO	P41518 calliphora
42	13	22.0	6	1 E101_LITRU	P82096 litorea rub
43	13	22.0	6	1 FARP_MONEX	P41966 moniezia ex
44	13	22.0	7	1 UN11_RAT	P56576 rattus norv
45	13	22.0	9	1 LIT0_LITRU	P08945 litorea aur

ALIGNMENTS

RESULT 1
ID TPIS_NICPL STANDARD: PRT: 10 AA.
AC P19118:
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).
OS Nicotiana glauca (L.) Link. (Leadwort-leaved tobacco).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicot:
OC Asteridae: euasterids I: Solanales: Solanaceae: Nicotiana.
OX NCBI_TaxID=4092;
RN [1]
RP SEQUENCE.
RA Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.:
RT "Alterations in the phenotype of plant cells studied by NH2-terminal
RT amino acid-sequence analysis of proteins electrophoretically from two-
RT dimensional gel-separated total extracts.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate -> glyceralone
CC phosphate.
CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
CC AND PLASTID.
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR PIR: A27617; A27617.
DR InterPro: IPR000652; Triophos_1smrse.
DR PROSITE: PS00171; TIM; PARTIAL.
KW isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW pentose shunt.
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1140 MW: 80890378629C9C9D1 CMC64:
Query Match 39.0%; Score 23; DB 1; Length 10;
Best local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GNM 9
Db 8 GNM 10
RESULT 2
ID UF01_MOUSE STANDARD: PRT: 5 AA.
AC P38639:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Rodentia: Sciurognathu: Muridae: Murinae: Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.6, ITS MW IS: 19 KDa.
 FT NON_TER 5
 SQ SEQUENCE 5 AA: 717 MW: 7364087043100000 CRC64;

 Query Match 35.6%; Score 21; DB 1; Length 5;
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 OY 6 IGMW 9
 DB 2 IGRW 5

 RESULT 3
 CAER_LITXA STANDARD; PRT; 10 AA.
 AC P56264;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Caerulein.
 OS Litoria xanthomera (Orange-thighed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Pelodyadinae; Litoria.
 OC NCBI_Taxid=79697;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-Skin secretion;
 RX MEDLINE=97374000; PubMed=9230483;
 RA Steinboerner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
 RA Ramsay S.L.;
 RT "New caerin antibacterial peptides from the skin glands of the
 RT Australian tree frog Litoria xanthomera.";
 RL J. Pept. Sci. 3:181-185(1997).
 CC -1- FUNCTION: HYPOTENSIVE NEUROPEPTIDE.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=1354; METHOD=FAH.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE: PS00259; GASTRIN; 1.
 KW Amphibian skin; Hypotensive agent; Amidation; Sulfation.
 FT MOD_RES 1 1
 FT MOD_RES 4 4
 FT MOD_RES 10 10
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA: 1290 MW: 99DBF8387861BB5A CRC64;

 Query Match 35.6%; Score 21; DB 1; Length 10;
 Best Local Similarity 42.9%; Pred. No. 3.9e+02;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 OY 4 ODIGMW 10
 DB 2 ODYGMW 8

 RESULT 4
 CA12_LITCI STANDARD; PRT; 10 AA.
 AC P82089;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Caerulein 1.2/1.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog), and
 OS Litoria splendida (Magnificent tree frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Pelodyadinae; Litoria.
 OX NCBI_Taxid=94770; 30345;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2 AND 1.2Y4).
 RC SPECIES=L.citropa; TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 RN [2]
 RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2).
 RC SPECIES=L.splendida;
 RX MEDLINE=20069371; PubMed=10601876;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Smith B.P.;
 RT "Differences in the skin peptides of the male and female Australian
 RT tree frog Litoria splendida. The discovery of the aquatic male sex
 RT phenomone splendipherin, together with Phe8 caerulein and the
 RT antibiotic peptide caerin 1.10.";
 RL Eur. J. Biochem. 267:269-275(2000).
 CC -1- FUNCTION: HYPOTENSIVE NEUROPEPTIDE (PROBABLE).
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- PTM: ISOCORM 1.2Y4 DIFFERS FROM ISOCORM 1.2 IN NOT BEING
 CC SULFATED.
 CC -1- MASS SPECTROMETRY: MW=1366; METHOD=Electrospray.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE: PS00259; GASTRIN; FALSE NEG.
 KW Amphibian skin; Hypotensive agent; Amidation; Sulfation.
 FT MOD_RES 1 1
 FT MOD_RES 4 4
 FT MOD_RES 10 10
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA: 1306 MW: 99DBFCD37861BB5A CRC64;

 Query Match 32.2%; Score 19; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 9.1e+02;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 OY 4 ODIGMW 9
 DB 2 ODYGMW 7

 RESULT 5
 CA31_LITCI STANDARD; PRT; 11 AA.
 AC P82089;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Caerulein 3.1/3.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Pelodyadinae; Litoria.
 OX NCBI_Taxid=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -1- FUNCTION: HYPOTENSIVE NEUROPEPTIDE (PROBABLE).
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

OC	HTFL_PERAM	STANDARD:	PRT:	8 AA.
AC	HTFL_PERAM			
DT	P04548:			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-FEB-1994 (Rel. 28, Last annotation update)			
DE	Hypertrehalosemic factor I (Neuropeptide M-I) (Periplanetin CC-1)			
DE	Pea-CAH-I (Ied-CC-1) (Hypertrehalosemic neuropeptide I).			
OS	Periplaneta americana (American cockroach),			
OS	Leptinotarsa decemlineata (Colorado potato beetle), and			
OC	Blattella orientalis (Oriental cockroach),			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda			

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OC Insecta;Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattellidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN (1)
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RT Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN (2)
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN (3)
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiacaum from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN (4)
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosemic neuropeptides isolated from
RT Gremphodrhina portulosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RC -I- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
RC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
RC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
CC CC
DR DR
DR PIR: A05169; A05169.
DR PIR: S08995; S08995.
DR PIR: A49823; A49823.
DR PIR: A44960; A44960.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
FT Neuropeptide: Amidation.
FT MOD_RES 1
FT MOD_RES 8 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 AMIDATION.
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 28.8%; Score 17; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. NO. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 NW 9
Db 7 NW 8

RESULT 8
HTFP2_PERAM
ID HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Hypertrehalosemic factor II (Neuropeptide W-II) (Periplanetin CC-2)

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DE (pea-CAH-II) (Lep-CC-II) (Hypertrehalosemic neuropeptide II).
 OS Periplaneta americana (American cockroach).
 OS Lepidoptera decemlineata (Colorado potato beetle), and
 OS Blatta orientalis (Oriental cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES-P. americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L., Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry."
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-P. americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarbrough R.M., Jamieson G.C., Kalish F., Kramer S.J., McInroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES-L. decemlineata; TISSUE-Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiacum from the potato
 RT beetle and the American cockroach are identical."
 RL Peptides 10:1287-1288(1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES-B. orientalis; TISSUE-Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L., Jr.;
 RT "Primary structures of hypertrehalosemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gryphonodonta portoricensis, Blattella germanica and Blatta orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry."
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 CC PIR: A05170; A05170.
 DR PIR: S08996; S08996.
 DR PIR: B44960; B44960.
 DR PIR: B49823; B49823.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 FT MOD_RES 86745771A5D1A736 CRC64;
 SQ SEQUENCE 8 AA: 1006 MW; 86745771A5D1A736 CRC64;
 QY 8 NW 9
 Db 7 NW 8
 RESULT 9
 HTF_TENMO 1
 ID HTF_TENMO STANDARD; PRT; 8 AA.
 Query Match 28.8%; Score 17; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.le+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC P25419;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypertrehalosemic factor (HRTN) (Hypertrehalosemic neuropeptide).
 OS Tenebrio molitor (Yellow mealworm), and
 OS Zophobas rugipes.
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 CC Cucujiformia; Tenebrionidae; Tenebrio.
 OX NCBI_TaxID=7067, 7073;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Corpora cardiaca;
 RX MEDLINE=90341081; PubMed=2381871;
 RA Gaede G., Rosinski G.;
 RT "The primary structure of the hypertrehalosemic neuropeptide from
 RT tenebrionid beetles: a novel member of the AKH/RPCH family."
 RL Peptides 11:455-459(1990).
 CC -1- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 CC PIR: A43976; A43976.
 DR PIR: B43976; B43976.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 FT MOD_RES 86745775B9C44736 CRC64;
 SQ SEQUENCE 8 AA: 1005 MW; 86745775B9C44736 CRC64;
 QY 8 NW 9
 Db 7 NW 8
 RESULT 10
 DL_NEPRNO STANDARD; PRT; 9 AA.
 ID DL_NEPRNO
 AC P24816;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-MAR-1992 (Rel. 21, Last annotation update)
 DE Gastrin/cholecystokinin-like peptide DL.
 CC Nephrops norvegicus (Norway lobster).
 OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 CC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 CC Astacidea; Nephropoidea; Nephropidae; Nephrops.
 OX NCBI_TaxID=6829;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Stomach;
 RX MEDLINE=92082847; PubMed=1747388;
 RA Favrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.;
 RT "Structure and biological activity of crustacean gastrointestinal
 RT peptides identified with antibodies to gastrin/cholecystokinin."
 RL Biochimie 73:1233-1239(1991).
 CC -1- FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 CC PIR: A48398; A48398.
 KW Hormone.
 SQ SEQUENCE 9 AA: 1038 MW; 60EC79CAB6D8787B CRC64;
 QY 1 QASDIGNWL 10
 Query Match 28.8%; Score 17; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.le+05;
 Matches 4; Conservative 1; Mismatches 3; Indels 2; Gaps 1;


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DB      2  EGGODE--WL 9

RESULT 11
NEF_HV128
ID      NEF_HV128      STANDARD;      PRT;      9  AA.
AC      P12481;
DT      01-OCT-1989 (Rel. 12, Created)
DT      01-OCT-1989 (Rel. 12, Last sequence update)
DE      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Negative factor (F-protein) (27 kDa protein) (3'ORF) (Fragment).
GN      NEF.
OS      Human immunodeficiency virus type 1 (2-84 isolate) (HIV-1).
OC      Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX      NCB1_TaxID=11681;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=88281278; PubMed=3395517;
RA      Youno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA      Gallo R.C.;
RT      "Nucleotide sequence analysis of the env gene of a new Zairian
RT      isolate of HIV-1";
RL      AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC      -1- FUNCTION: NEF has GTPase, GTP-binding and autophosphorylating
CC      activities. It seems to down-regulate the CD4(74) antigen.
CC      -1- MISCELLANEOUS: THE 2-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC      ZAIREAN MALE.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
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CC      or send an email to license@isb-sib.ch).
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DR      EMBL: J03653; AAA44687.1; -.
DR      HIV: J03653; NEFSU1.
KW      AIDS; Myristate; GTP-binding.
FT      LIPID
FT      NON_TER      2      9
FT      SEQUENCE      9  AA; 967 MW; 310CB325A3733878 CRC64;

Query Match      28.8%; Score 17; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches      2; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

OY      7  NMW 9
DB      3  GKW 5

RESULT 12
BPP2_BOTIN
ID      BPP2_BOTIN      STANDARD;      PRT;      10  AA.
AC      P30422;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      01-FEB-1994 (Rel. 28, Last annotation update)
DE      Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
DE      enzyme inhibitor).
OS      Bothrops insularis (Island jararaca) (Quelinada jararaca).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC      Viperidae; Crotalinae; Bothrops.
OX      NCB1_TaxID=8723;
RN      [1]
RP      SEQUENCE.
RX      TISSUE=Venom;
RA      MEDLINE=90351557; PubMed=2386615;
RA      Cintera A.C.O., Vieira C.A., Giglio J.R.;
RT      "Primary structure and biological activity of bradykinin potentiating

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RT      peptides from Bothrops insularis snake venom.";
RL      J. Protein Chem. 9:221-227(1990).
CC      -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC      ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC      BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC      IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR      PIR: B37196; B37196.
KW      Hypotensive agent; Venom.
FT      MOD_RES      1
FT      SEQUENCE      10  AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match      28.8%; Score 17; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

OY      8  NMW 9
DB      2  NMW 3

RESULT 13
BPP2_BOTJA
ID      BPP2_BOTJA      STANDARD;      PRT;      10  AA.
AC      P01022;
DT      21-JUL-1986 (Rel. 01, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      01-FEB-1994 (Rel. 28, Last annotation update)
DE      Bradykinin-potentiating peptide 10B (angiotensin-converting enzyme
DE      inhibitor V-6-II).
OS      Bothrops jararaca (Jararaca).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC      Viperidae; Crotalinae; Bothrops.
OX      NCB1_TaxID=8724;
RN      [1]
RP      SEQUENCE.
RX      TISSUE=Venom;
RA      MEDLINE=72118526; PubMed=4334402;
RA      Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA      Kocoy O.;
RT      "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT      jararaca. Isolation, elucidation of structure, and synthesis.";
RL      Biochemistry 10:4033-4039(1971).
CC      -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC      ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC      BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC      IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR      PIR: A01255; XAV16B.
KW      Hypotensive agent; Venom.
FT      MOD_RES      1
FT      SEQUENCE      10  AA; 1232 MW; 30C53546C741773 CRC64;

Query Match      28.8%; Score 17; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

OY      8  NMW 9
DB      2  NMW 3

RESULT 14
HTF1_ROMMI
ID      HTF1_ROMMI      STANDARD;      PRT;      10  AA.
AC      P18110;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      01-FEB-1994 (Rel. 28, Last annotation update)
DE      RO I (Hypertrichothalassaemic factor).
OS      Romalea microptera (Lumber grasshopper).
OC      Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC      Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC      Acridoidea; Acridoidea; Romaleidae; Romalea.

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OX NCBI_TaxID=7007;
 RN [1]
 RP SEQUENCE:
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89145002; PubMed-3226948;
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
 RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
 the lubber grasshopper, *Rhombia microptera*.";
 RL Peptides 9:681-688(1988).
 CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight.
 FT MOD.RES 1 10 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD.RES 1 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;
 Query Match 28.8%; Score 17; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 8 NW 9
 DB 7 NW 8
 RESULT 15
 HTF2_CARMO STANDARD; PRT; 10 AA.
 ID HTF2_CARMO
 AC p11385; Created
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Hypertrahalosaemic factor II (HTF-II) (HRTN-II) (Hypertrahalosaemic
 DE neuropeptide II).
 OS Carausius morosus (Indian stick insect), and
 OS Exaltosoma tiaratum (Stick insect).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Phasmatoidea;
 OC Heteronemidae; Carausius.
 OX NCBI_TaxID=7022, 7024;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C. morosus; TISSUE=Corpora cardiaca;
 RX MEDLINE=87157103; PubMed-3828078;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structure of the hypertrahalosaemic factor II from the
 RT corpus cardiacum of the Indian stick insect, *Carausius morosus*,
 RT determined by fast atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=E. tiaratum; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed-2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrahalosaemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches *Leucophaea maderae*,
 RT *Gromphadorhina portentosa*, *Blattella germanica* and *Blattella orientalis*
 RT and of the stick insect *Exaltosoma tiaratum* assigned by tandem fast
 RT atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 RN [3]
 RP CARBOHYDRATE-LINKAGE SITE.
 RC SPECIES=C. morosus; TISSUE=Corpora cardiaca;
 RX MEDLINE=93129188; PubMed-1482345;
 RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
 RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
 RT a stick insect corpus cardiacum";
 RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
 CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT

CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: S07157; S07157.
 DR PIR: S09138; S09138.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Glycoprotein.
 FT MOD.RES 1 10 PYRROLIDONE CARBOXYLIC ACID.
 FT CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).
 FT MOD.RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;
 Query Match 28.8%; Score 17; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 8 NW 9
 DB 7 NW 8

Search completed: February 25, 2003, 10:58:15
 Job time : 12 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:56:32 : Search time 14 seconds
(without alignments)

75.534 Million cell updates/sec

Title: US-09-743-482A-2

Perfect score: 59

Sequence: 1 QASQDIGNMILA 11

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 1326

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	44.1	11	2	PH0906
2	24	40.7	11	2	PH1343
3	23	39.0	6	2	PT0532
4	23	39.0	10	2	A40753
5	23	39.0	10	2	A27617
6	21.5	36.4	11	2	A49164
7	21	35.6	10	2	A61337
8	20	33.9	9	2	A43848
9	20	33.9	10	2	PT0289
10	19.5	33.1	9	2	A57444
11	19.5	33.1	9	2	PT0562
12	19	32.2	6	2	PT0619
13	19	32.2	6	2	PT0550
14	19	32.2	7	2	PT0524
15	19	32.2	7	2	PT0683
16	19	32.2	8	2	PT0627
17	19	32.2	8	2	PT0509
18	19	32.2	10	2	T17054
19	19	32.2	10	2	T17063
20	19	32.2	10	2	T12329
21	18	30.5	6	2	PT0629
22	18	30.5	7	2	PT0728
23	18	30.5	9	2	D57444
24	18	30.5	10	2	PH1344
25	18	30.5	10	2	PH0900
26	18	30.5	11	2	PH0891
27	17	28.8	5	2	PT0281
28	17	28.8	6	2	B31263
29	17	28.8	6	2	PT0630

30	17	28.8	6	2	PT0637	T-cell receptor be
31	17	28.8	6	2	PT0687	T-cell receptor be
32	17	28.8	7	2	PT0642	T-cell receptor be
33	17	28.8	7	2	PT0620	T-cell receptor be
34	17	28.8	7	2	PT0666	T-cell receptor be
35	17	28.8	7	2	PT0655	T-cell receptor be
36	17	28.8	7	2	PT0544	T-cell receptor be
37	17	28.8	8	2	S08995	hypertrehalosemic
38	17	28.8	8	2	S08996	hypertrehalosemic
39	17	28.8	8	2	A49823	adipokinetic hormo
40	17	28.8	8	2	B49823	neuropeptide led-c
41	17	28.8	8	2	A44960	neuropeptide led-c
42	17	28.8	8	2	B44960	hypertrehalosemic
43	17	28.8	8	2	A43976	hypertrehalosemic
44	17	28.8	8	2	B43976	hypertrehalosemic
45	17	28.8	8	2	A05169	neuropeptide M-I -

ALIGNMENTS

RESULT 1

PH0906
T-cell receptor beta chain V-D-J region (isolates 2, 8, 9) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0906
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0906
A:Molecule type: mRNA
A:Residues: 1-11 <COL>
A:Experimental source: myelin basic protein-immunized lymph node
C:Keywords: T-cell receptor

Query Match

Best Local Similarity 66.7%; Score 26; DB 2; Length 11;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ASQDIGNMIL 10
DB 2 ASSDSGNTL 10

RESULT 2

PH1343
Ig heavy chain DJ region (clone C100-91) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1343
R:Masserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor ly
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1343
A:Molecule type: DNA
A:Residues: 1-11 <MAS>
C:Keywords: heterodimer; immunoglobulin

Query Match

Best Local Similarity 40.7%; Score 24; DB 2; Length 11;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DIGNM 9
DB 3 DLDMW 7

RESULT 3

PT0532
T-cell receptor beta chain V-D-J region (100-4A1) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0532
 R:Peeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0532
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-6 <FEF>
 A:Experimental source: adult thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 39.0%; Score 23; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GNM 9
 |||
 Db 4 GNM 6

RESULT 4
 A:0753
 A:Idhyde ferredoxin oxidoreductase (EC 1.2.7.-) - Pyrococcus furiosus (fragment)
 N:Alternate names: glyceraldhyde:ferredoxin oxidoreductase; red tungsten protein (RTP)
 C:Species: Pyrococcus furiosus
 C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 13-Sep-1996
 C:Accession: A40753
 R:Mukund, S.; Adams, M.W.W.
 J. Biol. Chem. 266, 14208-14216, 1991
 A:Title: The novel tungsten-iron-sulfur protein of the hyperthermophilic archaeobacterium
 C:Keywords: iron-sulfur protein; oxidoreductase; tungsten
 A:Reference number: A40753; MUID:91317766; PMID:1907273
 A:Accession: A40753
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <MKK>
 C:Keywords: iron-sulfur protein; oxidoreductase; tungsten

Query Match 39.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GNM 9
 |||
 Db 3 GNM 5

RESULT 5
 A:27617
 A:triose-phosphate isomerase (EC 5.3.1.1) - curled-leaved tobacco (fragment)
 C:Species: Nicotiana glauca (curled-leaved tobacco)
 C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 28-Apr-1993
 C:Accession: A27617
 R:Baum, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
 A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-
 A:Reference number: A94167
 A:Accession: A27617
 A:Molecule type: protein
 A:Residues: 1-10 <BMU>
 C:Keywords: gluconeogenesis; glycolysis; intramolecular oxidoreductase; isomerase; pentose

Query Match 39.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GNM 9
 |||
 Db 8 GNM 10

RESULT 6
 A:49164
 A:chromogranin-B - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
 C:Accession: B49164
 R:Nielsen, E.; Mellander, B.S.; Madsen, O.D.
 Endocrinology 129, 3147-3156, 1991
 A:Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides
 A:Reference number: A49164; MUID:92063871; PMID:1954895
 A:Accession: B49164
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <NIE>
 A:Note: sequence extracted from NCBI backbone (NCBIP:66370)
 C:Superfamily: chromogranin B precursor

Query Match 36.4%; Score 21.5; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 8.8e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 3 SODIGNM 9
 |||
 Db 3 SEDV-NW 8

RESULT 7
 A:61337
 A:caerulein - frog (Hyla caerulea)
 C:Species: Hyla caerulea
 C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
 C:Accession: A61337
 R:Anastasi, A.; Erspamer, V.; Eide, R.
 Arch. Biochem. Biophys. 125, 57-68, 1968
 A:Title: Isolation and amino acid sequence of caerulein, the active decapeptide of the
 A:Reference number: A61337; MUID:68238534; PMID:5649531
 A:Accession: A61337
 A:Molecule type: protein
 A:Residues: 1-10 <NAN>
 C:Comment: The last five amino acids and the carboxyl terminal amide group of this ne
 C:Comment: This amphibian skin peptide can cause a sustained lowering of blood pressu
 C:Superfamily: gastrin
 C:Keywords: amidated carboxyl end; antihypertensive; neuropeptide; pyroglutamic acid;
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:4/Binding site: sulfate (Tyr) (covalent) #status experimental
 F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 35.6%; Score 21; DB 2; Length 10;
 Best Local Similarity 42.9%; Pred. No. 9.8e+02;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 ODIGNM 10
 |||
 Db 2 QDITGM 8

RESULT 8
 A:43848
 A:cell surface adhesin for heparan sulfate, 66k - Staphylococcus aureus (fragment)
 C:Species: Staphylococcus aureus
 C:Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995
 C:Accession: A43848
 R:Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
 Infect. Immun. 60, 899-906, 1992
 A:Title: Binding of heparan sulfate to Staphylococcus aureus.
 A:Reference number: A43848; MUID:92176005; PMID:1541563
 A:Accession: A43848
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <LIA>
 A:Note: sequence extracted from NCBI backbone (NCBIP:85442)

Query Match 33.9%; Score 20; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 DIGMMLA 11
| | | | |
Db 1 DWTGMLA 7

RESULT 9
PT0289
Ig heavy chain CRD3 region (clone 4-109) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0289
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0289
A:Molecule type: DNA
A:Residues: 1-10 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 33.9%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 8 NWLA 11
| | | | |
Db 3 NWIS 6

RESULT 10
A57444
neuropeptide Grb-AST B1 - two-spotted cricket
C:Species: Gryllus bimaculatus (two-spotted cricket)
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Accession: A57444
R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cr
A:Reference number: A57444; MUID:95403341; PMID:7673141
A:Accession: A57444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <LOR>

Query Match 33.1%; Score 19.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

OY 4 QDI-GMW 9
| | | | |
Db 3 QDLNGW 9

RESULT 11
PT0562
T-cell receptor beta chain V-D-J region (126-1AK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0562
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0562
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-9 <FEE>
A:Experimental source: day 18 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 33.1%; Score 19.5; DB 2; Length 9;
Best Local Similarity 62.5%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 2 ASDIGMW 9
| | | | |
Db 1 ASSD-DNW 7

RESULT 12
PT0619
T-cell receptor beta chain V-D-J region (120-2CN) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0619; PT0563; PT0598
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0619
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: newborn thymus, strain BALB/c, clone 120-2CN
A:Accession: PT0563
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 136-3A
A:Accession: PT0598
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: newborn thymus, strain BALB/c, clone 111-1Q
C:Keywords: T-cell receptor

Query Match 32.2%; Score 19; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ASDIG 7
| | | | |
Db 1 ASSDTG 6

RESULT 13
PT0550
T-cell receptor beta chain V-D-J region (126-1CF) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0550
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0550
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: day 18 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 32.2%; Score 19; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ASDIG 7
| | | | |
Db 1 ASSDAG 6

RESULT 14

PT0524
 T-cell receptor beta chain V-D-J region (100-4AD) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0524
 R:Reaney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0524
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-7 <FEF>
 A:Experimental source: adult thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match

32.2%; Score 19; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY

2 ASDIG 7
 1 1 1 1
 1 ASDAG 6

Db

1 ASDAG 6

RESULT 15

PT0683
 T-cell receptor beta chain V-D-J region (140-1N) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0683
 R:Reaney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0683
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-7 <FEF>
 A:Experimental source: day 18 fetal thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match

32.2%; Score 19; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY

2 ASDIG 7
 1 1 1 1
 1 ASDAG 6

Db

1 ASDAG 6

Search completed: February 25, 2003, 11:00:14
 Job time : 14 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:36:42 ; Search time 0.898333 Seconds
(Without alignments)
380.447 Million cell updates/sec

Title: US-09-743-482A-2
Sequence: 1 QASODIGNMILA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues
Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEM_PUB pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEM_PUB pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEM_PUB pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	78.0	88	10 US-09-905-243-63	Sequence 63, Appl
2	44	74.6	11	10 US-09-798-058-8	Sequence 8, Appl
3	44	74.6	109	10 US-09-798-058-4	Sequence 4, Appl
4	41	69.5	222	9 US-09-738-626-4206	Sequence 4206, Ap
5	40	67.8	76	9 US-09-187-693-36	Sequence 36, Appl
6	40	67.8	90	10 US-09-864-761-34739	Sequence 34739, A
7	40	67.8	99	10 US-09-925-297-864	Sequence 864, App
8	40	67.8	105	9 US-09-187-693-40	Sequence 40, Appl
9	40	67.8	105	9 US-09-187-693-44	Sequence 44, Appl
10	40	67.8	105	9 US-09-187-693-50	Sequence 50, Appl
11	40	67.8	105	9 US-09-187-693-54	Sequence 54, Appl
12	40	67.8	231	10 US-09-731-126-8	Sequence 8, Appl
13	40	67.8	232	9 US-10-003-035-49	Sequence 49, Appl
14	40	67.8	234	10 US-09-800-729-150	Sequence 150, App
15	40	67.8	261	9 US-10-003-035-50	Sequence 50, Appl
16	40	67.8	275	10 US-09-756-551A-4	Sequence 4, Appl
17	40	67.8	286	9 US-10-003-035-51	Sequence 51, Appl
18	40	67.8	294	10 US-09-827-822-3	Sequence 3, Appl
19	40	67.8	363	9 US-10-003-035-37	Sequence 37, Appl

20	40	67.8	363	9	US-09-943-722-130	Sequence 130, App
21	40	67.8	453	9	US-10-003-035-39	Sequence 39, Appl
22	40	67.8	492	9	US-10-003-035-18	Sequence 18, Appl
23	40	67.8	500	10	US-09-968-355-26	Sequence 26, Appl
24	40	67.8	515	10	US-09-968-355-20	Sequence 20, Appl
25	40	67.8	531	10	US-09-968-355-23	Sequence 23, Appl
26	40	67.8	583	10	US-09-968-355-17	Sequence 17, Appl
27	40	67.8	599	9	US-10-003-035-59	Sequence 59, Appl
28	39.5	66.9	109	10	US-09-943-906-74	Sequence 74, Appl
29	38.5	66.9	130	1	US-08-779-784-35	Sequence 35, Appl
30	39.5	66.9	243	9	US-09-887-853-6	Sequence 6, Appl
31	39.5	66.9	276	10	US-09-766-543-12	Sequence 12, Appl
32	38	64.4	95	10	US-09-158-120A-19	Sequence 19, Appl
33	38	64.4	95	10	US-09-158-120A-33	Sequence 33, Appl
34	38	64.4	109	10	US-09-229-200A-7	Sequence 7, Appl
35	38	64.4	232	10	US-09-731-126-7	Sequence 7, Appl
36	37	62.7	88	10	US-09-905-243-35	Sequence 35, Appl
37	37	62.7	97	9	US-09-796-692-700	Sequence 700, App
38	37	62.7	97	9	US-09-796-692-2120	Sequence 2120, App
39	37	62.7	102	9	US-09-796-692-774	Sequence 774, App
40	37	62.7	107	9	US-10-011-931-4	Sequence 4, Appl
41	37	62.7	107	10	US-09-997-574-12	Sequence 12, Appl
42	37	62.7	115	9	US-09-796-692-887	Sequence 887, App
43	37	62.7	118	9	US-09-796-692-883	Sequence 883, App
44	37	62.7	118	9	US-09-796-692-2167	Sequence 2167, Ap
45	37	62.7	122	9	US-09-796-692-985	Sequence 985, App

ALIGNMENTS

RESULT 1
US-09-905-243-63
Sequence 63, Application US/09905243
Patent No. US20020062009A1
GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 63
LENGTH: 88
TYPE: PRT
ORGANISM: Macaca cynomolgus
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (24)...(34)
OTHER INFORMATION: CDRI
NAME/KEY: DOMAIN
LOCATION: (50)...(56)
OTHER INFORMATION: CDR1
US-09-905-243-63

Query Match 78.0%; Score 46; DB 10; Length 88;
Best Local Similarity 81.8%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Caps 0;

QY 1 QASODIGNMILA 11
|||||
DB 24 QASODIGNMILA 34

RESULT 2
US-09-798-058-8
Sequence 8, Application US/09798058
Patent No. US20020098523A1
GENERAL INFORMATION:

APPLICANT: Vaughan, Tristan John
APPLICANT: Wilton, Alison Jane
APPLICANT: Smith, Stephen
APPLICANT: Main, Sarah Helen
TITLE OF INVENTION: Human antibodies against ectaxin and their use
FILE REFERENCE: 84632-000100
CURRENT APPLICATION NUMBER: US/09/798,058
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 60/187,246
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-798-058-8

Query Match 74.6%; Score 44; DB 10; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.085;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNMILA 11
Db 1 RASODISSMILA 11

RESULT 3
US-09-798-058-4
Sequence 4, Application US/09798058
Patent No. US20020098523A1
GENERAL INFORMATION:
APPLICANT: Vaughan, Tristan John
APPLICANT: Wilton, Alison Jane
APPLICANT: Smith, Stephen
APPLICANT: Main, Sarah Helen
TITLE OF INVENTION: Human antibodies against ectaxin and their use
FILE REFERENCE: 84632-000100
CURRENT APPLICATION NUMBER: US/09/798,058
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 60/187,246
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-798-058-4

Query Match 74.6%; Score 44; DB 10; Length 109;
Best Local Similarity 72.7%; Pred. No. 0.81;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNMILA 11
Db 24 RASODISSMILA 34

RESULT 4
US-09-738-626-4206
Sequence 4206, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHITAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO

APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 4206
LENGTH: 222
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-4206

Query Match 69.5%; Score 41; DB 9; Length 222;
Best Local Similarity 63.6%; Pred. No. 5.3;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNMILA 11
Db 206 QAAQLIGNMILS 216

RESULT 5
US-09-187-693-36
Sequence 36, Application US/09187693
Patent No. US20020173629A1
GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
FILE REFERENCE: Cell 4.20 CIP2
CURRENT APPLICATION NUMBER: US/09/187,693
CURRENT FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 09/162,280
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 08/851,362
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 76
TYPE: PRT
ORGANISM: human
US-09-187-693-36

Query Match 67.8%; Score 40; DB 9; Length 76;
Best Local Similarity 80.0%; Pred. No. 2.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNMIL 10
Db 5 QASODISSMIL 14

RESULT 6
US-09-864-761-34739
Sequence 34739, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR


```

: TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
: FILE REFERENCE: Aecmca-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
: SEQ ID NO 34739
: LENGTH: 90
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC009958.1
: OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.6
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 84
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 15
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.9
: OTHER INFORMATION: EST. HUMAN HIT: AM04507.1, EVALUE 4.00e-46
: OTHER INFORMATION: SWISSPROT HIT: P01608, EVALUE 3.00e-43
: US-09-864-761-34739

Query Match      67.8%: Score 40; DB 10; Length 90;
Best Local Similarity 80.0%: Pred. No. 3.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 1 QASODIGNWL 10
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Db 16 QASODISNYL 25

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RESULT 7
US-09-925-297-864
: Sequence 864, Application US/09925297
: Patent No. US20020081659A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.

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: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA105
: CURRENT APPLICATION NUMBER: US/09/925,297
: CURRENT FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05989
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 928
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 864
: LENGTH: 99
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (40)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (47)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (58)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (75)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (86)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: US-09-925-297-864

Query Match      67.8%: Score 40; DB 10; Length 99;
Best Local Similarity 72.7%: Pred. No. 3.5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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OY 1 QASODIGNWLA 11
   ||||| 1:1
Db 43 RASOXIENWLA 53

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RESULT 8
US-09-187-693-40
: Sequence 40, Application US/09187693
: Patent No. US20020173629A1
: GENERAL INFORMATION:
: APPLICANT: Jakobovits, Aya
: APPLICANT: Yang, Xiao-Dong
: APPLICANT: Gallo, Michael
: APPLICANT: Jia, Xiao-Chi
: TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
: FILE REFERENCE: Cell 4.20 C1P2
: CURRENT APPLICATION NUMBER: US/09/187,693
: CURRENT FILING DATE: 1998-11-05
: PRIOR APPLICATION NUMBER: 09/162,280
: PRIOR FILING DATE: 1998-09-29
: PRIOR APPLICATION NUMBER: 08/851,362
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 40
: LENGTH: 105
: TYPE: PRT
: ORGANISM: human
: US-09-187-693-40

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Query Match      67.8%: Score 40; DB 9; Length 105;
Best Local Similarity 80.0%: Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 1 QASODIGNWL 10
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Db 5 QASODIGNYL 14

RESULT 9

US-09-187-693-44
; Sequence 44, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; FILE REFERENCE: Cell 4.20 CIP2
; CURRENT APPLICATION NUMBER: US/09/187,693
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 105
; TYPE: PRT
; ORGANISM: human
US-09-187-693-44

Query Match

Best Local Similarity 67.8%; Score 40; DB 9; Length 105;
Best Local Similarity 80.0%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNYL 10
||||| 1:1
Db 5 QASODIGNYL 14

RESULT 10

US-09-187-693-50
; Sequence 50, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; FILE REFERENCE: Cell 4.20 CIP2
; CURRENT APPLICATION NUMBER: US/09/187,693
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 105
; TYPE: PRT
; ORGANISM: human
US-09-187-693-50

Query Match

Best Local Similarity 67.8%; Score 40; DB 9; Length 105;
Best Local Similarity 80.0%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNYL 10
||||| 1:1
Db 5 QASODIGNYL 14

RESULT 11

US-09-187-693-54
; Sequence 54, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; FILE REFERENCE: Cell 4.20 CIP2
; CURRENT APPLICATION NUMBER: US/09/187,693
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 105
; TYPE: PRT
; ORGANISM: human
US-09-187-693-54

Query Match

Best Local Similarity 67.8%; Score 40; DB 9; Length 105;
Best Local Similarity 80.0%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNYL 10
||||| 1:1
Db 5 QASODIGNYL 14

RESULT 12

US-09-731-126-8
; Sequence 8, Application US/09731126
; Patent No. US2002010636A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Lou, Sheng C.
; APPLICANT: Hunt, Jeffrey C.
; APPLICANT: Konrat, John G.
; APPLICANT: Qiu, Xiaoxing
; APPLICANT: Scheffel, James W.
; APPLICANT: Tyner, Joan D.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO HUMAN
; FILE REFERENCE: 6755.US.01
; CURRENT APPLICATION NUMBER: US/09/731,126
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-09-731-126-8

Query Match

Best Local Similarity 67.8%; Score 40; DB 10; Length 231;
Best Local Similarity 60.0%; Pred. No. 8.1;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNYL 10
||||| 1:1
Db 176 QASOEYKMMW 185

RESULT 13

US-10-003-035-49
; Sequence 49, Application US/10003035
; Patent No. US20020155127A1

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; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 22488-712
; CURRENT APPLICATION NUMBER: US/10/003,035
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-003-035-49

Query Match      67.8%; Score 40; DB 9; Length 232;
Best Local Similarity 60.0%; Pred. No. 8.1;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 QASODIGNWL 10
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Db      177 QASQEVKNMM 186

RESULT 14
US-09-800-729-150
; Sequence 150; Application US/09800729
; Patent No. US20020068319A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 150
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (120)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-800-729-150

Query Match      67.8%; Score 40; DB 10; Length 234;
Best Local Similarity 80.0%; Pred. No. 8.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QASODIGNWL 10
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Db      44 QASODIANYL 53

RESULT 15
US-10-003-035-50
; Sequence 50; Application US/10003035
; Patent No. US20020155127A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 22488-712
; CURRENT APPLICATION NUMBER: US/10/003,035
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 09/585,599

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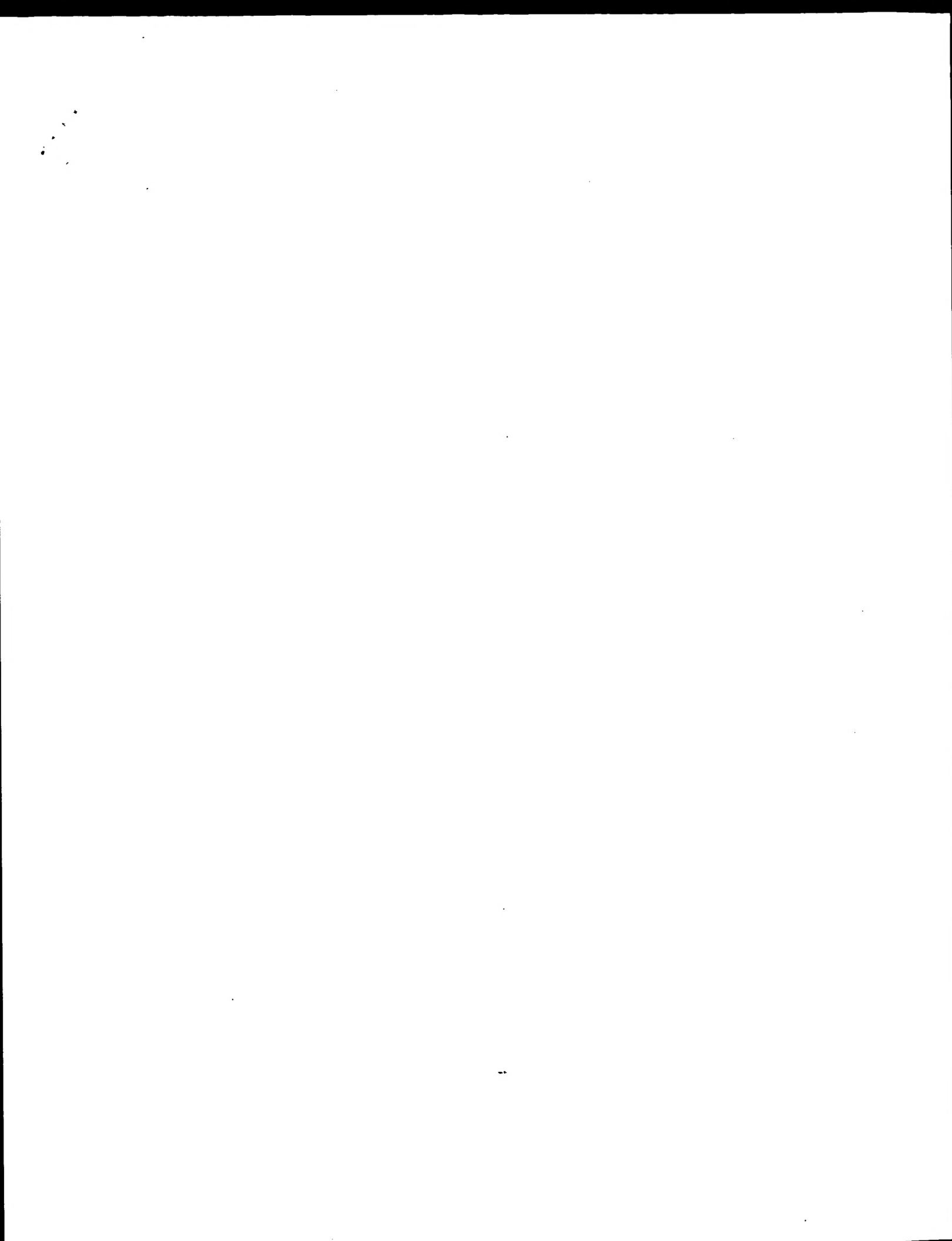
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; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 75
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; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-003-035-50

Query Match      67.8%; Score 40; DB 9; Length 261;
Best Local Similarity 60.0%; Pred. No. 9.1;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 QASODIGNWL 10
        |||||:|:|
Db      206 QASQEVKNMM 215

Search completed: February 25, 2003, 10:57:17
Job time : 1.89833 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:57 : Search time 3.63 seconds
(without alignments)
403.790 Million cell updates/sec

Title: US-09-743-482a-2
Perfect score: 59
Sequence: 1 QASODIGNMLA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	11	AAV78319	Anti-zeta-chain an
2	59	100.0	107	AAV78326	Anti-zeta-chain an
3	59	100.0	532	AAV78328	Bispecific anti-ze
4	47	79.7	105	AAV54310	Anti-HIV gp120 imm
5	47	79.7	105	AAV01268	VL region of HIV n
6	47	79.7	105	AAV95120	Anti-gp120 antibod
7	47	79.7	105	AAV98229	Anti-gp120 antibod
8	46	78.0	88	AAV56672	Partial peptide fr
9	46	78.0	130	AAV56737	Amino acid sequenc
10	44	74.6	11	AAE10819	Human antibody CAT

11	44	74.6	109	AAE10815	Human antibody CAT
12	44	74.6	231	AAW33610	p25gag protein clo
13	44	74.6	231	AAV77303	HIV-1 (ATCC CRL 85
14	44	74.6	232	AAV60177	Sequence encoded b
15	44	74.6	232	AAV29707	p25 gag protein fr
16	44	74.6	232	AAW33616	p25gag structural
17	44	74.6	232	AAV77310	HIV-1 (ATCC CRL 85
18	44	74.6	232	AAV98047	Synthetic HIV core
19	44	74.6	232	AAV80652	Viral protein sequ
20	44	74.6	368	AAV60178	Sequence of gag pr
21	44	74.6	368	AAV29708	p41 gag protein fr
22	44	74.6	368	AAV33611	GAG region of p41g
23	44	74.6	368	AAV77304	HIV-1 (ATCC CRL 85
24	44	74.6	494	AAV69271	HIV-1 non-subtype
25	44	74.6	497	AAV80840	Sequence deduced f
26	44	74.6	500	AAV80884	Sequence encoded b
27	44	74.6	502	AAV33108	GAG protein contai
28	44	74.6	502	AAV77294	HIV-1 (ATCC CRL 85
29	44	74.6	502	AAV77300	HIV-1 (ATCC CRL 85
30	44	74.6	506	AAV60176	Sequence of ARV-2
31	44	74.6	506	AAV29704	gag gene decoded f
32	43	72.9	11	AAV33617	Complementarily de
33	43	72.9	78	AAV33247	Novel human secret
34	43	72.9	111	AAV33628	Amino acid sequenc
35	43	72.9	299	AAV33632	Amino acid sequenc
36	43	72.9	299	AAV33637	Amino acid sequenc
37	42	71.2	9	AAV10298	T cell epitope/MHC
38	42	71.2	11	AAV23433	CDR-1 of rW12 ligh
39	42	71.2	42	AAV80686	Peptide 147 from t
40	42	71.2	108	AAV23439	Modified light cha
41	42	71.2	108	AAV23440	Modified light cha
42	42	71.2	108	AAV23436	rW12 light chain.
43	42	71.2	108	AAV23442	hW12 light chain.
44	41	69.5	10	ABP12844	HIV A02 super moti
45	41	69.5	10	ABP17875	HIV B58 super moti

ALIGNMENTS

RESULT 1
AAV78319
ID AAV78319 standard; Protein: 11 AA.
AC AAV78319;
XX 04-MAY-2000 (first entry)
XX Anti-zeta-chain antibody 2-B-5 VL-region CDR1 protein sequence.
DE
XX
XX Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
KW complementary determining region; CDR; autoimmune disease; cytostatic;
KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.
XX
XX Rattus norvegicus.
XX
XX WO200003016-A1.
XX
XX 20-JAN-2000.
XX
XX 09-JUL-1999; 99WO-EP04838.
XX
XX 10-JUL-1998; 98EP-0112867.
XX
XX (CONN-) CONNEX GMBH.
XX
XX Reiter C;
XX
XX WPI: 2000-150926/14.
XX N-PSDB: AA288317.
XX
XX New oligonucleotide, polypeptide, antibody useful for treating

PT autoimmune disease, immune deficiencies, T-cell malignancies and
 PT infectious diseases -
 XX
 PS Claim 10: Fig 7; 79pp; English.

CC The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is
 CC encoded by (I), is obtained by immunising a rat with jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,
 CC infectious diseases and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC or viral infections. The antibody, and fragments of it, can be useful for
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC treatment of NK-cell derived malignancies. It can also be useful for the
 CC determination of zeta-chain or eta-chain expression on NK-cells,
 CC T-lymphocytes or their precursors. The present sequence represents the
 CC CDR1 of the VL-region of the anti-zeta-chain antibody 2-B-5, produced
 CC by rats from the present invention.

XX Sequence 11 AA:

Query Match 100.0%; Score 59; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASODIGNWLA 11
 ID 1 QASODIGNWLA 11

RESULT 2
 AAY78326
 ID AAY78326 standard; Protein: 107 AA.

XX AAY78326;

DT 04-MAY-2000 (first entry)

DE Anti-zeta-chain antibody 2-B-5 VL-region protein sequence.

XX Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
 KW complementary determining region; CDR; autoimmune disease; cytostatic;
 KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
 KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.

OS Rattus norvegicus.

XX WO200003016-A1.

XX 20-JAN-2000.

XX 09-JUL-1999; 99WO-EP04838.

XX 10-JUL-1998; 98EP-0112867.

XX (CONN-) CONNEX GMBH.

XX Reiter C;

XX WPI: 2000-160926/14.

XX N-PSDB; AA288324.

XX New oligonucleotide, polypeptide, antibody useful for treating
 PT autoimmune disease, immune deficiencies, T-cell malignancies and
 PT infectious diseases -

PS Claim Fig 7; 79pp; English.

CC The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is
 CC encoded by (I), is obtained by immunising a rat with jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,
 CC infectious diseases and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC or viral infections. The antibody, and fragments of it, can be useful for
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC treatment of NK-cell derived malignancies. It can also be useful for the
 CC determination of zeta-chain or eta-chain expression on NK-cells,
 CC T-lymphocytes or their precursors. The present sequence represents the
 CC VL-region of the anti-zeta-chain antibody 2-B-5, produced by rats from
 CC the present invention.

XX Sequence 107 AA:

Query Match 100.0%; Score 59; DB 21; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.0053;
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASODIGNWLA 11
 ID 24 QASODIGNWLA 34

RESULT 3
 AAY78328
 ID AAY78328 standard; Protein: 532 AA.

XX AAY78328;

DT 04-MAY-2000 (first entry)

DE Bispecific anti-zeta-chain/anti-EpCAM antibody protein sequence.

XX Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
 KW complementary determining region; CDR; autoimmune disease; cytostatic;
 KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
 KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.

OS Rattus norvegicus.
 OS Synthetic.

XX WO200003016-A1.

XX 20-JAN-2000.

XX 09-JUL-1999; 99WO-EP04838.

XX 10-JUL-1998; 98EP-0112867.

XX (CONN-) CONNEX GMBH.

XX Reiter C;

XX WPI: 2000-160926/14.

XX N-PSDB; AA288358.

XX New oligonucleotide, polypeptide, antibody useful for treating
 PT autoimmune disease, immune deficiencies, T-cell malignancies and
 PT infectious diseases -

XX Example 9; Page 74-76; 79pp; English.

CC The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is

CC encoded by (1), is obtained by immunising a rat with jurkat cells and
CC subsequently with a conjugate comprising a carrier molecule and a
CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
CC anti-zeta-chain antibody is useful for the treatment and prevention of
CC autoimmune diseases, immune deficiencies, T-cell malignancies,
CC infectious diseases and the suppression of immune response preferably in
CC order to avoid graft rejection after organ transplantation, malignancies,
CC or viral infections. The antibody, and fragments of it, can be useful for
CC the enhancement or suppression of NK-cell dependent immunity or for the
CC treatment of NK-cell derived malignancies. It can also be useful for the
CC determination of zeta-chain or eta-chain expression on NK-cells,
CC T-lymphocytes or their precursors. The present sequence represents a
CC bspecific anti-zeta-chain/anti-EpCAM antibody, from an example from
CC the present invention.

SQ Sequence 532 AA;

Query Match 100.0%; Score 59; DB 21; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.029;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASODIGNWLA 11
IIIIIIIIII
DB 43 QASODIGNWLA 53

RESULT 4

AAR54310
ID AAR54310 standard; protein; 105 AA.

AC AAR54310;

DT 10-NOV-1994 (first entry)

DE Anti-HIV gp120 immunoglobulin light chain variable region b5.

KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;

KW neutralisation; monoclonal antibody; kappa light chain;

KW variable region; framework; complementarity determining region.

XX Homo sapiens.

FH Key Location/Qualifiers

FT 1..21
FT /label= FR1FT 22..33
FT /label= CDR1FT 34..48
FT /label= FR2FT 49..55
FT /label= CDR2FT 56..87
FT /label= FR3FT 88..94
FT /label= CDR3FT 95..105
FT /label= FR4

FT Region

FN WO9407922-A.

PD 14-APR-1994.

PE 30-SEP-1993; 93WO-US09328.

PR 30-SEP-1992; 92US-0954148.

PA (SCRI) SCRIPPS RES INST.

PI Barbas CF, Burton DR, Lerner RA;

DR WPI: 1994-135516/16.
XX New human monoclonal antibodies neutralising HIV - react with

PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
XX Example: Page 179-180; 248pp; English.

CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC distronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAb regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence AAR54310 is from a gp120-
CC specific clone.

SQ Sequence 105 AA;

Query Match 79.7%; Score 47; DB 15; Length 105;
Best Local Similarity 81.8%; Pred. No. 0.72;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNWLA 11
:IIIIIIIIII
DB 22 RASODIHWWLA 32

RESULT 5

AAW01268
ID AAW01268 standard; protein; 105 AA.

AC AAW01268;

DT 28-JAN-1997 (first entry)

DE VL region of HIV neutralising MAb, clone b5.

KW Heavy chain; light chain; variable region; VH; monoclonal antibody;

KW MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;

KW virus infectivity assay; precursor gp160; immunocompetence; human;

KW anti-HIV antibody; detection; HIV infection.

XX Homo sapiens.

FH Key Location/Qualifiers

FT 1..21
FT /label= FR1FT 22..32
FT /label= CDR1FT 33..47
FT /label= FR2FT 48..54
FT /label= CDR2FT 55..86
FT /label= FR3FT 87..94
FT /label= CDR3FT 95..105
FT /label= FR4

FN WO9602273-A1.

PD 01-FEB-1996.

PE 11-JUL-1995; 95WO-US08743.

PR 18-JUL-1994; 94US-0276852.

PA (SCRI) SCRIPPS RES INST.

PI Barbas CF, Burton DR, Lerner RA;

DR WPI: 1996-179601/18.
XX

PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PT passive immunotherapy and detection of HIV infection.
 XX
 PS Example; Fig 11: 366pp: English.
 CC The sequences given in AAW01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the Jk3
 CC gene clone, b5. A Mab containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50% at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The Mab
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 CC
 SO Sequence 105 AA:
 Query Match 79.7%; Score 47; DB 17; Length 105;
 Best Local Similarity 81.8%; Pred. No. 0.72;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 QASODIGNWLA 11
 :|||||
 Db 22 RASODIHNWLA 32
 RESULT 6
 AAY95120
 ID AAY95120 standard; Protein; 105 AA.
 AC AAY95120:
 DT 30-JUN-2000 (first entry)
 DE Anti-gp120 antibody light chain variable region from clone b5.
 DE
 XX
 KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody;
 XX
 OS Homo sapiens.
 XX
 PN AU9948756-A.
 PD 17-FEB-2000.
 PF 16-SEP-1999; 99AU-0048756.
 PR 16-SEP-1999; 99AU-0048756.
 PA (SCRI) SCRIPPS RES INST.
 PI Burton DR, Barbas CF, Lerner RA;
 PI
 DR WPI; 2000-293393/26.
 DR
 XX
 PT Novel human monoclonal antibodies which immunoreact with and neutralise
 PT human immunodeficiency virus useful for treating HIV infections -
 PS
 PS Example 9; Figure 11; 366pp: English.
 CC The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50% at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies

CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV.
 CC
 SO Sequence 105 AA:
 Query Match 79.7%; Score 47; DB 21; Length 105;
 Best Local Similarity 81.8%; Pred. No. 0.72;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 QASODIGNWLA 11
 :|||||
 Db 22 RASODIHNWLA 32
 RESULT 7
 AAY98229
 ID AAY98229 standard; Protein; 105 AA.
 AC AAY98229:
 DT 04-JUL-2000 (first entry)
 DE Anti-gp120 antibody light chain variable region from clone b5.
 DE
 XX
 KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX
 OS Homo sapiens.
 XX
 PN AU9948754-A.
 PD 17-FEB-2000.
 PF 16-SEP-1999; 99AU-0048754.
 PR 16-SEP-1999; 99AU-0048754.
 PA (SCRI) SCRIPPS RES INST.
 PI Burton DR, Barbas CF, Lerner RA;
 PI
 DR WPI; 2000-246867/22.
 DR
 XX
 PT Human neutralizing monoclonal antibodies to human immunodeficiency
 PT virus (HIV) used for providing passive immunotherapy to HIV are
 PT specific for glycoprotein-120 -
 PS
 PS Example 9; Figure 11; 374pp: English.
 CC This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody
 CC capable of reducing an HIV infectivity titre in an in vitro virus
 CC infectivity assay by 50% at a concentration of less than 70 ng/ml. The
 CC method for the production of the antibody comprises:
 CC (a) providing a first polynucleotide encoding a heavy chain
 CC immunoglobulin amino acid sequence (which does not comprise the sequence
 CC represented by AAY98206) and a second polynucleotide encoding a light

CC chain immunoglobulin amino acid sequence;
 CC (b) inserting the first and second polynucleotide sequences into a host
 CC cell;
 CC (c) maintaining the host cell in conditions which allow the amino acid
 CC sequences encoded by the polynucleotides to be expressed in the host
 CC cell; and
 CC (d) isolating the antibody comprising the heavy and light chain
 CC immunoglobulin amino acid sequences from the host cell.
 CC The anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used
 CC for neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting
 CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the
 CC antibodies associated with monoclonal antibodies of xenogeneic or
 CC chimeric derivation.

XX Sequence 105 AA;

Query Match 79.7%; Score 47; DB 21; Length 105;
 Best Local Similarity 81.8%; Pred. No. 0.72;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNMILA 11
 :|||||
 Db 22 RASQDINMILA 32

RESULT 8
 AAY56672
 ID AAY56672 standard; protein; 88 AA.

XX AAY56672;

DT 15-FEB-2000 (first entry)

XX Partial peptide fragment of Cynomolgus V kappa CDNA clone 4-10.

XX Complementarity determining region; antibody; primate; immunogenicity;

KM Old World ape; Old World monkey; antigen-binding affinity.

XX Macaca cynomolgus.

XX WO955369-A1.

PD 04-NOV-1999.

XX 28-APR-1999; 99WO-US09131.

XX 28-APR-1998; 98US-0083367.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Taylor AH;

XX WPI; 2000-023265/02.

DR N-PSDB; AA239340.

PT Antibodies containing donor complementarity determining regions and
 PT non-human primate acceptor frameworks, having reduced immunogenicity in
 PT humans -

XX Claim 26; Page 102; 123pp; English.

CC The invention provides an antibody (Ab) comprising donor CDRs
 CC (complementarity determining regions) derived from a non-human antigen-
 CC specific donor antibody, and an acceptor framework from a non-human
 CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
 CC specific donor antibody onto homologous Old World ape or monkey acceptor
 CC frameworks. The Abs have reduced immunogenicity and are better tolerated
 CC in humans (because of the close similarity between the human and primate
 CC proteins), but retain the full antigen-binding affinity of the donor
 CC antibody.

XX Sequence 88 AA;

Query Match 78.0%; Score 46; DB 21; Length 88;
 Best Local Similarity 81.8%; Pred. No. 0.9;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASODIGNMILA 11
 :|||||
 Db 24 QASQGISNMILA 34

RESULT 9
 AAY56737
 ID AAY56737 standard; protein; 130 AA.

XX AAY56737;

DT 15-FEB-2000 (first entry)

XX Amino acid sequence of Cynomolgus V kappa CDNA clone 4-10.

XX Complementarity determining region; antibody; primate; immunogenicity;

KM Old World ape; Old World monkey; antigen-binding affinity.

XX Macaca cynomolgus.

XX WO955369-A1.

PD 04-NOV-1999.

XX 28-APR-1999; 99WO-US09131.

XX 28-APR-1998; 98US-0083367.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Taylor AH;

XX WPI; 2000-023265/02.

DR N-PSDB; AA239340.

PT Antibodies containing donor complementarity determining regions and
 PT non-human primate acceptor frameworks, having reduced immunogenicity in
 PT humans -

XX Example 4; Page 96-97; 123pp; English.

CC The invention provides an antibody (Ab) comprising donor CDRs
 CC (complementarity determining regions) derived from a non-human antigen-
 CC specific donor antibody, and an acceptor framework from a non-human
 CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
 CC specific donor antibody onto homologous Old World ape or monkey acceptor
 CC frameworks. The Abs have reduced immunogenicity and are better tolerated
 CC in humans (because of the close similarity between the human and primate
 CC proteins), but retain the full antigen-binding affinity of the donor
 CC antibody.

XX Sequence 130 AA;

Query Match 78.0%; Score 46; DB 21; Length 130;
 Best Local Similarity 81.8%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 QASODIGNMILA 11
 DB 46 QASODISSMILA 56

RESULT 10
 AAE10819
 ID AAE10819 standard; peptide; 11 AA.

XX AAE10819;

DT 18-DEC-2001 (first entry)

DE Human antibody CAT-212 VL complementarity determining region-1 (CDR-1).

XX Human; eotaxin; CAT-212; antibody; light chain variable region; VL;
 KW eczema; asthma; atopic disease; dermatological; rhinitis; food allergy;
 KM vasculitis; conjunctivitis; allergic colitis; psoriasis; pemphigoid;
 KM eosinophil-mediated disease; cellulitis; drug eruption; vasculitis;
 KM inflammatory bowel disease; complementarity determining region-1; CDR-1;
 KM gastroenteritis.

XX Homo sapiens.

PN WO20016754-A1.

PD 13-SEP-2001.

PE 02-MAR-2001; 2001WO-GB00927.

PR 03-MAR-2000; 2000US-187246P.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Vaughan TJ, Willton AJ, Smith S;

DR WPI: 2001-589944/66.

XX Human antibodies against eotaxin useful for treating asthma, eczema and
 PT other atopic diseases, comprises an antibody variable heavy or variable
 PT light domain from CAT-212 or from complementary determining regions -

PS Claim 1; Page 102; 107pp; English.

XX The invention relates to a specific binding member which binds to human
 CC eotaxin. The binding member comprises an antibody variable heavy
 CC (VH)/variable light (VL) domain from CAT-212 VH/VL domain and a VH/VL
 CC domain comprising one or more VH/VL complementary determining regions
 CC (CDRs). Eotaxin is a chemoattractant protein that binds to a specific
 CC receptor which is expressed predominantly on eosinophils. The binding
 CC member is useful for neutralising eotaxin, which is useful in treating
 CC asthma, eczema and other atopic diseases such as rhinitis, food allergy,
 CC conjunctivitis, allergic colitis which are recognised as eosinophil-
 CC mediated diseases; for treating skin and other atopic conditions such as
 CC psoriasis, pemphigoid, wells' syndrome, cellulitis, drug eruptions;
 CC inflammatory bowel disease which includes eosinophilic colitis/enteritis/
 CC gastroenteritis/Shulman's syndrome; vasculitis including Hughes-Stovin
 CC syndrome, Churg-Strauss syndrome. The present sequence is human
 CC antibody CAT-212 light chain variable domain (VL) complementarity
 CC determining region (CDR).

XX Sequence 11 AA;

Query Match 74.6%; Score 44; DB 22; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.22; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNMILA 11
 DB 1 RASODISSMILA 11

RESULT 11

AAE10815
 ID AAE10815 standard; Protein; 109 AA.

XX AAE10815;

DT 18-DEC-2001 (first entry)

DE Human antibody CAT-212 light chain variable domain.

XX Human; eotaxin; CAT-212; antibody; light chain variable region; VL;
 KW eczema; asthma; atopic disease; dermatological; rhinitis; food allergy;
 KM vasculitis; conjunctivitis; allergic colitis; psoriasis; pemphigoid;
 KM eosinophil-mediated disease; cellulitis; drug eruption; vasculitis;
 KM inflammatory bowel disease; gastroenteritis.

XX Homo sapiens.

FN Key Location/Qualifiers

FT Misc-difference 1..2 /note="Encoded by ACATC"

PN WO20016754-A1.

PD 13-SEP-2001.

PE 02-MAR-2001; 2001WO-GB00927.

PR 03-MAR-2000; 2000US-187246P.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Vaughan TJ, Willton AJ, Smith S;

DR WPI: 2001-589944/66.

DR N-PSDB: AAD18149.

XX Human antibodies against eotaxin useful for treating asthma, eczema and
 PT other atopic diseases, comprises an antibody variable heavy or variable
 PT light domain from CAT-212 or from complementary determining regions -

PS Claim 1; Page 102; 107pp; English.

XX The invention relates to a specific binding member which binds to human
 CC eotaxin. The binding member comprises an antibody variable heavy
 CC (VH)/variable light (VL) domain from CAT-212 VH/VL domain and a VH/VL
 CC domain comprising one or more VH/VL complementary determining regions
 CC (CDRs). Eotaxin is a chemoattractant protein that binds to a specific
 CC receptor which is expressed predominantly on eosinophils. The binding
 CC member is useful for neutralising eotaxin, which is useful in treating
 CC asthma, eczema and other atopic diseases such as rhinitis, food allergy,
 CC conjunctivitis, allergic colitis which are recognised as eosinophil-
 CC mediated diseases; for treating skin and other atopic conditions such as
 CC psoriasis, pemphigoid, wells' syndrome, cellulitis, drug eruptions;
 CC inflammatory bowel disease which includes eosinophilic colitis/enteritis/
 CC gastroenteritis/Shulman's syndrome; vasculitis including Hughes-Stovin
 CC syndrome, Churg-Strauss syndrome. The present sequence is human
 CC antibody CAT-212 light chain variable domain (VL) which binds to eotaxin.

XX Sequence 109 AA;

Query Match 74.6%; Score 44; DB 22; Length 109;

Best Local Similarity 72.7%; Pred. No. 2.6; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNMILA 11
 DB 24 RASODISSMILA 34

RESULT 12

AAW33610
 ID AAW33610 standard; Protein; 231 AA.

XX

DE HIV-1 (ATCC CRL 8597) p25gag protein encoded by plasmid pGAG25-10.

XX LAV; HIV; ARV; HTLR; vaccine; AIDS; immunoassay; diagnosis;
KW Lymphadenopathy syndrome.

```

OS Human T-cell lymphotropic virus III.
XX
XX EPI81150-A.
XX
XX 14-MAY-1986.
XX
XX 30-OCT-1985; 85EP-0307860.
XX
XX 06-SEP-1985; 85US-0773447.
XX
XX 31-OCT-1984; 84US-0667501.
XX
XX 30-JAN-1985; 85US-0696534.
XX
XX (CHIR-) CHIRON CORP.
XX
XX Luciw PA, Dina D, Steimer K, Pescador RS, George-Nascimento C;
XX
XX Parkes D, Hallewell R, Barr PJ, Truett M;
XX
XX WPI: 1986-126568/20.
XX
XX N-PSDB: AAN60141.
XX
XX
XX New recombinant human T-cell lymphotropic retro virus proteins -
XX
XX useful in diagnostic immunoassays for antibodies in humans, and
XX
XX in prodn. of monoclonal antibodies, as vaccines etc.
XX
XX Disclosure: Fig 4; 67pp; English.
XX
XX
XX The inventors claim a DNA construct contg. a DNA sequence
XX
XX substantially as set forth in AAN60141, AAN60142, AAN60143, AAN60144,
XX
XX which are each derived from AIDS-associated retroviruses. For the
XX
XX purposes of this application, HTLV-III, LAV and ARV are generically
XX
XX referred to as human T-cell lymphotropic retrovirus (HTLR). The
XX
XX following recombinant polypeptides are also claimed: (a) ARV-2 p16 gag;
XX
XX (b) ARV-2 p25 gag; (c) ARV-2 env; (d) ARV-2 p31 pol.
XX
XX
XX Sequence 232 AA:
XX
XX
XX Query Match 74.6%; Score 44; DB 7; Length 232;
XX
XX Best Local Similarity 70.0%; Pred. No. 5.7;
XX
XX Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX
XX QY 1 QASODIGNWL 10
XX
XX 11111: 11
XX
XX Db 177 QASODVKNMM 186
XX
XX
XX RESULT 15
XX
XX AAR29707
XX
XX ID AAR29707 standard; Protein: 232 AA.
XX
XX
XX AAR29707;
XX
XX
XX 26-APR-1993 (first entry)
XX
XX
XX p25 gag protein from HTLR.
XX
XX
XX express proteins; lymphadenopathy syndrome; AIDS; HIV; HTLV;
XX
XX serological immunoassays; antibodies to HTLR; monoclonal antibodies;
XX
XX probes; ss.
XX
XX
XX Human T cell lymphotropic retrovirus.
XX
XX
XX EP518443-A.
XX
XX
XX 16-DEC-1992.
XX
XX
XX 30-OCT-1985; 85EP-0201711.
XX
XX
XX 31-OCT-1984; 84US-0667501.
XX
XX 30-JAN-1985; 85US-0696534.
XX
XX 06-SEP-1985; 85US-0773447.
XX
XX
XX (CHIR-) CHIRON CORP.
XX
XX

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PI Barr PJ, Dina D, George-Nascimento C, Hallewell R;
PI
PI Luciw PA, Parkes D, Pescador RS, Steimer K, Truett M;
XX
XX WPI: 1992-417329/51.
XX
XX N-PSDB: AAO31937.
XX
XX
XX Recombinant DNA construct including replication system recognised
XX
XX by unicellular microorganism - used to form recombinant proteins
XX
XX for diagnosing AIDS and lymphadenopathy syndrome
XX
XX
XX Example 9; Fig 4; 32pp; English.
XX
XX
XX This sequence was decoded from the p25 gag gene from HTLR DNA.
XX
XX Proteins associated with lymphadenopathy syndrome and/or AIDS may
XX
XX be used in serological immunoassays to detect antibodies to HTLR.
XX
XX The polypeptides can be used alone or in fusion constructs to
XX
XX produce antisera or monoclonal antibodies which may be used for
XX
XX therapy or diagnosis.
XX
XX
XX Sequence 232 AA:
XX
XX
XX
XX Query Match 74.6%; Score 44; DB 13; Length 232;
XX
XX Best Local Similarity 70.0%; Pred. No. 5.7;
XX
XX Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX
XX QY 1 QASODIGNWL 10
XX
XX 11111: 11
XX
XX Db 177 QASODVKNMM 186
XX
XX
XX Search completed: February 25, 2003, 10:32:25
XX
XX Job time : 4.63 secs

```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 2.78667 Seconds

(without alignments)
813.344 Million cell updates/sec

Title: US-09-743-482a-2

Perfect score: 59

Sequence: 1 OASQDIGNMILA 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	81.4	104	15	O99CA9	O99CA9 human immun
2	48	81.4	492	15	O99AK0	O99AK0 human immun
3	45	76.3	491	15	O90D04	O90D04 human immun
4	44	74.6	97	15	O9W0T5	O9W0T5 human immun
5	44	74.6	104	15	O99C95	O99C95 human immun
6	44	74.6	104	15	O99C97	O99C97 human immun
7	44	74.6	104	15	O99C99	O99C99 human immun
8	44	74.6	104	15	O99CA1	O99CA1 human immun
9	44	74.6	104	15	O99CA4	O99CA4 human immun
10	44	74.6	104	15	O99CA6	O99CA6 human immun
11	44	74.6	104	15	O99CB0	O99CB0 human immun
12	44	74.6	104	15	O99CB1	O99CB1 human immun
13	44	74.6	104	15	O99CB2	O99CB2 human immun
14	44	74.6	104	15	O99CB4	O99CB4 human immun
15	44	74.6	104	15	O99CB6	O99CB6 human immun
16	44	74.6	104	15	O99CB8	O99CB8 human immun

17	44	74.6	104	15	O99CB9	O99CB9 human immun
18	44	74.6	104	15	O99CC0	O99CC0 human immun
19	44	74.6	104	15	O99CC1	O99CC1 human immun
20	44	74.6	104	15	O99CC3	O99CC3 human immun
21	44	74.6	104	15	O99CC4	O99CC4 human immun
22	44	74.6	104	15	O99CC5	O99CC5 human immun
23	44	74.6	104	15	O99CC6	O99CC6 human immun
24	44	74.6	104	15	O99CC7	O99CC7 human immun
25	44	74.6	104	15	O99CC8	O99CC8 human immun
26	44	74.6	104	15	O99CC9	O99CC9 human immun
27	44	74.6	104	15	O99CC0	O99CC0 human immun
28	44	74.6	104	15	O99CC1	O99CC1 human immun
29	44	74.6	104	15	O99CC2	O99CC2 human immun
30	44	74.6	104	15	O99CC3	O99CC3 human immun
31	44	74.6	104	15	O99CC4	O99CC4 human immun
32	44	74.6	104	15	O99CC5	O99CC5 human immun
33	44	74.6	104	15	O99CC6	O99CC6 human immun
34	44	74.6	104	15	O99CC7	O99CC7 human immun
35	44	74.6	104	15	O99CC8	O99CC8 human immun
36	44	74.6	104	15	O99CC9	O99CC9 human immun
37	44	74.6	104	15	O99CC0	O99CC0 human immun
38	44	74.6	104	15	O99CC1	O99CC1 human immun
39	44	74.6	104	15	O99CC2	O99CC2 human immun
40	44	74.6	104	15	O99CC3	O99CC3 human immun
41	44	74.6	104	15	O99CC4	O99CC4 human immun
42	44	74.6	104	15	O99CC5	O99CC5 human immun
43	44	74.6	104	15	O99CC6	O99CC6 human immun
44	44	74.6	104	15	O99CC7	O99CC7 human immun
45	44	74.6	104	15	O99CC8	O99CC8 human immun

ALIGNMENTS

RESULT 1

O99CA9 PRELIMINARY; PRT; 104 AA.
ID O99CA9
AC O99CA9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GAG polypeptide [Contains: core protein(s) P24] (Fragment).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21102912; PubMed=11157057;
RA Kelleher A.D., Long C., Holmes E.C., Allen R.L., Wilson J., Conlon C.,
RA Workman C., Shanak S., Olson K., Goulder P., Brander C., Ogg G.,
RA Sullivan J.S., Dyer W., Jones I., McMichael A.J., Rowland-Jones S.,
RA Phillips R.E.;
RT "Clustered Mutations in HIV-1 gag Are Consistently Required for Escape
RT from HLA-B27-restricted cytotoxic T Lymphocyte Responses.";
RL J. Exp. Med. 193:375-386(2001).
CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
DR EMBL: AF319382; AA07390.1;
DR InterPro: IPR000721; GAG_P24.
DR Pfam: PF00607; GAG_P24; 1.
KW Core protein; Polypeptide.
FT NON_TER
FT NON_TER
SQ SEQUENCE 104 AA; 11943 MW; 658DEAA852CF448C CRC64;

Query Match 81.4%; Score 48; DB 15; Length 104;

Best Local Similarity 72.7%; Pred. NO. 0.31;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 OASQDIGNMILA 11
| | | | | : | : |
DB 63 OASQDVKNMMA 73

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RESULT 2
0994KO ID 0994KO PRELIMINARY; PRT; 492 AA.
AC 0994KO;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE GAG polypeptide [contains: core protein(s) p24].
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98IN012; PubMed=11177395;
RA MEDLINE=21094715;
RA Rodenburg C.M., Li Y., Trask S.A., Chen Y., Decker J., Robertson D.L.,
RA Kallish M.L., Shaw G.M., Allen S., Hahn B.H., Gao F.;
RT "Near full-length clones and reference sequences for subtype C
RT isolates for HIV type 1 from three different continents.";
RL AIDS Res. Hum. Retroviruses 17:161-168(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=98IN012;
RA Rodenburg C.M., Li Y., Trask S.A., Chen Y., Decker J., Robertson D.L.,
RA Allen S., Shaw G.M., Hahn B.H., Gao F.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
DR EMBL: AN286231; AAK31026.1; -
DR HSSP: P05888; 1AAF.
DR InterPro: IPR000721; Gag_P24.
DR InterPro: IPR000071; Retrovir_p17.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00540; Gag_p17; 1.
DR Pfam: PF00607; Gag_P24; 1.
DR Pfam: PF00098; Zf-CCHC; 2.
DR PRINTS: PRO0234; HIVMATRIX.
DR SMART: SM00343; ZNF_C2HC; 2.
DR AIDS: Core protein; Polypeptide.
SQ SEQUENCE 492 AA; 55054 MW; 78CCAF1A33F52FF CRC64;

Query Match 81.4%; Score 48; DB 15; Length 492;
Best Local Similarity 72.7%; Pred. No. 1.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNM1A 11
Db 306 QASODVKNMMA 316

RESULT 3
090D04 ID 090D04 PRELIMINARY; PRT; 491 AA.
AC 090D04;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE GAG polypeptide [contains: core protein(s) p24] (Fragment).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97T204;
RA MEDLINE=21395692; PubMed=11504977;
RA Hoelscher M., Kim B., Maboko L., Mhalu F., von Sonnenburg F.,
RA Birx D.L., McCutchan F.E.;
RT the UNAIDS Network for HIV Isolation Characterization;
RT "High proportion of unrelated HIV-1 intersubtype recombinants in the
RT AIDS 15:1461-1470(2001).
RL

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CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
DR EMBL: AF361874; AAK94237.1; -
DR InterPro: IPR000721; Gag_P24.
DR InterPro: IPR000071; Retrovir_p17.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00540; Gag_p17; 1.
DR Pfam: PF00607; Gag_P24; 1.
DR Pfam: PF00098; Zf-CCHC; 2.
DR AIDS: Core protein; Polypeptide.
FT NON_TER 1
SQ SEQUENCE 491 AA; 54926 MW; 4B1FF79615F67DB9 CRC64;

Query Match 76.3%; Score 45; DB 15; Length 491;
Best Local Similarity 63.6%; Pred. No. 6.3;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNM1A 11
Db 303 QATODVKNMMA 313

RESULT 4
09WJT5 ID 09WJT5 PRELIMINARY; PRT; 97 AA.
AC 09WJT5;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE GAG polypeptide [contains: core protein(s) p24] (Fragment).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TW382;
RA Chang K.S.S., Lin C.-I., Salminen M.O., Liao S.-K., Wu A.M.,
RA Lin H.-C., Lin R.-Y., Tzu S.-C.;
RT "HIV type 1 env gene diversity detected in Taiwan.";
RT Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
DR EMBL: U73086; AAD0201.1; -
DR InterPro: IPR000721; Gag_P24.
DR Pfam: PF00607; Gag_P24; 1.
DR Core protein; Polypeptide.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 97 AA; 11276 MW; EDDDB0B92C69E5EF1 CRC64;

Query Match 74.6%; Score 44; DB 15; Length 97;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNM1A 10
Db 66 QASODVKNMMA 75

RESULT 5
099C95 ID 099C95 PRELIMINARY; PRT; 104 AA.
AC 099C95;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE GAG polypeptide [contains: core protein(s) p24] (Fragment).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21102912; PubMed=11157057;

```

RA Kelleher A.D., Long C., Holmes E.C., Allen R.L., Wilson J., Conlon C.,
 RA Workman C., Shaunak S., Olson K., Goulder P., Brander C., Ogg G.,
 RA Sullivan J.S., Dyer W., Jones I., McMichael A.J., Rowland-Jones S.,
 RA Phillips R.E.;
 RT "Clustered Mutations in HIV-1 gag Are Consistently Required for Escape
 from HLA-B27-restricted Cytotoxic T Lymphocyte Responses.";
 RL J. Exp. Med. 193:375-386(2001).
 CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
 DR EMBL: AF319396; AAK07404.1; -.
 DR HSSP: P03351; IEIA.
 DR InterPro: IPR000721; Gag_p24.
 DR Pfam: PF00607; Gag_p24; 1.
 KW Core protein; Polyprotein.
 FT NON_TER 1 104
 FT NON_TER 1 104
 SQ SEQUENCE 104 AA; 11957 MW; 92CA581152DE1DF CRC64;

Query Match
 Best Local Similarity 74.6%; Score 44; DB 15; Length 104;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNML 10
 |||||: ||:
 DB 63 QASQDVKNMM 72

RESULT 6
 Q99C97 PRELIMINARY; PRT; 104 AA.
 AC 099C97;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Gag polyprotein [contains: core protein(s) p24] (Fragment).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21102912; PubMed=11157057;
 RA Kelleher A.D., Long C., Holmes E.C., Allen R.L., Wilson J., Conlon C.,
 RA Workman C., Shaunak S., Olson K., Goulder P., Brander C., Ogg G.,
 RA Sullivan J.S., Dyer W., Jones I., McMichael A.J., Rowland-Jones S.,
 RA Phillips R.E.;
 RT "Clustered Mutations in HIV-1 gag Are Consistently Required for Escape
 from HLA-B27-restricted Cytotoxic T Lymphocyte Responses.";
 RL J. Exp. Med. 193:375-386(2001).
 CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
 DR EMBL: AF319394; AAK07402.1; -.
 DR HSSP: P03351; IEIA.
 DR InterPro: IPR000721; Gag_p24.
 DR Pfam: PF00607; Gag_p24; 1.
 KW Core protein; Polyprotein.
 FT NON_TER 1 104
 FT NON_TER 1 104
 SQ SEQUENCE 104 AA; 11973 MW; 13569AA852CF4498 CRC64;

Query Match
 Best Local Similarity 74.6%; Score 44; DB 15; Length 104;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNML 10
 |||||: ||:
 DB 63 QASQDVKNMM 72

RESULT 7
 Q99C99 PRELIMINARY; PRT; 104 AA.
 AC 099C99;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Gag polyprotein [contains: core protein(s) p24] (Fragment).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21102912; PubMed=11157057;
 RA Kelleher A.D., Long C., Holmes E.C., Allen R.L., Wilson J., Conlon C.,
 RA Workman C., Shaunak S., Olson K., Goulder P., Brander C., Ogg G.,
 RA Sullivan J.S., Dyer W., Jones I., McMichael A.J., Rowland-Jones S.,
 RA Phillips R.E.;
 RT "Clustered Mutations in HIV-1 gag Are Consistently Required for Escape
 from HLA-B27-restricted Cytotoxic T Lymphocyte Responses.";
 RL J. Exp. Med. 193:375-386(2001).
 CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
 DR EMBL: AF319390; AAK07398.1; -.
 DR HSSP: P03351; IEIA.
 DR InterPro: IPR000721; Gag_p24.
 DR Pfam: PF00607; Gag_p24; 1.
 KW Core protein; Polyprotein.
 FT NON_TER 1 104
 FT NON_TER 1 104
 SQ SEQUENCE 104 AA; 11973 MW; 13569AA852CF4498 CRC64;

Query Match
 Best Local Similarity 74.6%; Score 44; DB 15; Length 104;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNML 10
 |||||: ||:
 DB 63 QASQDVKNMM 72

RESULT 8
 Q99C97 PRELIMINARY; PRT; 104 AA.
 AC 099C97;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Gag polyprotein [contains: core protein(s) p24] (Fragment).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21102912; PubMed=11157057;
 RA Kelleher A.D., Long C., Holmes E.C., Allen R.L., Wilson J., Conlon C.,
 RA Workman C., Shaunak S., Olson K., Goulder P., Brander C., Ogg G.,
 RA Sullivan J.S., Dyer W., Jones I., McMichael A.J., Rowland-Jones S.,
 RA Phillips R.E.;
 RT "Clustered Mutations in HIV-1 gag Are Consistently Required for Escape
 from HLA-B27-restricted Cytotoxic T Lymphocyte Responses.";
 RL J. Exp. Med. 193:375-386(2001).
 CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
 DR EMBL: AF319390; AAK07398.1; -.
 DR HSSP: P03351; IEIA.
 DR InterPro: IPR000721; Gag_p24.
 DR Pfam: PF00607; Gag_p24; 1.
 KW Core protein; Polyprotein.
 FT NON_TER 1 104
 FT NON_TER 1 104
 SQ SEQUENCE 104 AA; 11973 MW; 13569AA852CF4498 CRC64;

Query Match
 Best Local Similarity 74.6%; Score 44; DB 15; Length 104;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNML 10
 |||||: ||:
 DB 63 QASQDVKNMM 72

Db 63 QASODVKNMM 72

RESULT 9

Q99CA4

PRELIMINARY: PRT: 104 AA.

AC Q99CA4:

01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE GAG polyprotein [Contains: core protein(s) p24] (Fragment).

GN GAG.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21102912; PubMed=11157057;

RA Kelleher A.D., Long C., Holmes E.C., Allen R.L., Wilson J., Conlon C.,

RA Workman C., Shaunak S., Olson K., Goulder P., Brander C., Ogg G.,

RA Sullivan J.S., Dyer W., Jones I., McMichael A.J., Rowland-Jones S.,

RA Phillips R.E.;

RT "Clustered Mutations in HIV-1 gag Are Consistently Required for Escape

from HLA-B27-restricted Cytotoxic T Lymphocyte Responses.";

RL J. Exp. Med. 193:375-386(2001).

CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).

DR EMBL: AF319387; AAK07395.1; -.

DR HSP: P03351; IEIA.

DR InterPro: IPR000721; Gag_p24.

DR Pfam: PF00607; Gag_p24; 1.

KW Core protein; Polyprotein.

FT NON_TER 1 1

FT NON_TER 104 104

SQ SEQUENCE 104 AA: 11945 MW: 92DF822152DDEIDF CRC64;

Query Match 74.6%; Score 44; DB 15; Length 104;

Best Local Similarity 70.0%; Pred. No. 1.7;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNWL 10

11111: 11:

Db 63 QASODVKNMM 72

RESULT 10

Q99CA6

PRELIMINARY: PRT: 104 AA.

AC Q99CA6:

01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE GAG polyprotein [Contains: core protein(s) p24] (Fragment).

GN GAG.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21102912; PubMed=11157057;

RA Kelleher A.D., Long C., Holmes E.C., Allen R.L., Wilson J., Conlon C.,

RA Workman C., Shaunak S., Olson K., Goulder P., Brander C., Ogg G.,

RA Sullivan J.S., Dyer W., Jones I., McMichael A.J., Rowland-Jones S.,

RA Phillips R.E.;

RT "Clustered Mutations in HIV-1 gag Are Consistently Required for Escape

from HLA-B27-restricted Cytotoxic T Lymphocyte Responses.";

RL J. Exp. Med. 193:375-386(2001).

CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).

DR EMBL: AF319385; AAK07393.1; -.

DR HSP: P03351; IEIA.

DR InterPro: IPR000721; Gag_p24.

DR Pfam: PF00607; Gag_p24; 1.

KW Core protein; Polyprotein.

FT NON_TER 1 1

FT NON_TER 104 104

SQ SEQUENCE 104 AA: 11945 MW: 92DF822152DDEIDF CRC64;

Query Match 74.6%; Score 44; DB 15; Length 104;

Best Local Similarity 70.0%; Pred. No. 1.7;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNWL 10

11111: 11:

Db 63 QASODVKNMM 72

FT NON_TER 104 104

SQ SEQUENCE 104 AA: 11945 MW: 92DF822152DDEIDF CRC64;

Query Match 74.6%; Score 44; DB 15; Length 104;

Best Local Similarity 70.0%; Pred. No. 1.7;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNWL 10

11111: 11:

Db 63 QASODVKNMM 72

RESULT 11

Q99CB0

PRELIMINARY: PRT: 104 AA.

AC Q99CB0:

01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE GAG polyprotein [Contains: core protein(s) p24] (Fragment).

GN GAG.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21102912; PubMed=11157057;

RA Kelleher A.D., Long C., Holmes E.C., Allen R.L., Wilson J., Conlon C.,

RA Workman C., Shaunak S., Olson K., Goulder P., Brander C., Ogg G.,

RA Sullivan J.S., Dyer W., Jones I., McMichael A.J., Rowland-Jones S.,

RA Phillips R.E.;

RT "Clustered Mutations in HIV-1 gag Are Consistently Required for Escape

from HLA-B27-restricted Cytotoxic T Lymphocyte Responses.";

RL J. Exp. Med. 193:375-386(2001).

CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).

DR EMBL: AF319381; AAK07389.1; -.

DR HSP: P03351; IEIA.

DR InterPro: IPR000721; Gag_p24.

DR Pfam: PF00607; Gag_p24; 1.

KW Core protein; Polyprotein.

FT NON_TER 1 1

FT NON_TER 104 104

SQ SEQUENCE 104 AA: 11945 MW: 92DF822152DDEIDF CRC64;

Query Match 74.6%; Score 44; DB 15; Length 104;

Best Local Similarity 70.0%; Pred. No. 1.7;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNWL 10

11111: 11:

Db 63 QASODVKNMM 72

RESULT 12

Q99CB1

PRELIMINARY: PRT: 104 AA.

AC Q99CB1:

01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE GAG polyprotein [Contains: core protein(s) p24] (Fragment).

GN GAG.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21102912; PubMed=11157057;

RA Kelleher A.D., Long C., Holmes E.C., Allen R.L., Wilson J., Conlon C.,

RA Workman C., Shaunak S., Olson K., Goulder P., Brander C., Ogg G.,

RA Sullivan J.S., Dyer W., Jones I., McMichael A.J., Rowland-Jones S.,

RA Phillips R.E.;

RT "Clustered Mutations in HIV-1 gag Are Consistently Required for Escape

RT from HLA-B27-restricted cytotoxic T lymphocyte Responses."
 RL J. Exp. Med. 193:375-386(2001).
 CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
 DR EMBL: AF319380; AAK07388.1; -
 DR HSSP: P03351; IEIA.
 DR InterPro: IPR000721; Gag_p24.
 DR Pfam: PF00607; Gag_p24; 1.
 KW Core protein; Polyprotein.
 FT NON_TER 1
 FT NON_TER 104
 SQ SEQUENCE 104 AA; 11955 MW; 135740032315EF8 CRC64;
 Query Match 74.6%; Score 44; DB 15; Length 104;
 Best Local Similarity 70.0%; Pred. No. 1.7;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 13

ID 099CB2 PRELIMINARY; PRT; 104 AA.
 AC 099CB2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE GAG polyprotein [contains: core protein(s) p24] (Fragment).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21102912; PubMed=11157057;
 RA Kelleher A.D., Long C., Holmes E.C., Allen R.L., Wilson J., Conlon C.,
 RA Workman C., Shaunak S., Olson K., Goulder P., Brander C., Ogg G.,
 RA Sullivan J.S., Dyer W., Jones I., McMichael A.J., Rowland-Jones S.,
 RA Phillips R.E.;
 RT "Clustered Mutations in HIV-1 gag Are Consistently Required for Escape
 RT from HLA-B27-restricted cytotoxic T lymphocyte Responses.";
 RL J. Exp. Med. 193:375-386(2001).
 CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
 DR EMBL: AF319379; AAK07387.1; -
 DR HSSP: P03351; IEIA.
 DR InterPro: IPR000721; Gag_p24.
 DR Pfam: PF00607; Gag_p24; 1.
 KW Core protein; Polyprotein.
 FT NON_TER 1
 FT NON_TER 104
 SQ SEQUENCE 104 AA; 11973 MW; 13569AA852CF4498 CRC64;

Query Match 74.6%; Score 44; DB 15; Length 104;
 Best Local Similarity 70.0%; Pred. No. 1.7;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNWL 10
 Db 63 QASODVKNM 72

RESULT 14

ID 099CB4 PRELIMINARY; PRT; 104 AA.
 AC 099CB4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE GAG polyprotein [contains: core protein(s) p24] (Fragment).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21102912; PubMed=11157057;
 RA Kelleher A.D., Long C., Holmes E.C., Allen R.L., Wilson J., Conlon C.,
 RA Workman C., Shaunak S., Olson K., Goulder P., Brander C., Ogg G.,
 RA Sullivan J.S., Dyer W., Jones I., McMichael A.J., Rowland-Jones S.,
 RA Phillips R.E.;
 RT "Clustered Mutations in HIV-1 gag Are Consistently Required for Escape
 RT from HLA-B27-restricted cytotoxic T lymphocyte Responses.";
 RL J. Exp. Med. 193:375-386(2001).
 CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
 DR EMBL: AF319377; AAK07385.1; -
 DR HSSP: P03351; IEIA.
 DR InterPro: IPR000721; Gag_p24.
 DR Pfam: PF00607; Gag_p24; 1.
 KW Core protein; Polyprotein.
 FT NON_TER 1
 FT NON_TER 104
 SQ SEQUENCE 104 AA; 11945 MW; 2BD34DCB733C0BF8 CRC64;

Query Match 74.6%; Score 44; DB 15; Length 104;
 Best Local Similarity 70.0%; Pred. No. 1.7;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNWL 10
 Db 63 QASODVKNM 72

RESULT 15

ID 099CB6 PRELIMINARY; PRT; 104 AA.
 AC 099CB6;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE GAG polyprotein [contains: core protein(s) p24] (Fragment).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21102912; PubMed=11157057;
 RA Kelleher A.D., Long C., Holmes E.C., Allen R.L., Wilson J., Conlon C.,
 RA Workman C., Shaunak S., Olson K., Goulder P., Brander C., Ogg G.,
 RA Sullivan J.S., Dyer W., Jones I., McMichael A.J., Rowland-Jones S.,
 RA Phillips R.E.;
 RT "Clustered Mutations in HIV-1 gag Are Consistently Required for Escape
 RT from HLA-B27-restricted cytotoxic T lymphocyte Responses.";
 RL J. Exp. Med. 193:375-386(2001).
 CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
 DR EMBL: AF319375; AAK07383.1; -
 DR HSSP: P03351; IEIA.
 DR InterPro: IPR000721; Gag_p24.
 DR Pfam: PF00607; Gag_p24; 1.
 KW Core protein; Polyprotein.
 FT NON_TER 1
 FT NON_TER 104
 SQ SEQUENCE 104 AA; 11973 MW; 13569AA852CF4498 CRC64;

Query Match 74.6%; Score 44; DB 15; Length 104;
 Best Local Similarity 70.0%; Pred. No. 1.7;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNWL 10
 Db 63 QASODVKNM 72

Search completed: February 25, 2003, 10:36:25
 Job time : 3.78667 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 : Search time 0.971667 Seconds
(without alignments)
469.543 Million cell updates/sec

Title: US-09-743-482A-2
Perfect score: 59
Sequence: 1 QASQDIGNWLA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	44	74.6	92 1 KV09_RABIT	P01690 oryctolagus
2	44	74.6	108 1 KVIS_HUMAN	P01611 homo sapien
3	44	74.6	496 1 GAG_HV1ND	P18800 human immun
4	44	74.6	498 1 GAG_HV10Y	P20889 human immun
5	44	74.6	499 1 GAG_HV1EL	P04592 human immun
6	44	74.6	500 1 GAG_HV1RH	P05890 human immun
7	44	74.6	501 1 GAG_HV1A2	P03349 human immun
8	42	71.2	109 1 KV03_RABIT	P01684 oryctolagus
9	41	69.3	492 1 GAG_HV1U4	P24736 human immun
10	40	67.8	499 1 GAG_HV1H2	P05887 human immun
11	40	67.8	499 1 GAG_HV1H2	P04591 human immun
12	40	67.8	499 1 GAG_HV1J3	P12494 human immun
13	40	67.8	499 1 GAG_HV1LW	O70622 human immun
14	40	67.8	499 1 GAG_HV1N5	P14493 human immun
15	40	67.8	499 1 GAG_HV1Y2	P33962 human immun
16	40	67.8	506 1 GAG_HV1M1	P05888 human immun
17	40	67.8	508 1 GAG_HV1C2	P17282 chimpanzee
18	40	67.8	511 1 GAG_HV1B1	P03347 human immun
19	40	67.8	511 1 GAG_HV1B5	P04593 human immun
20	40	67.8	511 1 GAG_HV1BR	P03348 human immun
21	40	67.8	511 1 GAG_HV1PV	P03350 human immun
22	39.5	66.9	130 1 KVIS_MOUSE	P01639 mus musculu
23	39	66.1	107 1 KVIS_HUMAN	P01596 homo sapien
24	39	66.1	246 1 YNUO_YEAST	P40165 saccharomyc
25	39	66.1	360 1 MANB_BACSU	P55278 bacillus su
26	39	66.1	396 1 NIDL_RHIME	P56907 rhizobium m
27	39	66.1	513 1 GAG_STVAL	O02843 simian immu
28	39	66.1	1926 1 LPH_RABIT	P09849 oryctolagus
29	39	66.1	1927 1 LPH_HUMAN	P09848 homo sapien
30	39	66.1	1928 1 LPH_RAT	O02401 rattus norv
31	38	64.4	117 1 KVIS_HUMAN	P01562 homo sapien
32	37	62.7	108 1 KVIS_HUMAN	P01598 homo sapien
33	37	62.7	140 1 GSPG_KLEBN	P15746 klebsiella

34	37	62.7	388 1	GAG_HV1W2	P05889 human immun
35	37	62.7	503 1	GAG_HV1JR	P20873 human immun
36	37	62.7	504 1	GAG_HV1MA	P04594 human immun
37	37	62.7	578 1	VIPC_SALTI	O04975 salmonella
38	37	62.7	613 1	UBID_VIBCH	O9K448 vibrio chol
39	37	62.7	926 1	CHS2_SCHPO	O74756 schizosacch
40	36	61.0	108 1	KV5K_MOUSE	P01644 mus musculu
41	36	61.0	108 1	KV5L_MOUSE	P01645 mus musculu
42	36	61.0	108 1	KV5M_MOUSE	P01646 mus musculu
43	36	61.0	108 1	KV5N_MOUSE	P01647 mus musculu
44	36	61.0	108 1	KV5O_MOUSE	P01648 mus musculu
45	36	61.0	111 1	KV12_RABIT	P01693 oryctolagus

ALIGNMENTS

RESULT 1					
ID	Sequence	STANDARD	PRT	92 AA	
AC	KV09_RABIT				
AC	P01690:				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V region 3381 (Fragment).				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX	NCBI_TaxID=9986;				
RN	(1)				
RP	SEQUENCE.				
RX	MEDLINE=75176905; PubMed=1094456;				
RA	Marcolini M.N., Cannon L.E. III, Strosberg A.D., Haber E.;				
RT	"Diversity of light chain variable region sequences among rabbit				
RT	antibodies elicited by the same antigens."				
RC	Proc. Natl. Acad. Sci. U.S.A. 72:2180-2184(1975).				
CC	-I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III				
CC	PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.				
CC	PIR: A01953; KVRB38.				
DR	HSSP: P01607; 1RET.				
DR	InterPro: IPR003006; Ig_MHC.				
DR	InterPro: IPR003596; Ig_V.				
DR	Pfam: PF00047; 1g; 1.				
DR	SMART: SM00406; 1GV; 1.				
KW	Immunoglobulin V region.				
FT	DOMAIN 1 23				FRAMEWORK-1.
FT	DOMAIN 24 34				COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 35 49				FRAMEWORK-2.
FT	DOMAIN 50 56				COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 57 88				FRAMEWORK-3.
FT	DOMAIN 89 >92				COMPLEMENTARITY-DETERMINING-3.
FT	NON_TER 92 92				
SQ	SEQUENCE 92 AA; 9730 MW; 9A36B15913C3BEE CXC64;				
Query Match					
	Best Local Similarity	74.6%;	Score 44;	DB 1;	Length 92;
	Matches 8; Conservative		Pred. No. 0.23;		
			1; Mismatches	2; Indels	0; Gaps
Oy	1 QASQDIGNWLA 11				
Db	24 QASESISNMLA 34				
RESULT 2					
KVIS_HUMAN					
ID	KVIS_HUMAN	STANDARD	PRT	108 AA	
AC	P01611:				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-I region Wes.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				

```
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolyzate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclinal L-chain of k-type, subgroup I (Bence-Jones Protein
RT Mes).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR: A01877; KIHUWS.
DR HSSP: P80362; IWT.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KM Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 49 FRAMEWORK-2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 57 FRAMEWORK-3.
FT DOMAIN 6 88 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 97 FRAMEWORK-4.
FT DOMAIN 8 107 COMPLEMENTARITY-DETERMINING-4.
FT DISULFID 23 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 74.6%; Score 44; DB 1; Length 108;
Best Local Similarity 72.7%; Pred. No. 0.27;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNML 11
DB 24 RASODISHMLA 34

RESULT 3
GAG_HVIND STANDARD; PRT; 496 AA.
ID GAG_HVIND
AC P18800;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE GAG polypeptide [Contains: Core proteins p17, p24, p7, p1, p6].
GN GAG.
OS Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11695;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90034200; PubMed=2806917;
RA Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F.,
RA Hampe A., Chermann J.C.;
RT "Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the
RT human immunodeficiency virus.";
RL Gene 81:275-284(1989).
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- P17: THE P24 PROTEIN IS PHOSPHORYLATED.
CC -1- MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH
CC AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M27323; AAA44868.1;
DR PIR: J00065; FOLJND.
DR HSSP: P05888; IAAF.
DR HIV: M27323; GAGSNDK.
DR InterPro: IPR000721; Gag_P24.
DR InterPro: IPR000071; Retrovir_P17.
DR InterPro: IPR01878; ZnF_CCHC.
DR Pfam: PF00098; zf-CCHC; 2.
DR Pfam: PF00540; Gag_P17; 1.
DR Pfam: PF00607; Gag_P24; 1.
DR PRINTS: PR00939; C2HCZNFINGER.
DR PRINTS: PR00234; HIVMTRIX.
DR SMART: SM00343; ZnF_C2HC; 2.
DR PROSITE: PS0158; ZF_CCHC; 2.
KM AIDS: Core protein; Polypeptide; Myristate; Phosphorylation;
KM Zinc-finger; Repeat.
FT INIT_MET 0 BY SIMILARITY.
FT CHAIN 1 128 CORE PROTEIN P17 (MATRIX PROTEIN).
FT CHAIN 129 359 CORE PROTEIN P24 (CORE ANTIGEN).
FT CHAIN 360 374 CORE PROTEIN P2.
FT CHAIN 375 429 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
FT CHAIN 430 445 CORE PROTEIN P1.
FT CHAIN 446 496 CORE PROTEIN P6.
FT ZN_FING 387 404 CCHC-TYPE 1.
FT ZN_FING 408 425 CCHC-TYPE 2.
FT LIPID 1 MYRISTATE (BY SIMILARITY).
SQ SEQUENCE 496 AA; 55152 MW; F50A42E42CCE20AA CRC64;

Query Match 74.6%; Score 44; DB 1; Length 496;
Best Local Similarity 70.0%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNML 10
DB 304 QASODVKNMM 313

RESULT 4
GAG_HVIOY STANDARD; PRT; 498 AA.
ID GAG_HVIOY
AC P20889;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE GAG polypeptide [Contains: Core proteins p17, p24, p7, p1, p6].
GN GAG.
OS Human immunodeficiency virus type 1 (OY isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11699;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90148544; PubMed=2559749;
RA Hueb T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Main-Hobson S.;
RT "A highly defective HIV-1 strain isolated from a healthy Gabonese
RT individual presenting an atypical western blot.";
RL AIDS 3:707-715(1989).
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- P17: THE P24 PROTEIN IS PHOSPHORYLATED.
CC -1- MISCELLANEOUS: THE OY1 ISOLATE WAS TAKEN FROM THE BLOOD OF A
CC HEALTHY GABONESE INDIVIDUAL.
```

CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
 CC -----
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 CC -----
 CC EMBL: M26727; AAA83391.1; -
 CC HSSP: P05888; 1AAR.
 CC HIV: M26727; GAGSOY1.
 CC InterPro: IPR000721; Gag_P24.
 CC InterPro: IPR000071; Retrovir_p17.
 CC InterPro: IPR001878; Znf_CCHC.
 CC Pfam: PF00098; zf_CCHC; 2.
 CC Pfam: PF00540; Gag_P17; 1.
 CC Pfam: PF00607; Gag_P24; 1.
 CC PRINTS: PR00939; C2HC2NFINGER.
 CC PRINTS: PR00234; HIVMATRIX.
 CC SMART: SM00343; Znf_C2HC; 2.
 CC PROSITE: PS50158; ZF_CCHC; 2.
 CC AIDS: Core protein; Polyprotein; Myristate; Phosphorylation;
 CC Zinc-finger; Repeat.
 CC INIT_MET 0
 CC CHAIN 1 131 BY SIMILARITY.
 CC CHAIN 132 362 CORE PROTEIN P17 (MATRIX PROTEIN).
 CC CHAIN 363 376 CORE PROTEIN P24 (CORE ANTIGEN).
 CC CHAIN 377 430 CORE PROTEIN P2.
 CC CHAIN 431 446 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
 CC CHAIN 447 498 CORE PROTEIN P1.
 CC ZN_FING 388 405 CORE PROTEIN P6.
 CC ZN_FING 409 426 CCHC-TYPE 1.
 CC LIPID 1 1 MYRISTATE (BY SIMILARITY).
 CC SEQUENCE 498 AA; 55451 MW; BDFE20658DEB2081 CRC64;
 SQ
 Query Match 74.6%; Score 44; DB 1; Length 498;
 Best Local Similarity 70.0%; Pred. No. 1.3;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASODIGNML 10
 Db 307 QASODVKNMW 316
 RESULT 5
 GAG_HV1EL STANDARD; PRT; 499 AA.
 ID GAG_HV1EL
 AC P04592;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE GAG polyprotein [contains: Core proteins p17, p24, p2, p7, p1, p6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
 OC Viruses; Retrovirdae; Lentivirus.
 OX NCBI_TaxID=11689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86245056; PubMed=2424612;
 RA Alizon M., Main-Hobson S., Montagnier L., Sonigo P.;
 RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
 RT of two isolates from African patients.";
 RL Cell 46:63-74(1986).
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
 CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
 CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
 CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
 CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
 CC -1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
 CC -----
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 CC -----
 CC EMBL: K03454; AAA44324.1; -
 CC EMBL: A07108; CA00611.1; -
 CC HSSP: P05888; 1AAR.
 CC HIV: K03454; GAGSEL1.
 CC InterPro: IPR000721; Gag_P24.
 CC InterPro: IPR000071; Retrovir_p17.
 CC InterPro: IPR001878; Znf_CCHC.
 CC Pfam: PF00098; zf_CCHC; 2.
 CC Pfam: PF00540; Gag_P17; 1.
 CC Pfam: PF00607; Gag_P24; 1.
 CC PRINTS: PR00939; C2HC2NFINGER.
 CC PRINTS: PR00234; HIVMATRIX.
 CC SMART: SM00343; Znf_C2HC; 2.
 CC PROSITE: PS50158; ZF_CCHC; 2.
 CC AIDS: Core protein; Polyprotein; Myristate; Phosphorylation;
 CC Zinc-finger; Repeat.
 CC INIT_MET 0
 CC CHAIN 1 131 BY SIMILARITY.
 CC CHAIN 132 362 CORE PROTEIN P17 (MATRIX PROTEIN).
 CC CHAIN 363 377 CORE PROTEIN P24 (CORE ANTIGEN).
 CC CHAIN 378 431 CORE PROTEIN P2.
 CC CHAIN 432 447 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
 CC CHAIN 448 499 CORE PROTEIN P1.
 CC ZN_FING 390 407 CORE PROTEIN P6.
 CC ZN_FING 411 428 CCHC-TYPE 1.
 CC LIPID 1 1 MYRISTATE (BY SIMILARITY).
 CC SEQUENCE 499 AA; 55582 MW; 8A1785A59EAE08D CRC64;
 SQ
 Query Match 74.6%; Score 44; DB 1; Length 499;
 Best Local Similarity 70.0%; Pred. No. 1.3;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASODIGNML 10
 Db 307 QASODVKNMW 316
 RESULT 6
 GAG_HV1RH STANDARD; PRT; 500 AA.
 ID GAG_HV1RH
 AC P05890;
 DT 01-NOV-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE GAG polyprotein [contains: Core proteins p17, p24, p2, p7, p1, p6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
 OC Viruses; Retrovirdae; Lentivirus.
 OX NCBI_TaxID=11701;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,
 RA Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
 RA Wong-Staal F.;
 RL Submitted (XXY-1987) to the HIV data bank.
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
 CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
 CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
 CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
 CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
 CC -1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M17451; AAA5052.1; -
CC HSSP: P05888; IAAF.
CC HIV: M17451; GAGSRF.
DR InterPro: IPR000721; Gag_p24.
DR InterPro: IPR000071; Retrovir_p17.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF000098; zf-CCHC; 2.
DR Pfam: PF00540; Gag_p17; 1.
DR Pfam: PF00607; Gag_p24; 1.
DR PRINTS: PR00939; C2HCZNFINGER.
DR PRINTS: PR00234; HIVMATRIX.
DR SMART: SM00343; ZNF_C2HC; 2.
DR PROSITE: PS0158; ZF_CCHC; 2.
KW AIDS: Core protein; Polyprotein; Myristate; Phosphorylation;
KW Zinc-finger; Repeat.
FT INIT_MET 0 BY SIMILARITY.
FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
FT CHAIN 363 376 CORE PROTEIN P2.
FT CHAIN 377 433 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
FT CHAIN 434 449 CORE PROTEIN P1.
FT CHAIN 450 500 CORE PROTEIN P6.
FT ZN_FING 389 406 CORE PROTEIN P1.
FT ZN_FING 410 427 CCHC-TYPE 2.
FT LIPID 1 MYRISTATE (BY SIMILARITY).
SQ SEQUENCE 500 AA: 55825 MW: 44AA0CB5CDAEF7B CRC64;
Query Match 74.6%; Score 44; DB 1; Length 500;
Best Local Similarity 70.0%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 QASODIGNWL 10
Db 309 QASQDVKNWM 316
RESULT 7
GAG_HV1A2 STANDARD: PRT; 501 AA.
ID GAG_HV1A2
AC P03349;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Gag polyprotein [Contains: Core proteins P17, P24, P2, P7, P1, P6].
GN Gag.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11685;
RN [1]
RP MEDLINE=85090453; PubMed=2578227;
RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
RA Stempien M.W., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
RA Levy J.A., Dina D., Luciw P.A.;
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
RT (ARV-2)."
RL Science 227:484-492(1985).
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FORM DURING VIRAL ASSEMBLY TO SELECTIVELY

CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- P17: THE P24 PROTEIN IS PHOSPHORYLATED.
CC
CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
CC
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CC
CC EMBL: K02007; AAB59875.1; -
CC PIR: A03947; FOVWA2.
CC HSSP: P05888; IAAF.
DR HIV: K02007; GAGSSF2.
DR InterPro: IPR000721; Gag_p24.
DR InterPro: IPR000071; Retrovir_p17.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF000098; zf-CCHC; 2.
DR Pfam: PF00540; Gag_p17; 1.
DR Pfam: PF00607; Gag_p24; 1.
DR PRINTS: PR00939; C2HCZNFINGER.
DR PRINTS: PR00234; HIVMATRIX.
DR SMART: SM00343; ZNF_C2HC; 2.
DR PROSITE: PS0158; ZF_CCHC; 2.
KW AIDS: Core protein; Polyprotein; Myristate; Phosphorylation;
KW Zinc-finger; Repeat.
FT INIT_MET 0 BY SIMILARITY.
FT CHAIN 1 133 CORE PROTEIN P17 (MATRIX PROTEIN).
FT CHAIN 134 364 CORE PROTEIN P24 (CORE ANTIGEN).
FT CHAIN 365 378 CORE PROTEIN P2.
FT CHAIN 379 433 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
FT CHAIN 434 449 CORE PROTEIN P1.
FT CHAIN 450 501 CORE PROTEIN P6.
FT ZN_FING 391 408 CORE PROTEIN P1.
FT ZN_FING 412 429 CCHC-TYPE 2.
FT LIPID 1 MYRISTATE (BY SIMILARITY).
SQ SEQUENCE 501 AA: 55935 MW: 8F36C928D5EBDA5 CRC64;
Query Match 74.6%; Score 44; DB 1; Length 501;
Best Local Similarity 70.0%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 QASODIGNWL 10
Db 309 QASQDVKNWM 318
RESULT 8
KV03_RABIT STANDARD: PRT; 109 AA.
ID KV03_RABIT
AC P01684;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region 3374.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP MEDLINE=75176905; PubMed=1094456;
RA Mariolles M.N., Cannon L.E., Haber E.;
RT "Diversity of light chain variable region sequences among rabbit
RT antibodies elicited by the same antigens."
RL Proc. Natl. Acad. Sci. U.S.A. 72:2180-2184(1975).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III
CC PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.
DR PIR: A01947; KVRB37.
DR HSSP: P80362; IMTL.
DR InterPro: IPR003006; Ig_MHC.

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DR InterPro: IPR003596; 19-V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; IGV: 1.
KW Immunoglobulin V region.
FT DOMAIN 1
FT 25 24 FRAMEWORK-1.
FT 35 35 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 2
FT 36 50 FRAMEWORK-2.
FT 51 57 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 3
FT 58 89 FRAMEWORK-3.
FT 90 98 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 4
FT 99 108 FRAMEWORK-4.
FT NON_TER
FT 109 109
SQ SEQUENCE 109 AA: E79294813E118AF CRC64;
Query Match 71.2%; Score 42; DB 1; Length 109;
Best Local Similarity 72.7%; Pred. No. 0.64;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 QASODIGMMLA 11
DB 25 QASQNDISMLA 35

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RESULT 9
GAG_HV1U4 STANDARD; PRT; 492 AA.
AC P24736;
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE GAG polypeptide [contains: Core proteins p17, p24, p2, p7, p1, p6].
GN GAG.
OS Human immunodeficiency virus type 1 (strain Ugandan / isolate 0455)
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11703;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9109081; PubMed=2265025;
RA Oram J.D., Downing R.G., Roff M., Clegg J.C.S., Serrada D.,
RA Carswell J.W.;
RT "Nucleotide sequence of a Ugandan HIV-1 provirus reveals genetic
RT diversity from other HIV-1 isolates."
RL AIDS Res. Hum. Retroviruses 6:1073-1078(1990).
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
CC
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CC
CC EMBL: M6320; AAA75018.1; -
CC HSSP: P05888; 1AAE.
CC InterPro: IPR000721; Gag_p24.
CC InterPro: IPR000071; Retrovir_p17.
CC Pfam: PF00098; zf-CCHC; 2.
CC Pfam: PF00540; Gag_p17; 1.
CC Pfam: PF00607; Gag_p24; 1.
CC PRINTS: PR00939; C2HCZNFINGER.
CC PRINTS: PR00234; HIVMATRIX.
CC SMART: SM00343; ZNF_C2HC; 2.

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DR PROSITE: PS50158; ZF_CCHC; 2.
KW AIDS; Core protein; Polypeptide; Myristate; Phosphorylation;
KW Zinc-finger; Repeat.
FT INIT_MET 0
FT CHAIN 1 127 BY SIMILARITY.
FT CHAIN 128 358 CORE PROTEIN P17 (MATRIX PROTEIN).
FT CHAIN 359 371 CORE PROTEIN P24 (CORE ANTIGEN).
FT CHAIN 372 425 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
FT CHAIN 426 441 CORE PROTEIN P1.
FT CHAIN 442 492 CORE PROTEIN P6.
FT ZN_FING 383 400 CCHC-TYPE 1.
FT ZN_FING 404 421 CCHC-TYPE 2.
FT LIPID 1
SQ SEQUENCE 492 AA: 54791 MW: E4A3B4D633B6972 CRC64;
Query Match 69.5%; Score 41; DB 1; Length 492;
Best Local Similarity 60.0%; Pred. No. 4.6;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 QASODIGMML 10
DB 303 QATQDVKNMM 312

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RESULT 10
GAG_HV1C4 STANDARD; PRT; 499 AA.
AC P05887;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE GAG polypeptide [contains: Core proteins p17, p24, p2, p7, p1, p6].
GN GAG.
OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11687;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87041461; PubMed=3490666;
RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
RA Andersen P.R., Devare S.G.;
RT "Molecular cloning and primary nucleotide sequence analysis of a
RT distinct human immunodeficiency virus isolate reveal significant
RT divergence in its genomic sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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CC
CC EMBL: M13136; AAA44306.1; -
CC PIR: A25523; FOVMH4.
CC HSSP: P05888; 1AAE.
CC HIV: M13136; GAGSCD45.
CC InterPro: IPR000721; Gag_p24.
CC InterPro: IPR000071; Retrovir_p17.
CC Pfam: PF00098; zf-CCHC; 2.
CC Pfam: PF00540; Gag_p17; 1.
CC Pfam: PF00607; Gag_p24; 1.

```

DR PRINTS: PR00939; C2HCZNFINGER.
 DR PRINTS: PR00234; HIVMATRIX.
 DR SMART: SM00343; ZNF_C2HC; 2.
 DR PROSITE: PS50158; ZF_CCHC; 2.
 KW AIDS: Core protein: Polyprotein; Myristate; Phosphorylation;
 ZINC-finger; Repeat.
 FT INIT_MET 0
 FT CHAIN 1 131
 FT CHAIN 132 362
 FT CHAIN 363 376
 FT CHAIN 377 431
 FT CHAIN 432 447
 FT CHAIN 448 489
 FT CHAIN 389 406
 FT ZN_FING 410 427
 FT LIPID 1
 SQ SEQUENCE 499 AA; 55796 MW; 023CA76C9C6F22AD CRC64;

Query Match 67.8%; Score 40; DB 1; Length 499;
 Best Local Similarity 60.0%; Pred. No. 7.1;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWL 10
 |||||: ||:
 DB 307 QASQEVKNWM 316

RESULT 11
 GAG_HV1H2 STANDARD; PRT; 499 AA.
 ID GAG_HV1H2
 AC P04591:
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE GAG polyprotein [contains: Core proteins p17, p24, p2, p7, p1, p6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
 OC Viruses: Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11706;
 RN [1]
 RP MEDLINE=8729196; PubMed=3040055;
 RA Retner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
 RA Gallo R.C., Wong-Staal F.;
 RT "Complete nucleotide sequences of functional clones of the AIDS
 RT virus";
 RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
 CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
 CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
 CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
 CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
 CC -1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
 CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
 CC
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 CC
 CC EMBL: K03455; AAB50258.1; -
 CC HSSP: P05888; IAAF.
 CC HIV: K03455; GAGSHXB2.
 CC InterPro: IPR000721; Gag_p24.
 CC InterPro: IPR000071; Retroviral_p17.
 CC InterPro: IPR001878; ZNF_CCHC.
 CC Pfam: PF00098; ZF-CCHC; 2.
 CC Pfam: PF00540; Gag_p17; 1.

DR Pfam: PF00607; Gag_p24; 1.
 DR PRINTS: PR00939; C2HCZNFINGER.
 DR PRINTS: PR00234; HIVMATRIX.
 DR SMART: SM00343; ZNF_C2HC; 2.
 DR PROSITE: PS50158; ZF_CCHC; 2.
 KW AIDS: Core protein: Polyprotein; Myristate; Phosphorylation;
 ZINC-finger; Repeat.
 FT INIT_MET 0
 FT CHAIN 1 131
 FT CHAIN 132 362
 FT CHAIN 363 376
 FT CHAIN 377 431
 FT CHAIN 432 447
 FT CHAIN 448 489
 FT CHAIN 389 406
 FT ZN_FING 410 427
 FT LIPID 1
 SQ SEQUENCE 499 AA; 55798 MW; 774C384D6EACB108 CRC64;

Query Match 67.8%; Score 40; DB 1; Length 499;
 Best Local Similarity 60.0%; Pred. No. 7.1;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASQDIGNWL 10
 |||||: ||:
 DB 307 QASQEVKNWM 316

RESULT 12
 GAG_HV1J3 STANDARD; PRT; 499 AA.
 ID GAG_HV1J3
 AC P12494:
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE GAG polyprotein [contains: Core proteins p17, p24, p2, p7, p1, p6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).
 OC Viruses: Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11694;
 RN [1]
 RP MEDLINE=89552108; PubMed=2669897;
 RA Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
 RT "Nucleotide sequences of gag and env genes of a Japanese isolate of
 RT HIV-1 and their expression in bacteria";
 RL AIDS Res. Hum. Retroviruses 5:411-419(1989).
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
 CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
 CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
 CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
 CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
 CC -1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
 CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: M21137; AAB03522.1; -
 CC HSSP: P05888; IAAF.
 CC HIV: M21137; GAGSHXB3.
 CC InterPro: IPR000721; Gag_p24.
 CC InterPro: IPR000071; Retroviral_p17.
 CC InterPro: IPR001878; ZNF_CCHC.
 CC Pfam: PF00098; ZF-CCHC; 2.
 CC Pfam: PF00540; Gag_p17; 1.

PFam: PF00607; Gag_p24: 1.
 DR PRINTS: PR00939; C2HC2NFINGER.
 DR PRINTS: PR00234; HIVMATR1X.
 DR SMART: SM00343; znf_C2HC; 2.
 DR PROSITE: PS50158; ZF_C2HC; 2.
 KW AIDS: Core protein; Polypeptide; Myristate; Phosphorylation;
 zinc-finger; Repeat.
 FT INIT_MET 0
 FT CHAIN 1 131
 FT CHAIN 132 362
 FT CHAIN 363 376
 FT CHAIN 377 431
 FT CHAIN 432 447
 FT CHAIN 448 499
 FT CHAIN 389 406
 FT ZN_FING 410 427
 FT LIPID 1
 SQ SEQUENCE 499 AA; 55725 MW; 52E2812D4424AE9 CRC64;
 Query Match 67.8%; Score 40; DB 1; Length 499;
 Best Local Similarity 60.0%; Pred. No. 7.1;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QASODIGNWL 10
 Db 307 QASOEKNNM 316

RESULT 13
 GAG_HYLM STANDARD; PRT: 499 AA.
 ID GAG_HYLM 070622;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE GAG polypeptide [contains: Core proteins p17, p24, p2, p7, p1, p6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=82834;
 RN [1]
 RP MEDLINE=95127297; PubMed=7826699;
 RA Reltz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
 RA Shaw G.M., Kong L.T., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker
 infected with HIV type 1 (HIV type IIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
 CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
 CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
 CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
 CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
 CC -1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
 CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
 CC -----
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 CC -----
 CC EMBL: U12055; AAA76886.1; -
 CC HSSP: P05888; IAAF.
 DR InterPro: IPR000721; Gag_p24.
 DR InterPro: IPR00071; Retroviral_p17.
 DR InterPro: IPR001878; Znf_C2HC.
 DR Pfam: PF00098; zf-C2HC; 2.
 DR Pfam: PF00607; Gag_p17; 1.
 DR PRINTS: PR00234; HIVMATR1X.

PFam: PF00607; Gag_p24: 1.
 DR PRINTS: PR00939; C2HC2NFINGER.
 DR PRINTS: PR00234; HIVMATR1X.
 DR SMART: SM00343; znf_C2HC; 2.
 DR PROSITE: PS50158; ZF_C2HC; 2.
 KW AIDS: Core protein; Polypeptide; Myristate; Phosphorylation;
 zinc-finger; Repeat.
 FT INIT_MET 0
 FT CHAIN 1 131
 FT CHAIN 132 362
 FT CHAIN 363 376
 FT CHAIN 377 431
 FT CHAIN 432 447
 FT CHAIN 448 499
 FT CHAIN 389 406
 FT ZN_FING 410 427
 FT LIPID 1
 SQ SEQUENCE 499 AA; 55772 MW; AA2F683546EDCA9 CRC64;
 Query Match 67.8%; Score 40; DB 1; Length 499;
 Best Local Similarity 60.0%; Pred. No. 7.1;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QASODIGNWL 10
 Db 307 QASOEKNNM 316

RESULT 14
 GAG_HYLN5 STANDARD; PRT: 499 AA.
 ID GAG_HYLN5 P12493;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE GAG polypeptide [contains: Core proteins p17, p24, p2, p7, p1, p6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11698;
 RN [1]
 RP SEQUENCE FROM N.A. (CLONE PNL4-3).
 RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
 RL Submitted (JUN-1988) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
 CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
 CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
 CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
 CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
 CC -1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
 CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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 CC -----
 CC EMBL: M19921; AAA44987.1; -
 CC HSSP: P05888; IAAF.
 DR HIV: M19921; GAGSNL43.
 DR InterPro: IPR000721; Gag_p24.
 DR InterPro: IPR00071; Retroviral_p17.
 DR InterPro: IPR001878; Znf_C2HC.
 DR Pfam: PF00098; zf-C2HC; 2.
 DR Pfam: PF00540; Gag_p17; 1.
 DR Pfam: PF00607; Gag_p24; 1.
 DR PRINTS: PR00939; C2HC2NFINGER.
 DR PRINTS: PR00234; HIVMATR1X.

DR SMART; SM00343; ZNF_C2HC; 2.
 DR PROSITE; PS50158; ZF_CCHC; 2.
 KW AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
 DR ZINC-finger; Repeat.
 FT INIT_MET 0 0
 FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
 FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
 FT CHAIN 363 376 CORE PROTEIN P2.
 FT CHAIN 377 431 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
 FT CHAIN 432 447 CORE PROTEIN P1.
 FT CHAIN 448 499 CORE PROTEIN P6.
 FT ZN_FING 389 406 CCHC-TYPE 1.
 FT ZN_FING 410 427 CCHC-TYPE 2.
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 SQ SEQUENCE 499 AA; 55687 MW; C8EC1302FE2C1E2 CRC64;
 Query Match 67.8%; Score 40; DB 1; Length 499;
 Best Local Similarity 60.0%; Pred. No. 7.1;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASODIGNWL 10
 Db 307 QASOEVRKMM 316
 RESULT 15
 GAG_HV1Y2 STANDARD; PRT; 499 AA.
 ID GAG_HV1Y2
 AC P35962;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE GAG polyprotein [contains: Core proteins p17, p24, p2, p7, p1, p6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=36377;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93021387; PubMed=1404605;
 RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
 Shaw G.M.;
 RT "Complete nucleotide sequence, genome organization, and biological
 properties of human immunodeficiency virus type 1 in vivo: evidence
 for limited defectiveness and complementation."
 RT J. Virol. 66:6587-6600(1992).
 RL
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
 MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
 RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
 CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
 BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
 CC -1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
 CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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 CC
 DR EMBL; M93258; .; NOT_ANNOTATED_CDS.
 DR PIR; A44001; A44001.
 DR HSSP; P05888; IAAF.
 DR InterPro: IPR000721; Gag_p24.
 DR InterPro: IPR000071; Retrovir_p17.
 DR InterPro: IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf-CCHC; 2.
 DR Pfam; PF00540; Gag_p17; 1.
 DR Pfam; PF09607; Gag_p24; 1.

DR PRINTS; PR00939; C2HCZNFINGER.
 DR PRINTS; PR00234; HIVMATRIX.
 DR SMART; SM00343; ZNF_C2HC; 2.
 DR PROSITE; PS50158; ZF_CCHC; 2.
 KW AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
 DR ZINC-finger; Repeat.
 FT INIT_MET 0 0
 FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
 FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
 FT CHAIN 363 376 CORE PROTEIN P2.
 FT CHAIN 377 431 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
 FT CHAIN 432 447 CORE PROTEIN P1.
 FT CHAIN 448 499 CORE PROTEIN P6.
 FT ZN_FING 389 406 CCHC-TYPE 1.
 FT ZN_FING 410 427 CCHC-TYPE 2.
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 SQ SEQUENCE 499 AA; 55660 MW; 278E65F5405CD99 CRC64;
 Query Match 67.8%; Score 40; DB 1; Length 499;
 Best Local Similarity 60.0%; Pred. No. 7.1;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASODIGNWL 10
 Db 307 QASOEVRKMM 316

Search completed: February 25, 2003, 10:37:25
 Job time : 0.971667 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 : Search time 1.39333 Seconds
(without alignments)
758.956 Million cell updates/sec

Title: US-09-743-482A-2

Perfect score: 59

Sequence: 1 QASQDIGNMFLA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	83.1	125	2 S04936	Ig kappa chain pre
2	49	83.1	130	2 PLO113	Ig kappa chain pre
3	44	74.6	92	1 KYR838	Ig kappa chain V r
4	44	74.6	108	1 K1HUMS	Ig kappa chain V-I
5	44	74.6	117	2 S46376	Ig kappa chain V-J
6	44	74.6	129	2 S40332	Ig kappa chain - h
7	44	74.6	146	2 S60702	gag protein - huma
8	44	74.6	146	2 S60704	gag protein - huma
9	44	74.6	146	2 S60703	gag protein - huma
10	44	74.6	146	2 S60698	gag protein - huma
11	44	74.6	146	1 FOLVMD	gag polyprotein -
12	44	74.6	502	1 FOVMA2	gag polyprotein -
13	43	72.9	103	2 S41321	Ig kappa chain V-J
14	43	72.9	122	2 S40351	Ig kappa chain V-J
15	43	72.9	139	2 S40365	Ig kappa chain V r
16	42	71.2	109	1 KYR837	Ig kappa chain V r
17	42	71.2	130	2 S40368	Ig kappa chain V r
18	40	67.8	62	2 S42265	Ig kappa chain V r
19	40	67.8	87	2 I52592	Ig kappa chain V r
20	40	67.8	88	2 S34088	Ig kappa chain V r
21	40	67.8	88	2 S34087	Ig kappa chain V r
22	40	67.8	95	2 PH0862	Ig kappa chain V r
23	40	67.8	108	2 S36277	Ig kappa chain V r
24	40	67.8	110	2 S4118	Ig kappa chain V r
25	40	67.8	117	2 S43528	Ig kappa chain V r
26	40	67.8	117	2 S4263	Ig kappa chain V r
27	40	67.8	129	2 S52789	Ig kappa chain V r
28	40	67.8	146	2 S60700	gag protein - huma
29	40	67.8	146	2 S60697	gag protein - huma

30	40	67.8	146	2 S60699	gag protein - huma
31	40	67.8	146	2 S60708	gag protein - huma
32	40	67.8	478	1 FOVWVL	gag polyprotein -
33	40	67.8	498	2 T09436	gag polyprotein -
34	40	67.8	500	1 FOVWLV	gag polyprotein -
35	40	67.8	500	1 A44001	gag polyprotein -
36	40	67.8	500	1 FOVWH4	gag polyprotein -
37	40	67.8	500	2 S33979	gag polyprotein -
38	40	67.8	506	1 A38068	gag polyprotein -
39	40	67.8	508	1 FOLVST	gag polyprotein -
40	40	67.8	512	1 FOVWH3	gag polyprotein -
41	40	67.8	709	2 AD2843	methy1-accepting c
42	40	67.8	717	2 E97620	methy1-accepting c
43	39.5	66.9	88	2 PLO261	Ig kappa chain V r
44	39.5	66.9	106	2 PLO260	Ig kappa chain V r
45	39.5	66.9	106	2 PLO259	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S04936

Ig kappa chain precursor V-J region (1H1) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000

C:Accession: S04936

R:Levy, S.; Mendel, E.; Kon, S.; Aynur, Z.; Levy, R.

J. Exp. Med. 168, 475-489, 1988

A:Title: Mutational hot spots in Ig V region genes of human follicular lymphomas.

A:Reference number: S04936; MUID:88316166; PMID:3045247

A:Accession: S04936

A:Molecule type: mRNA

A:Residues: 1-125 <LEV>

A:Cross-references: EMBL:X13076; NID:g33173; PIDN:CAA31477.1; PID:g736243

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:1-17/Domain: signal sequence (fragment) #status predicted <STG>

F:18-125/Product: Ig kappa chain (fragment) #status predicted <MAT>

F:33-107/Domain: Immunoglobulin homology <IMM>

Query Match 83.1%; Score 49; DB 2; Length 125;

Best Local Similarity 81.8%; Pred. No. 0.18; Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQDIGNMFLA 11

DB 41 RASQSIGNMFLA 51

RESULT 2

PLO113

Ig kappa chain precursor V-I region (CJ) - human

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000

C:Accession: PLO113

R:Levy, S.; Mendel, E.; Kon, S.; Aynur, Z.; Levy, R.

J. Exp. Med. 168, 475-489, 1988

A:Title: Mutational hot spots in Ig V region genes of human follicular lymphomas.

A:Reference number: S04936; MUID:88316166; PMID:3045247

A:Accession: PLO113

A:Molecule type: mRNA

A:Residues: 1-130 <LEV>

A:Experimental source: follicular lymphoma cells

A>Note: the sequence shown here is derived from the consensus nucleotide sequence of

om tumor cells of a single patient

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; hybridoma; Immunoglobulin

F:1-22/Domain: signal sequence #status predicted <STG>

F:23-130/Product: Ig kappa chain V-I region CJ #status predicted <MAT>

F:38-112/Domain: Immunoglobulin homology <IMM>

F:46-56/Region: complementarity-determining 1

F:72-78/Region: complementarity-determining 2

F:111-130/Region: complementarity-determining 3
F:118-130/Region: J1

Query Match 83.1%; Score 49; DB 2; Length 130;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWLA 11
:|||||:|||||
DB 46 RASODISWLA 56

RESULT 3

KVRB38
Ig kappa chain V region (3381) - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 21-Jan-2000
C:Accession: A01953
R:Margolies, M.N.; Cannon III, L.E.; Strosberg, A.D.; Haber, E.
Proc. Natl. Acad. Sci. U.S.A. 72, 2180-2184, 1975
A:Title: Diversity of light chain variable region sequences among rabbit antibodies elicited by sheep erythrocytes
A:Reference number: A93789; MUID:75176905; PMID:1094456
A:Accession: A01953
A:Molecule type: protein
A:Residues: 1-92 <MAR>

C:Comment: This chain was obtained from antibody to type III pneumococci and was isolated from a rabbit. The chain consists of two identical light (K) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 12 C:Superfamily: heterotetramer
C:Keywords: heterotetramer
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match 74.6%; Score 44; DB 1; Length 92;
Best Local Similarity 72.7%; Pred. No. 0.99;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QASODIGNWLA 11
:|||||:|||||
DB 24 QASESISWLA 34

RESULT 4

K1HWMS
Ig kappa chain V-I region (Wes) - human (tentative sequence)

C:Species: Homo sapiens (man)
C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 31-Mar-2000
C:Accession: A01877

R:Kratz, H.; Yang, C.; Krusche, J.U.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 361, 1591-1598, 1980

A:Title: Preparative separation of the tryptic hydrolysate of a protein by high-pressure
A:Reference number: A01877; MUID:81092279; PMID:6778806

A:Accession: A01877

A:Molecule type: protein

A:Residues: 1-108 <KRA>

A:Note: the C region of this chain has the Inv (3) marker

C:Comment: This is a Bence Jones protein.

C:Genetics:

A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (K) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 12 C:Superfamily: heterotetramer

C:Keywords: heterotetramer
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match 74.6%; Score 44; DB 1; Length 108;
Best Local Similarity 72.7%; Pred. No. 1.2;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWLA 11
:|||||:|||||
DB 24 RASODISWLA 34

RESULT 5
S46376
Ig kappa chain V-J region (T33-14) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46376; S36649

R:Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene
A:Reference number: S46369; MUID:94333975; PMID:8039491

A:Accession: S46376

A:Molecule type: mRNA

A:Residues: 1-117 <BEN>

A:Cross-references: EMBL:227177; NID:9415969; PIDN:CAA81701.1; PID:9415970

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:25-99/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 44; DB 2; Length 117;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWLA 11
:|||||:|||||
DB 33 RASODISWLA 43

RESULT 6

S40332
Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40332

R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40332

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-129 <KLE>

A:Cross-references: EMBL:X72442; NID:9441352; PIDN:CAA51110.1; PID:9441353

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 44; DB 2; Length 129;
Best Local Similarity 72.7%; Pred. No. 1.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWLA 11
:|||||:|||||
DB 41 RASODISWLA 51

RESULT 7

S60702
gag protein - human immunodeficiency virus type 1 (isolate 3005) (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 26-Aug-1999
C:Accession: S60702

R:Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.

Virus Res. 31, 331-342, 1994

A:Title: Molecular epidemiology of HIV-1 in Madrid.

A:Reference number: S60687; MUID:94249284; PMID:7545926

A:Accession: S60702

A>Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-146 <ROJ>
A:Cross-references: EMBL:Z29699; NID:9809013; PIDN:CAA82794.1; PID:9809014
C:Superfamily: AIDS-related virus gag polyprotein

Query Match 74.6%; Score 44; DB 2; Length 146;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWL 10
|||||:|:
Db 94 QASODVKNMW 103

RESULT 8

S60704
gag protein - human immunodeficiency virus type 1 (isolate 2051) (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 26-Aug-1999
C:Accession: S60704

R:Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.;
Virus Res. 31, 331-342, 1994

A:Title: Molecular epidemiology of HIV-1 in Madrid.

A:Reference number: S60687; MUID:94249284; PMID:7545926

A:Accession: S60704

A>Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-146 <ROJ>

A:Cross-references: EMBL:Z29700; NID:9809015; PIDN:CAA82795.1; PID:9809016
C:Superfamily: AIDS-related virus gag polyprotein

Query Match 74.6%; Score 44; DB 2; Length 146;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWL 10
|||||:|:
Db 94 QASODVKNMW 103

RESULT 9

S60703
gag protein - human immunodeficiency virus type 1 (isolate 2080) (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 26-Aug-1999
C:Accession: S60703

R:Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.;
Virus Res. 31, 331-342, 1994

A:Title: Molecular epidemiology of HIV-1 in Madrid.

A:Reference number: S60687; MUID:94249284; PMID:7545926

A:Accession: S60703

A>Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-146 <ROJ>

A:Cross-references: EMBL:Z29701; NID:9809017; PIDN:CAA82796.1; PID:9809018
C:Superfamily: AIDS-related virus gag polyprotein

Query Match 74.6%; Score 44; DB 2; Length 146;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWL 10
|||||:|:
Db 94 QASODVKNMW 103

RESULT 10

S60698
gag protein - human immunodeficiency virus type 1 (isolate 306) (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 26-Aug-1999
C:Accession: S60698

R:Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.;
Virus Res. 31, 331-342, 1994

A:Title: Molecular epidemiology of HIV-1 in Madrid

A:Reference number: S60687; MUID:94249284; PMID:7545926

A:Accession: S60698

A>Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-146 <ROJ>

A:Cross-references: EMBL:Z29695; NID:9809005; PIDN:CAA82790.1; PID:9809006
C:Superfamily: AIDS-related virus gag polyprotein

Query Match 74.6%; Score 44; DB 2; Length 146;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWL 10
|||||:|:
Db 94 QASODVKNMW 103

RESULT 11

FOUJND

gag polyprotein - human immunodeficiency virus type 1 (isolate NDK)

N:Alternate names: core polyprotein

N:Contains: core protein p15; core protein p17; core protein p24

C:Species: human immunodeficiency virus type 1, HIV-1

A>Note: host Homo sapiens (man)

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C:Accession: J00065

R:Spire, B.; Sife, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe,
Gene 81, 275-284, 1989

A:Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human imm

A:Reference number: J00065; MUID:90034200; PMID:2806917

A:Accession: J00065

A:Molecule type: DNA

A:Residues: 1-497 <SP1>

A:Cross-references: GB:M27323; NID:9328154; PIDN:AAA44868.1; PID:9328157

C:Genetics:

A:Gene: gag

C:Superfamily: AIDS-related virus gag polyprotein

C:Keywords: AIDS: core protein; immunodeficiency: polyprotein

F:1-129/Product: core protein p17 #status predicted <C17>

F:130-369/Product: core protein p24 #status predicted <C24>

F:390-497/Product: core protein p15 #status predicted <C15>

Query Match 74.6%; Score 44; DB 1; Length 497;
Best Local Similarity 70.0%; Pred. No. 5.9;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWL 10
|||||:|:
Db 305 QASODVKNMW 314

RESULT 12

FOVMA2
gag polyprotein - human immunodeficiency virus type 1 (isolate ARV-2)

N:Alternate names: core polyprotein

N:Contains: core protein p15; core protein p17; core protein p24

C:Species: human immunodeficiency virus type 1, HIV-1

A>Note: host Homo sapiens (man)

C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C:Accession: A03947

R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stemple, M.M.; Brown
Science 227, 484-492, 1985

A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).

A:Reference number: A04003; MUID:85090453; PMID:2578227

A:Accession: A03947

A:Molecule type: DNA

A:Residues: 1-502 <SAN>

A:Cross-references: GB:K02007; NID:9328658; PIDN:AAB59875.1; PID:9328661

C:Comment: Cleavage sites that yield the mature core proteins remain to be determined

C:Genetics:

A:Gene: gag

C:Superfamily: AIDS-related virus gag polyprotein

C:Keywords: AIDS: core protein; immunodeficiency: polyprotein
 E:1-144/Product: core protein p17 #status predicted <P17>
 F:135-393/Product: core protein p24 #status predicted <P24>
 F:394-502/Product: core protein p15 #status predicted <P15>

Query Match
 Best Local Similarity 74.6%; Score 44; DB 1; Length 502;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNMNL 10
 :||||:|:
 DB 310 QASODVKNM 319

RESULT 13

S44121
 Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C:Accession: S44121

R:Klein, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

submitted to the EMBL Data Library, March 1994

A:Description: Idiolytic vaccination against human B-cell lymphoma: rescue of variable

A:Reference number: S44105

A:Accession: S44121

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-103 <MAN>

A:Cross-references: EMBL:231385; NID:g472975; PIDN:CAA83260.1; PID:g940532

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 72.9%; Score 43; DB 2; Length 103;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 14

S40351
 Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40351

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chl genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40351

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-122 <KLE>

A:Cross-references: EMBL:X72461; NID:g441390; PIDN:CAA51129.1; PID:g441391

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-106/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 72.9%; Score 43; DB 2; Length 122;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNMNL 11
 :||||:|:
 DB 40 RASQVGTWLA 50

RESULT 15

S40365
 Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40365

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chl genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40365

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-139 <KLE>

A:Cross-references: EMBL:X72475; NID:g441418; PIDN:CAA51143.1; PID:g441419

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:31-105/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 72.9%; Score 43; DB 2; Length 139;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 QASODIGNMNL 10
 :||||:|:
 DB 39 QATVDIGNYL 48

Search completed: February 25, 2003, 10:33:47
 Job time : 2.39333 secs

GenCore version 5.1.4.p5 4578
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 22:21:19 : Search time 75 Seconds
(Without alignments)
1508.850 Million cell updates/sec

Title: US-09-743-482A-13

Perfect score: 369

Sequence: 1 caggtacagtcgacgaac.....ctctgtcactgtcttca 369

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NM:*

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	247.8	67.2	363	3 US-08-881-037-47	Sequence 47, Appl
2	246.6	66.8	831	2 US-08-403-853-17	Sequence 17, Appl
3	244.6	66.3	363	1 US-08-040-204-1	Sequence 1, Appl
4	243.2	65.9	366	1 US-08-040-204-7	Sequence 7, Appl
5	242.6	65.7	366	1 US-08-236-520-8	Sequence 8, Appl
6	242.6	65.5	366	5 PCT-US95-05262-8	Sequence 8, Appl
7	241.6	65.5	366	1 US-08-040-204-6	Sequence 6, Appl
8	240.2	65.1	423	4 US-09-438-954-45	Sequence 45, Appl
9	240.2	65.1	858	2 US-08-428-257A-71	Sequence 71, Appl
10	240.2	65.1	858	2 US-08-491-988-2	Sequence 2, Appl
11	240.2	65.1	1257	2 US-08-491-988-8	Sequence 8, Appl
12	240.2	65.1	1257	2 US-08-491-988-10	Sequence 10, Appl
13	240.2	65.1	1257	2 US-08-491-988-6	Sequence 6, Appl
14	240.2	65.1	1257	2 US-08-491-988-4	Sequence 4, Appl
15	240.2	65.1	1257	2 US-08-491-988-13	Sequence 13, Appl
16	238.6	64.7	454	2 US-08-737-560A-12	Sequence 12, Appl
17	238.6	64.7	454	2 US-08-737-560A-6	Sequence 6, Appl
18	238.4	64.6	366	1 US-08-040-204-5	Sequence 5, Appl
19	238.2	64.6	420	1 US-08-149-099C-9	Sequence 9, Appl
20	238.2	64.6	420	2 US-08-478-967A-9	Sequence 9, Appl
21	238.2	64.6	420	4 US-08-475-815B-10	Sequence 10, Appl
22	238.2	64.6	9209	1 US-08-149-099C-3	Sequence 3, Appl
23	238.2	64.6	9209	1 US-08-476-275-2	Sequence 2, Appl
24	238.2	64.6	9209	2 US-08-478-967A-3	Sequence 3, Appl
25	238.2	64.6	9209	4 US-08-475-815B-3	Sequence 3, Appl
26	238.2	64.6	18986	2 US-08-819-866-2	Sequence 2, Appl
27	238.2	64.6	18986	2 US-09-023-715-2	Sequence 2, Appl

ALIGNMENTS

28	238.2	64.6	18986	4	US-09-143-485A-2	Sequence 2, Appl
29	237	64.2	417	2	US-08-452-164A-7	Sequence 7, Appl
30	236.6	64.1	420	1	US-08-476-275-5	Sequence 5, Appl
31	236.2	64.0	416	1	US-08-253-877C-7	Sequence 7, Appl
32	236.2	64.0	416	3	US-08-603-024-1	Sequence 1, Appl
33	235.6	63.8	363	1	US-08-318-970B-34	Sequence 34, Appl
34	235.4	63.8	417	2	US-08-656-586-3	Sequence 3, Appl
35	235	63.7	429	1	US-08-236-520-6	Sequence 6, Appl
36	235	63.7	429	5	PCT-US95-05262-6	Sequence 6, Appl
37	234	63.4	363	1	US-08-040-204-2	Sequence 2, Appl
38	234	63.4	420	4	US-08-579-378A-3	Sequence 3, Appl
39	234	63.4	420	5	PCT-US93-11612-3	Sequence 3, Appl
40	233	63.1	366	3	US-08-767-128-3	Sequence 3, Appl
41	232.8	63.1	340	3	US-08-881-037-9	Sequence 9, Appl
42	232.2	62.9	348	2	US-08-888-366-1	Sequence 2, Appl
43	232	62.9	360	3	US-09-065-059-2	Sequence 2, Appl
44	232	62.9	426	2	US-08-678-194-7	Sequence 7, Appl
45	232	62.9	426	4	US-08-890-011-7	Sequence 7, Appl

RESULT 1

US-08-881-037-47

Sequence 47, Application US/08881037

Patent No. 6080588

GENERAL INFORMATION:

APPLICANT: Gluck, Gary D.

APPLICANT: Swanson, Patrick C.

TITLE OF INVENTION: DNA BINDING ANTIBODIES

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSER: Morrison & Foerster

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/881,037

FILING DATE: 23-JUN-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/443,540

FILING DATE: 18-MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Kanski, Antoinette F.

REGISTRATION NUMBER: 34,202

REFERENCE/DOCKET NUMBER: 203442110710

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX:

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 363 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-881-037-47

Query Match

Best Local Similarity 81.6% Pred. No. 2.6e-70:

Matches 301: Conservative 0: Mismatches 62: Indels 6: Gaps 1:

QY 1 CAGGTACAGTCGACGAACCTGCGCTGAGTGAACCTGCGCTGCTCACTGAAATT 60

```

Db      1  CAGGTCCAGCTGCTCCAGAGTCTGGGGCTGAGCTGGCAGGCGCTTGAGGCTTCAGTGAAGCTG 60
Qy      61  TCCTGCAAGGCTTCTGGCTACACATTCACCAAGTTAGCATATGAGTAAACAGCAG 120
Db      61  TCCTGCAAGGCTTCTGGCTACACATTCACCAAGTTAGCATATGAGTAAACAGCAG 120
Qy      121  CCGGAAGTGGCTTGGAGTGGATTTATCCCTGGGAATGGTAACTAGTAC 180
Db      121  ACTGGACAGGCGCTTGGAGTGGATTTATCCCTGGGAATGGTAACTAGTAC 180
Qy      181  AATCAAAAGTTCAATGGGAAGCAACACTGACAGACAATCTCCAGCAGCGCTAT 240
Db      181  AATGAGAGTTCAAGGCGCAAGGCCACACTGACAGACAATCTCCAGCAGCGCTAC 240
Qy      241  ATGCAGCTCAGACCGCTGACATCTGAGAGCTGCAAGCTATTTCTGGCAAGATGG 300
Db      241  ATGCAGCTCAGACCGCTGACATCTGAGAGCTGCAAGCTATTTCTGGCAAGA----- 294
Qy      301  CATTACTATAGCAGTATATCCCTGCTTGTACTGGGGCCAGGCAAGCCTGTGCTAC 360
Db      295  CAGTCTACTATAGTACTACTCTCTGTTGCTTACTGGGGCCAGGCAAGCCTGTGCTAC 354
Qy      361  GTCTCTTCA 369
Db      355  GTCTCTTCA 363

```

RESULT 2

US-08-403-853-17

; Sequence 17, Application US/08403853

; Patent No. 5844094

; GENERAL INFORMATION:

; APPLICANT: HUDSON, Peter J.

; APPLICANT: LAH, Maria

; APPLICANT: KORRT, Alex A.

; APPLICANT: IRVING, Robert A.

; APPLICANT: ATWELL, John L.

; APPLICANT: MALBY, Robyn L.

; APPLICANT: POWER, Barbara E.

; APPLICANT: COLMAN, Peter M.

; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/403,853

; FILING DATE: 30-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/AU93/00491

; FILING DATE: 24-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: AU PL 4973

; FILING DATE: 25-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 16786/189/CHAC

; TELEPHONE: (202) 672-5300

; TELEFAX: (202) 672-5399

; TELETYPE: 904136

```

; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: mat.peptide
; LOCATION: 1..819
; NAME/KEY: CDS
; LOCATION: 1..819
; US-08-403-853-17

```

```

Query Match          66.8%; Score 246.6; DB 2; Length 831;
Best Local Similarity 81.6%; Pred. No. 8.7e-70;
Matches 298; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

```

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Qy      1  CAGTACAGCTGACAGCAATCTGGGGCTGAGTGAAGCCTGGGCTCCAGTGAATTT 60
Db      67  CAGTGCAGCTGACAGCACTGTGGGCTGAGTGAAGCCTGGGCTCCAGTGAATTT 126
Qy      61  TCCTGCAAGGCTTCTGGCTACACATTCACCAAGTTACGATATGACATGATTAACAGCAG 120
Db      127  TCCTGCAAGGCTTCTGGCTACACATTCACCAAGTTACGATATGATTAACAGCAGTCA 186
Qy      121  CCTGAAATATGCGCTTGGAGTGGATTTATCTCTGGAATGTAATACTAAGTAC 180
Db      187  CCTGCAAGGCTTCTGGAGTGGATTTATCTCTGGAATGTAATACTAAGTAC 246
Qy      181  AATCAAAAGTTCAATGGGAAGCAACACTGACAGACAATCTCCAGCAGCGCTAT 240
Db      247  AATCAAAAGTTCAATGGGAAGCAACACTGACAGACAATCTCCAGCAGCGCTAT 306
Qy      241  ATGCAGCTCAGACCGCTGACATCTGAGAGCTGCAAGCTATTTCTGGCAAGATGG 300
Db      307  ATGCAGCTCAGACCGCTGACATCTGAGAGCTGCAAGCTATTTCTGGCAAGATGG 366
Qy      301  CATTACTATAGCAGTATATCCCTGCTTGTACTGGGGCCAGGCAAGCCTGTGCTACT 360
Db      367  GGCTCTAT---AGATAGCAGCGAGGCTTTGACTACTGGGGCCAGGCAAGCAGCGTAC 423
Qy      361  GTCTC 365
Db      424  GTCTC 428

```

RESULT 3

US-08-040-204-1

; Sequence 1, Application US/08040204

; Patent No. 5641488

; GENERAL INFORMATION:

; APPLICANT: Wysocki, Lawrence

; TITLE OF INVENTION: Method For Producing An Antibody To

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felle & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/040,204

; FILING DATE: 01-APRIL-1993

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:


```

ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MMV92-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..366
US-08-236-520-8

```

```

Query Match      65.7%; Score 242.6; DB 1; Length 366;
Best Local Similarity 80.5%; Pred. No. 1.2e-68;
Matches 297; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

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QY 1 CAGGTACAGCTGACGACATCTGGGGCTGAGTGAAGCCTGGCTCCTCACTGAAATT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 CAGGTCAACCTGACGACGCTGGAGCTGAAGCTGGAAGCCTGGGCTTCACTGAAGCTG 60
QY 61 TCCTGCAAGCTTCTGGCTGACATTCACCACTTACGATATGACGAGTAAACAGCAG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 TCCTGCAAGCTTCTGGCTGACATTCACCACTTACGATATGACGAGTAAACAGCAG 120
QY 121 CCTGGAATGCGCTTGAGTGTGATGGGTGATTTATCCTGAAATGTAATTAAGTAC 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 CCTGGAATGCGCTTGAGTGTGATGGGTGATTTATCCTGAAATGTAATTAAGTAC 180
QY 181 AATCAAAAGTTCAATGGGAGGCAACACACTGACGAGCAAAATCTCCAGACACACTAT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 AATGAGAATTTCAAGAGCAAGCCACACTGACTGTAGCAAAATCTCCAGACACACTAT 240
QY 241 ATGCAAGCTGACGACGCTGACATCTGAGACTCTGCACTGATTTCTGTGCAAGAGATTGG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 ATGCAAGCTGACGACGCTGACATCTGAGACTCTGCACTGATTTCTGTGCAAGAGATTGG 300
QY 301 CATTACTATAGACACTATATCCGCTTCTTACTGAGGGGCAAGGCAACTCTGTCTACT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 301 CATTACTATAGACACTATATCCGCTTCTTACTGAGGGGCAAGGCAACTCTGTCTACT 360
QY 361 GTCTCTCA 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 358 GTCTCTCA 366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 6
PCT-US95-05262-8

```

Sequence 8, Application PC/TUS9505262
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education Research
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smitty & Reynolds, P.C.
STREET: Two Millia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05262

```

```

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/236,520
FILING DATE: April 29, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MMV92-01 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..366
PCT-US95-05262-8

```

```

Query Match      65.7%; Score 242.6; DB 5; Length 366;
Best Local Similarity 80.5%; Pred. No. 1.2e-68;
Matches 297; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

```

```

QY 1 CAGGTACAGCTGACGACATCTGGGGCTGAGTGAAGCCTGGCTCCTCACTGAAATT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 CAGGTCAACCTGACGACGCTGGAGCTGAAGCTGGAAGCCTGGGCTTCACTGAAGCTG 60
QY 61 TCCTGCAAGCTTCTGGCTGACATTCACCACTTACGATATGACGAGTAAACAGCAG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 TCCTGCAAGCTTCTGGCTGACATTCACCACTTACGATATGACGAGTAAACAGCAG 120
QY 121 CCTGGAATGCGCTTGAGTGTGATGGGTGATTTATCCTGAAATGTAATTAAGTAC 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 CCTGGAATGCGCTTGAGTGTGATGGGTGATTTATCCTGAAATGTAATTAAGTAC 180
QY 181 AATCAAAAGTTCAATGGGAGGCAACACACTGACGAGCAAAATCTCCAGACACACTAT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 AATGAGAATTTCAAGAGCAAGCCACACTGACTGTAGCAAAATCTCCAGACACACTAT 240
QY 241 ATGCAAGCTGACGACGCTGACATCTGAGACTCTGCACTGATTTCTGTGCAAGAGATTGG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 ATGCAAGCTGACGACGCTGACATCTGAGACTCTGCACTGATTTCTGTGCAAGAGATTGG 300
QY 301 CATTACTATAGACACTATATCCGCTTCTTACTGAGGGGCAAGGCAACTCTGTCTACT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 301 CATTACTATAGACACTATATCCGCTTCTTACTGAGGGGCAAGGCAACTCTGTCTACT 360
QY 361 GTCTCTCA 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 358 GTCTCTCA 366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 7

```

US-08-040-204-6
Sequence 6, Application US/08040204
Patent No. 5641488
GENERAL INFORMATION:
APPLICANT: Wysocki, Lawrence
TITLE OF INVENTION: Method For Producing An Antibody To
TITLE OF INVENTION: A Chosen Antigen
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:

```


TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE: NO
NAME/KEY: CDS
LOCATION: 40..846
US-08-428-257A-71

Query Match 65.1%; Score 240.2; DB 2; Length 858;
Best Local Similarity 80.5%; Pred. No. 1e-67;
Matches 297; Conservative 0; Mismatches 63; Indels 9; Gaps 1;

QY 1 CAGGTACAGCTGCAGCAATCTGGGGCTGAACCTAGTGAAGCCTGGCTCCTCAGTGAATTT 60
DB 106 CAGGTACAGCTGCAGCAAGCTGGGGCTGAGCTGTGAAGCCTGGGGCTTCAAGTGAAGCTG 165
QY 61 TCCGCAAGGCTTCTGGCTACACATTCACCAAGTACATATGCACTGGATTAACAGCAG 120
DB 166 TCCGCAAGGCTTCTGGCTACACCTTCAACAGTACAGTACAGTACAGTACAGTACAG 225
QY 121 CCTGGAATGAGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
DB 226 CCTGGAATGAGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 285
QY 181 AATCAAAAGTTCAATGGAAGGCAACACTCAGTACAGCAAAATCCTCAGCAGACGCTAT 240
DB 286 AATGAGAAGTTCAAGAGCAAGGCAACACTCAGTACAGCAAAATCCTCAGCAGACGCTAT 345
QY 241 ATGCAAGCTCAGCAGCCTGACATCTGAGGACTCTGCACTATTTCTGCAAGGATTTGG 300
DB 346 ATGCAAGCTCAGCAGCCTGACATCTGAGGACTCTGCACTATTTCTGCAAGGATTTGG 405
QY 301 CATTACTATGACAGCTATATCCCTTGGCTTACTGGGGCAAGGACCTGCTCACT 360
DB 406 TACTACGCTAGTACTA-----CTTTGACTACTGGGGCAAGGACGACGCTCACT 456
QY 361 GTCTCTTCA 369
DB 457 GTCTCTTCA 465

RESULT 10
US-08-491-988-2
Sequence 2, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMENNON A.
APPLICANT: SPOONER, ROBERT A.
TITLE OF INVENTION: Deonarin, Mahendra
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090

TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 858 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 40..846
US-08-491-988-2

Query Match 65.1%; Score 240.2; DB 2; Length 858;
Best Local Similarity 80.5%; Pred. No. 1e-67;
Matches 297; Conservative 0; Mismatches 63; Indels 9; Gaps 1;

QY 1 CAGGTACAGCTGCAGCAATCTGGGGCTGAACCTAGTGAAGCCTGGCTCCTCAGTGAATTT 60
DB 106 CAGGTACAGCTGCAGCAAGCTGGGGCTGAGCTGTGAAGCCTGGGGCTTCAAGTGAAGCTG 165
QY 61 TCCGCAAGGCTTCTGGCTACACATTCACCAAGTACATATGCACTGGATTAACAGCAG 120
DB 166 TCCGCAAGGCTTCTGGCTACACCTTCAACAGTACAGTACAGTACAGTACAGTACAG 225
QY 121 CCTGGAATGAGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
DB 226 CCTGGAATGAGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 285
QY 181 AATCAAAAGTTCAATGGAAGGCAACACTCAGTACAGCAAAATCCTCAGCAGACGCTAT 240
DB 286 AATGAGAAGTTCAAGAGCAAGGCAACACTCAGTACAGCAAAATCCTCAGCAGACGCTAT 345
QY 241 ATGCAAGCTCAGCAGCCTGACATCTGAGGACTCTGCACTATTTCTGCAAGGATTTGG 300
DB 346 ATGCAAGCTCAGCAGCCTGACATCTGAGGACTCTGCACTATTTCTGCAAGGATTTGG 405
QY 301 CATTACTATGACAGCTATATCCCTTGGCTTACTGGGGCAAGGACCTGCTCACT 360
DB 406 TACTACGCTAGTACTA-----CTTTGACTACTGGGGCAAGGACGACGCTCACT 456
QY 361 GTCTCTTCA 369
DB 457 GTCTCTTCA 465

RESULT 11
US-08-491-988-8
Sequence 8, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMENNON A.
APPLICANT: SPOONER, ROBERT A.
TITLE OF INVENTION: Deonarin, Mahendra
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 40..1245
US-08-491-988-8

Query Match 65.1% Score 240.2; DB 2; Length 1257;
Best Local Similarity 80.5%; Pred. No. 1.2e-67;
Matches 297; Conservative 0; Mismatches 63; Indels 9; Gaps 1;

QY 1 CAGGTACAGCTGACGACATCTGGGGCTGAGTGAAGCCTGGGCTCCTCAGTGAATAAT 60
106 CAGGTGACGCTGACGACGCTGGGGCTGAGTGAAGCCTGGGCTCCTCAGTGAATAAT 165
QY 61 TCCTGCAAGCTTCTGGCTACACATTCACACGATTACATGACACTGATAAAGACGAG 120
166 TCCTGCAAGCTTCTGGCTACACATTCACACGATTACATGACACTGATAAAGACGAG 225
QY 121 CCTGGAATAGGCTTGAAGGATTTGATTCCTGGAATAGTAACTAATAGTAC 180
226 CCTGGAATAGGCTTGAAGGATTTGATTCCTGGAATAGTAACTAATAGTAC 285
DB 181 AATCAAAAGTTCAATGGGAAGGCAACACTCAGTGAAGCAAAATCCTCAGCAGAGCTAT 240
286 AATGAGAAATTCAGAGCAAGGCAACACTCAGTGAAGCAAAATCCTCAGCAGAGCTAT 345
QY 241 ATGCAAGCTCAGAGCTGACATCTGAGAGCTGACAGTATTTCTGTGCAAGAGATTGG 300
346 ATGCAAGCTCAGAGCTGACATCTGAGAGCTGACAGTATTTCTGTGCAAGAGATTGG 405
DB 301 CATTAATAGAGCTATATCCGCTTCTGCTTACTGGGGCAAGGCAAGCTGCTGACAT 360
406 TACTACGAGTAGTACTA-----CTTTGACTACTGGGGCAAGGCAAGGCTGACAT 456
QY 361 GTCTCTTCA 369
457 GTCTCTTCA 465

RESULT 12

US-08-491-988-10
Sequence 10, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMENON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
US-08-491-988-10

Query Match 65.1% Score 240.2; DB 2; Length 1259;
Best Local Similarity 80.5%; Pred. No. 1.2e-67;
Matches 297; Conservative 0; Mismatches 63; Indels 9; Gaps 1;

QY 1 CAGGTACAGCTGACGACATCTGGGGCTGAGTGAAGCCTGGGCTCCTCAGTGAATAAT 60
106 CAGGTGACGCTGACGACGCTGGGGCTGAGTGAAGCCTGGGCTCCTCAGTGAATAAT 165
QY 61 TCCTGCAAGCTTCTGGCTACACATTCACACGATTACATGACACTGATAAAGACGAG 120
166 TCCTGCAAGCTTCTGGCTACACATTCACACGATTACATGACACTGATAAAGACGAG 225
QY 121 CCTGGAATAGGCTTGAAGGATTTGATTCCTGGAATAGTAACTAATAGTAC 180
226 CCTGGAATAGGCTTGAAGGATTTGATTCCTGGAATAGTAACTAATAGTAC 285
DB 181 AATCAAAAGTTCAATGGGAAGGCAACACTCAGTGAAGCAAAATCCTCAGCAGAGCTAT 240
286 AATGAGAAATTCAGAGCAAGGCAACACTCAGTGAAGCAAAATCCTCAGCAGAGCTAT 345
QY 241 ATGCAAGCTCAGAGCTGACATCTGAGAGCTGACAGTATTTCTGTGCAAGAGATTGG 300
346 ATGCAAGCTCAGAGCTGACATCTGAGAGCTGACAGTATTTCTGTGCAAGAGATTGG 405
DB 301 CATTAATAGAGCTATATCCGCTTCTGCTTACTGGGGCAAGGCAAGCTGCTGACAT 360
406 TACTACGAGTAGTACTA-----CTTTGACTACTGGGGCAAGGCAAGGCTGACAT 456
QY 361 GTCTCTTCA 369
457 GTCTCTTCA 465

RESULT 13

US-08-491-988-6
Sequence 6, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMENON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 40..1284
US-08-491-988-6

Query Match 65.1%; Score 240.2; DB 2; Length 1296;
Best Local Similarity 80.5%; Pred. No. 1.2e-67;
Matches 297; Conservative 0; Mismatches 63; Indels 9; Gaps 1;

QY 1 CAGGTACAGTGCAGCAATCTGGGGCTGAACTAGTGAAGCCTGGCTCCTAGTGAATTT 60
DB 106 CAGGTACAGTGCAGCAAGCCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAAGTGAAGCTG 165
QY 61 TCCTGCAAGGCTTCTGGCTTACACATTCACAGTTAGATATGCGATGATTAAGCAAGCAG 120
DB 166 TCCTGCAAGGCTTCTGGCTTACACATTCACAGTTAGATATGCGATGATTAAGCAAGCAG 225
QY 121 CCGTGAAGTGGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
DB 226 CCGTGAAGTGGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 285
QY 181 AATCAAAAGTTCAAGGCAAGCAACATTCACAGTTAGATATGCGATGATTAAGCAAGCAG 240
DB 286 AATCAAAAGTTCAAGGCAAGCAACATTCACAGTTAGATATGCGATGATTAAGCAAGCAG 345
QY 241 ATGCAAGTGGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
DB 346 ATGCAAGTGGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 405
QY 301 CATTACTATAGCAGCTATATCCGTCCTTGGCTTACTGAGGCGCAAGGCACTCTGGTCACT 360
DB 406 TACTAGGTAAGTAACTA-----CTTTGACTACTGAGGCGCAAGGCACTCTGGTCACT 456
QY 361 GTCTCTTCA 369
DB 457 GTCTCTTCA 465

RESULT 14
US-08-491-988-4
Sequence 4, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMENNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK

STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1356 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 40..1344
US-08-491-988-4

Query Match 65.1%; Score 240.2; DB 2; Length 1356;
Best Local Similarity 80.5%; Pred. No. 1.2e-67;
Matches 297; Conservative 0; Mismatches 63; Indels 9; Gaps 1;

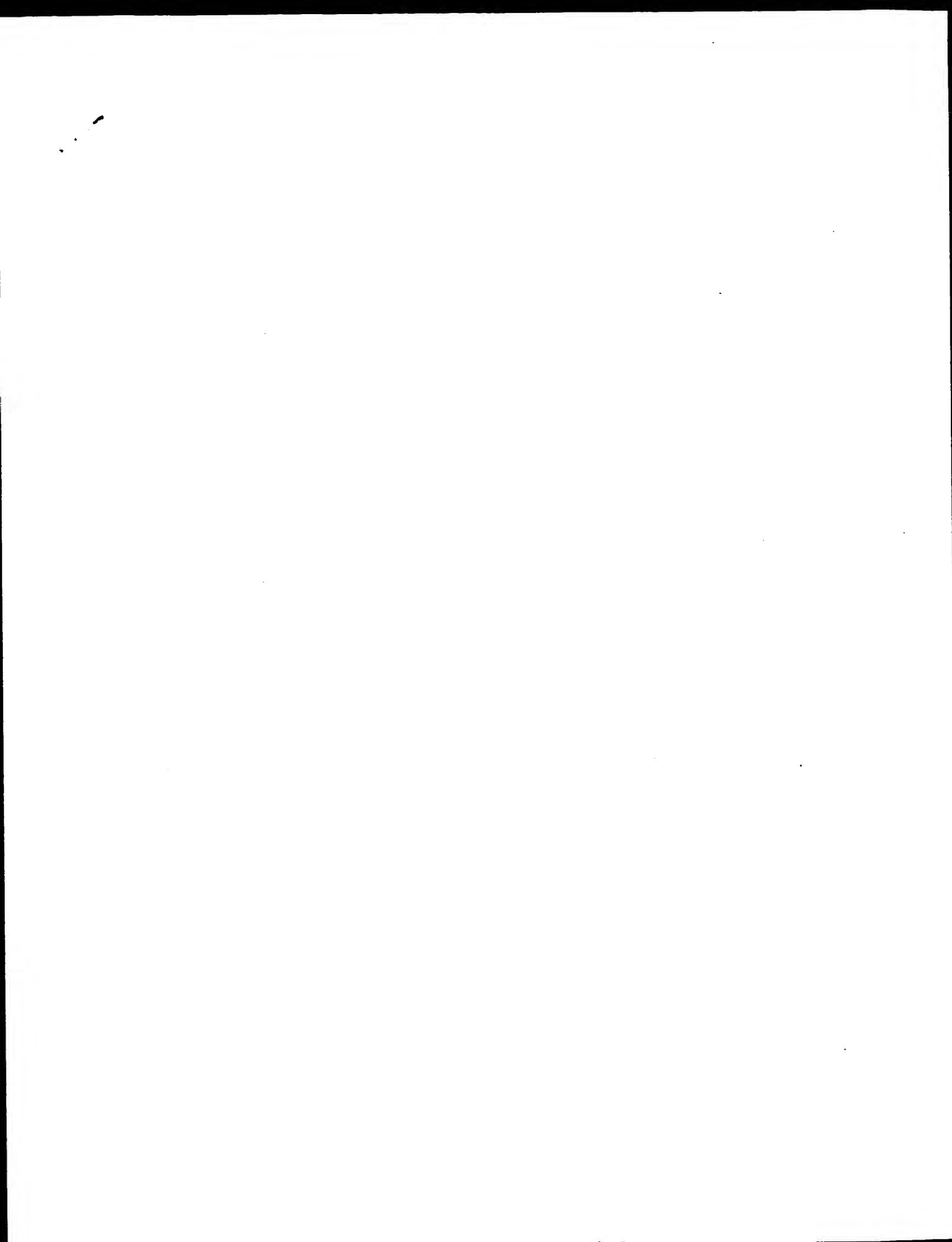
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DB 106 CAGGTACAGTGCAGCAAGCCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAAGTGAAGCTG 165
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DB 286 AATCAAAAGTTCAAGGCAAGCAACATTCACAGTTAGATATGCGATGATTAAGCAAGCAG 345
QY 241 ATGCAAGTGGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
DB 346 ATGCAAGTGGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 405
QY 301 CATTACTATAGCAGCTATATCCGTCCTTGGCTTACTGAGGCGCAAGGCACTCTGGTCACT 360
DB 406 TACTAGGTAAGTAACTA-----CTTTGACTACTGAGGCGCAAGGCACTCTGGTCACT 456
QY 361 GTCTCTTCA 369
DB 457 GTCTCTTCA 465

RESULT 15
US-08-491-988-13
Sequence 13, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMENNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1648 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-08-491-988-13

Query Match 65.1%; Score 240.2; DB 2; Length 1648;
Best Local Similarity 80.5%; Pred. No. 1.3e-67;
Matches 297; Conservative 0; Mismatches 63; Indels 9; Gaps 1;
QY 1 CAGGTACGCTGCGACCATCTGGGGCTGAAGGCTGCTCCTCAGTGAATTT 60
DB 106 CAGGTACGCTGCGACCATCTGGGGCTGAAGGCTGCTCCTCAGTGAATTT 165
QY 61 TCCTGCAAGGCTTCTGGCTACACATTCACAGTTACGATATGCACTGGATTAACAGCAG 120
DB 166 TCCTGCAAGGCTTCTGGCTACACATTCACAGTTACGATATGCACTGGATTAACAGCAG 225
QY 121 CCTGGAATGCGCTTGAAGTGGGATTTATCCTGGAATGTAATTAAGTAC 180
DB 226 CCTGGAATGCGCTTGAAGTGGGATTTATCCTGGAATGTAATTAAGTAC 285
QY 181 AATCAAAAGTTCATGGGAAGCAACACTGACAGCAAAATCCTCCAGCAGCCTAT 240
DB 286 AATCAAAAGTTCATGGGAAGCAACACTGACAGCAAAATCCTCCAGCAGCCTAT 345
QY 241 ATGAGCTCAGACCTGACATCTGAGACTCTGAGTCTATTTCTGCAAGAGATTGG 300
DB 346 ATGAGCTCAGACCTGACATCTGAGACTCTGAGTCTATTTCTGCAAGAGATTGG 405
QY 301 CATTACTATAGCACTATATCCGTCCTTGGCTTACTGGGGCCAAGGCACTTGTCAC 360
DB 406 TACTAGCTAGTACTA-----CTTGTACTACTGGGGCCAAGGCACTTGTCAC 456
QY 361 GTCTCTCA 369
DB 457 GTCTCTCA 465

Search completed: February 28, 2003, 23:11:12
Job time : 80 secs



GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 22:46:39 : Search time 88 Seconds
(without alignments)
2614.947 Million cell updates/sec

Title: US-09-743-482a-13
Perfect score: 369
Sequence: 1 caggtacagctgcagcaatc.....ctctgctactgtctctca 369

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 460893 seqs, 311809382 residues

Total number of hits satisfying chosen parameters: 921786

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCR_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCRUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	242.6	65.7	366	7 US-08-779-784-27	Sequence 27, Appl
2	238.2	64.6	420	9 US-09-911-703-9	Sequence 9, Appl
3	238.2	64.6	9209	9 US-09-911-703-3	Sequence 9, Appl
4	238.2	64.6	9209	9 US-09-905-928-2	Sequence 2, Appl
5	238.2	64.6	18986	9 US-10-109-853-2	Sequence 2, Appl
6	236.6	63.7	420	9 US-09-905-928-5	Sequence 3, Appl
7	235	63.7	429	7 US-08-779-784-25	Sequence 25, Appl
8	234.2	63.5	420	7 US-08-779-784-1	Sequence 1, Appl
9	233.2	63.2	351	7 US-08-779-784-9	Sequence 9, Appl
10	232.2	62.9	736	12 US-10-006-773-12	Sequence 12, Appl
11	232	62.9	426	10 US-09-772-120-7	Sequence 7, Appl
12	229.8	62.3	5691	10 US-09-897-006-11	Sequence 11, Appl
13	226.2	61.3	360	10 US-09-905-243-75	Sequence 75, Appl
14	224.8	60.9	756	9 US-10-237-667-17	Sequence 17, Appl
15	224.8	60.9	756	9 US-10-237-708-17	Sequence 17, Appl
16	224.8	60.9	756	9 US-10-237-866-17	Sequence 17, Appl
17	224.8	60.9	756	9 US-10-237-871-17	Sequence 17, Appl
18	224.8	60.9	756	10 US-09-984-186-17	Sequence 17, Appl
19	224.2	60.8	478	9 US-10-040-739-911	Sequence 911, App

20	224	60.7	920	10 US-09-742-693-28	Sequence 28, Appl
21	223.8	60.7	420	10 US-09-748-960-3	Sequence 3, Appl
22	223	60.4	461	10 US-09-861-294-3	Sequence 3, Appl
23	222.6	60.3	426	10 US-09-584-329A-12	Sequence 12, Appl
24	222.6	60.3	426	10 US-09-855-153-12	Sequence 12, Appl
25	222.6	60.3	426	10 US-09-854-811-12	Sequence 12, Appl
26	222.6	60.3	426	10 US-09-934-773-12	Sequence 12, Appl
27	222.6	60.3	426	10 US-09-963-620-12	Sequence 12, Appl
28	220.8	59.8	381	10 US-09-998-831-6	Sequence 6, Appl
29	220.6	59.8	996	10 US-09-742-693-27	Sequence 27, Appl
30	220.4	59.7	351	7 US-08-779-784-29	Sequence 29, Appl
31	217.2	58.9	348	9 US-09-894-839-3	Sequence 3, Appl
32	217.2	58.9	348	10 US-09-741-843-3	Sequence 3, Appl
33	217	58.8	759	10 US-09-978-752-10	Sequence 10, Appl
34	217	58.8	879	10 US-09-978-752-22	Sequence 10, Appl
35	216.6	58.7	422	10 US-09-753-436-77	Sequence 77, Appl
36	213.2	57.8	482	10 US-09-881-823-19	Sequence 19, Appl
37	213	57.7	354	9 US-10-141-908-1	Sequence 1, Appl
38	212.8	57.7	354	10 US-09-905-243-71	Sequence 71, Appl
39	212.8	57.7	375	10 US-09-978-752-8	Sequence 8, Appl
40	211.8	57.4	405	9 US-09-726-258-36	Sequence 36, Appl
41	211.8	57.4	762	9 US-09-726-258-43	Sequence 43, Appl
42	210.4	57.0	690	10 US-09-995-693-4	Sequence 43, Appl
43	209	56.6	414	9 US-10-146-305-6	Sequence 6, Appl
44	209	56.6	717	8 US-08-940-544-3	Sequence 3, Appl
45	207.6	56.3	351	9 US-09-982-992A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-779-784-27
Sequence 27, Application US/08779784
Patent No. US20020164325A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779, 784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..366
US-08-779-784-27

Query Match

Best Local Similarity 80.5%; Score 242.6; DB 7; Length 366;
Matches 297; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

QY 1 CAGGTACAGCTGACAGCAATCTGGGGCTGAGCTAGAGCCCTGGGCTCCTCAGTGAATTT 60
DB 1 CAGGTACAGCTGACAGCAATCTGGGGCTGAGCTAGAGCCCTGGGCTCCTCAGTGAATTT 60
QY 61 TCCTGCAAGGCTTCTGGCTACACATTCACAGTTACGATATGCACTGGATTAACAGCAG 120
DB 61 TCCTGCAAGGCTTCTGGCTACACATTCACAGTTACGATATGCACTGGATTAACAGCAG 120
QY 121 CCTGGAATGCGCTTGAAGTGGATTTATCCTGGAATGTAATACTAATAGTAC 180
DB 121 CCTGGAATGCGCTTGAAGTGGATTTATCCTGGAATGTAATACTAATAGTAC 180
QY 181 AATCAAAAGTTCAATGGAGGCAACACTGCTGACAGCAAAATCCTCAGACAGCCTAT 240
DB 181 AATCAAAAGTTCAATGGAGGCAACACTGCTGACAGCAAAATCCTCAGACAGCCTAT 240
QY 241 ATGAGAGCTGACAGCTGACATCTGAGAGCTGACGCTATTTCTGTCGAAGAGATTGG 300
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QY 301 CATTAAGTACAGCTATATCCGTCCTTACTGAGGCGCAAGGCAAGCTGCTGACT 360
DB 299 -ACTAGAGTACTGAGGCTGAGTACTTACTTACTGAGGCGCAAGGCAAGCTGCTGACT 357
QY 361 GTCCTCTCA 369
DB 358 GTCCTCTCA 366

RESULT 2

US-09-911-703-9
Sequence 9, Application US/09911703
Publication No. US20020197255A1
GENERAL INFORMATION:

APPLICANT: ANDERSON, Darrell R.

HANNA, Nabill
LEONARD, John E.
NEWMAN, Roland A.
REFE, Mitchell E.
RASPEJTER, William H.
THERAPEUTIC APPLICATION OF CHIMERIC AND
RADIO-LABELLED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
LYMPHOMA

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/911.703

FILING DATE: 25-Jul-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/149,099

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-014

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 420 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 1..420

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 58..420

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Query Match

Best Local Similarity 64.6%; Score 238.2; DB 9; Length 420;
Matches 295; Conservative 0; Mismatches 68; Indels 6; Gaps 1;

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DB 58 CAGGTACAGCTGACAGCAATCTGGGGCTGAGCTAGAGCCCTGGGCTCCTCAGTGAATTT 60
QY 61 TCCTGCAAGGCTTCTGGCTACACATTCACAGTTACGATATGCACTGGATTAACAGCAG 120
DB 118 TCCTGCAAGGCTTCTGGCTACACATTCACAGTTACGATATGCACTGGATTAACAGCAG 117
QY 121 CCTGGAATGCGCTTGAAGTGGATTTATCCTGGAATGTAATACTAATAGTAC 180
DB 178 CCTGGAATGCGCTTGAAGTGGATTTATCCTGGAATGTAATACTAATAGTAC 177
QY 181 AATCAAAAGTTCAATGGAGGCAACACTGCTGACAGCAAAATCCTCAGACAGCCTAT 240
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QY 241 ATGAGAGCTGACAGCTGACATCTGAGAGCTGACGCTATTTCTGTCGAAGAGATTGG 300
DB 298 ATGAGAGCTGACAGCTGACATCTGAGAGCTGACGCTATTTCTGTCGAAGAGATTGG 300
QY 301 CATTAAGTACAGCTATATCCGTCCTTACTGAGGCGCAAGGCAAGCTGCTGACT 360
DB 358 TACTA-----CGGCGTACTGAGTCTTCAATGCTGGGGCGCAGGACACAGGCTCAC 411
QY 361 GTCCTCTCA 369
DB 412 GTCCTCTCA 420

RESULT 3

US-09-911-703-3
Sequence 3, Application US/09911703
Publication No. US20020197255A1
GENERAL INFORMATION:

APPLICANT: ANDERSON, Darrell R.

HANNA, Nabill

LEONARD, John E.

NEWMAN, Roland A.

REFE, Mitchell E.

RASTETTER, William H.
THERAPEUTIC APPLICATION OF CHIMERIC AND
RADIOLABELLED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
LYMPHOMA

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria

STATE: Virginia
COUNTRY: United States
ZIP: 2213-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/911,703
FILING DATE: 25-JUL-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/149,099

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-014

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 9209 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-911-703-3

Query Match 64.6%; Score 238.2; DB 9; Length 9209;
Best Local Similarity 79.9%; Pred. No. 2e-66; Indels 6; Gaps 1;
Matches 295; Conservative 0; Mismatches 68;

QY 1 CAGGTACAGCTGACGACATCTGGGGCTGAAGTGAAGCCTGGTCTCAGTGAAGAATT 60
DB 2458 CAGGTACAGCTGACGACGCTGGGGCTGAAGTGAAGCCTGGTCTCAGTGAAGAATT 2517
QY 61 TCCCTGCAAGGCTTGGCTGACATTCACCACTTACGATATGCGATGATTAACAAGCAG 120
DB 2518 TCCCTGCAAGGCTTGGCTGACATTCACCACTTACGATATGCGATGATTAACAAGCAG 2577
QY 121 CCGGAATAGGCGCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 2578 CCGGATGAGGCGCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2637
QY 181 AATCAAAAGTCAATGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 240
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QY 241 ATGCACTGACGACGCTGACATCTGAGGACTGCGAGTCTATTCTGTGCAAGAGATTGG 300
DB 2698 ATGCACTGACGACGCTGACATCTGAGGACTGCGAGTCTATTCTGTGCAAGAGATTGG 2757
QY 301 CATTACTATAGCAGCTATATCCCTTCTTACTGAGGCGCAAGGCAAGGCAAGGCAAGGCAAGG 360
DB 2758 TACTA-----CGGCGGTGACTGTGTTACTTAATGTCTGGGGCGCAGGAGACAGGTTACC 2811
QY 361 GTCTCTTCA 369

DB 2812 GTCTCTGCA 2820
|||||

RESULT 4
US-09-905-928-2

Sequence 2, Application US/09905928

Publication No. US20030021781A1

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

APPLICANT: Hanna, Nabil

APPLICANT: Leonard, John E.

APPLICANT: Newman, Roland A.

APPLICANT: Reff, Mitchell E.

APPLICANT: Rastetter, William H.

TITLE OF INVENTION: Therapeutic Application of Chimeric and

TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted

TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lymphoma

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince St.

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/905,928

FILING DATE: 17-JUL-2001

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/475,813

FILING DATE: 07-JUN-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/149,099

FILING DATE: 03-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/978,891

FILING DATE: 13-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-158

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 9209 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

POSITION IN GENOME:

CHROMOSOME/SEGMENT: anti-CD20 in TCRAE 8

US-09-905-928-2

Query Match 64.6%; Score 238.2; DB 9; Length 9209;
Best Local Similarity 79.9%; Pred. No. 2e-66; Indels 6; Gaps 1;
Matches 295; Conservative 0; Mismatches 68;

QY 1 CAGGTACAGCTGACGACATCTGGGGCTGAAGTGAAGCCTGGTCTCAGTGAAGAATT 60
DB 2458 CAGGTACAGCTGACGACGCTGGGGCTGAAGTGAAGCCTGGGCGCTGAGTGAAGAATT 2517

QY 61 TCTGCAAGCCTTGGCTACACATTCACAGTACAGTATGACATGATTAACAGCAG 120
|||||
Db 2518 TCTGCAAGCCTTGGCTACACATTCACAGTATGACATGATTAACAGCAG 2577
QY 121 CTTGGAATGCTTGTGATGATGCTGATGATTTATCTGGAATGATTAAGTAC 180
|||||
Db 2578 CTTGGAATGCTTGTGATGATGCTGATGATTTATCTGGAATGATTAAGTAC 2637
QY 181 AATCAAAAGTTGATGGAGGCAAGCAGTACAGCAGCAAAATCTGACAGCAGCTAT 240
|||||
Db 2638 AATCAAAAGTTGATGGAGGCAAGCAGTACAGCAGCAAAATCTGACAGCAGCTAT 2697
QY 241 ATGAGCTGACAGCAGCTGACATCTGAGAGCTGACAGCTATTTCTGTGCAAGAGATTGG 300
|||||
Db 2698 ATGAGCTGACAGCAGCTGACATCTGAGAGCTGACAGCTATTTCTGTGCAAGAGATTGG 2757
QY 301 CATTAATAGCAGCTATATCCCTTTGCTTACTGGGGCCAGAGCAGCTGTGCTACT 360
|||||
Db 2758 TACTA-----CGGCGGTGAGCTGTACTTCAATGTCTGGGGCCAGAGCAGCAGCTGACC 2811
QY 361 GTCTCTTCA 369
|||||
Db 2812 GTCTCTGCA 2820

RESULT 5

US-109-853-2
; Sequence 2, Application US/10109853
; Publication No. US20020192820A1
GENERAL INFORMATION:

APPLICANT: REEF, Mitchell E.
BARNETT, Richard Spence
MCLACHLAN, Karen Rella

TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/109,853

FILING DATE: 01-APR-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/023,715

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/819,866

FILING DATE: 14-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-352

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 18986 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-109-853-2

Query Match

Best Local Similarity 79.9%;

Matches 295; Conservative

Score 238.2; DB 9; Length 18986;

Pred. No. 2.9e-66;

Mismatches 68; Indels 6; Gaps 1;

QY 1 CAGGTACAGCTTCAGCAATCTGGGCTGACATGAGAGGCTGGGCTCTGAGTAAATT 60
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Db 9490 CAGGTACAGCTTCAGCAATCTGGGCTGACATGAGAGGCTGGGCTCTGAGTAAATTG 9549
QY 61 TCTGCAAGCCTTGGCTACACATTCACAGTATGACATGATTAACAGCAG 120
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Db 9550 TCTGCAAGCCTTGGCTACACATTCACAGTATGACATGATTAACAGCAG 9609
QY 121 CTTGGAATGCTTGTGATGATGCTGATGATTTATCTGGAATGATTAAGTAC 180
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Db 9610 CTTGGAATGCTTGTGATGATGCTGATGATTTATCTGGAATGATTAAGTAC 9669
QY 181 AATCAAAAGTTGATGGAGGCAAGCAGTACAGCAGCAAAATCTGACAGCAGCTAT 240
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Db 9670 AATCAAAAGTTGATGGAGGCAAGCAGTACAGCAGCAAAATCTGACAGCAGCTAT 9729
QY 241 ATGAGCTGACAGCAGCTGACATCTGAGAGCTGACAGCTATTTCTGTGCAAGAGATTGG 300
|||||
Db 9730 ATGAGCTGACAGCAGCTGACATCTGAGAGCTGACAGCTATTTCTGTGCAAGAGATTGG 9789
QY 301 CATTAATAGCAGCTATATCCCTTTGCTTACTGGGGCCAGAGCAGCTGTGCTACT 360
|||||
Db 9790 TACTA-----CGGCGGTGAGCTGTACTTCAATGTCTGGGGCCAGAGCAGCAGCTGACC 9843
QY 361 GTCTCTTCA 369
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Db 9844 GTCTCTGCA 9852

RESULT 6

US-09-905-928-5

; Sequence 5, Application US/09905928
; Publication No. US20030021781A1
GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

APPLICANT: Hanna, Nabill

APPLICANT: Leonard, John E.

APPLICANT: Newman, Roland A.

APPLICANT: Reef, Mitchell E.

APPLICANT: Rastetter, William H.

TITLE OF INVENTION: Therapeutic Application of Chimeric and

TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince St.

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/905,928

FILING DATE: 17-JUL-2001

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/475,813

FILING DATE: 07-JUN-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/149,099

FILING DATE: 03-NOV-1993

```

PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/978,891
: FILING DATE: 13-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Teskin, Robin L.
: REGISTRATION NUMBER: 35,030
: REFERENCE/DOCKET NUMBER: 012712-158
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6620
: TELEFAX: 703-836-2021
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 420 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
: POSITION IN GENOME:
: CHROMOSOME/SEGMENT: murine variable region heavy chain
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..420
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 58..420
:
: US-09-905-928-5
:
Query Match      64.1%; Score 236.6; DB 9; Length 420;
Best Local Similarity 79.7%; Pred. No. 1.5e-66;
Matches 294; Conservative 0; Mismatches 69; Indels 6; Gaps 1;

OY 1 CAGGTACAGCTGACCAATCTGGGGCTGAGTGAAGCCTGGTCTCAGTGAATAAT 60
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Db 58 CAGGTACAGCTGACCAATCTGGGGCTGAGTGAAGCCTGGTCTCAGTGAATAAT 117
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OY 61 TCCTGCAAGGCTTCTGGCTACACATTCACGATTAACGATATGCACTGATTAACAGCAG 120
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Db 118 TCCTGCAAGGCTTCTGGCTACACATTCACGATTAACGATTAACGATTAACAGCAG 177
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OY 121 CCTGGAATGGCCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
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Db 178 CCTGGAATGGCCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 181 AATCAAAAGTTCAATGGGAAGGCAACACTGCTGACAGCAAAATCCTCCAGCAGCCTAT 240
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Db 238 AATCAAAAGTTCAATGGGAAGGCAACACTGCTGACAGCAAAATCCTCCAGCAGCCTAT 297
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OY 241 ATGCACTGACAGCCTGACATCTGAGGACTCTGAGTCTATTTCTGTGCAAGAGATTGG 300
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Db 298 ATGCACTGACAGCCTGACATCTGAGGACTCTGAGTCTATTTCTGTGCAAGAGATTGG 357
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OY 301 CATTAATATAGCAGCTATATCCGTCCTTGGCTTACTGGGGCCAAAGCAGCTGTGCTACT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 TACTATA-----CGGCGGTGAGTGGTACTTCAATGCTGTGGGGCCGAGGACACAGGTCACC 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 361 GTCTCTTCA 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 412 GTCTCTGCA 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-08-779-784-25
: Sequence 25. Application US/08779784
: Patent No. US20020164325A1
: GENERAL INFORMATION:
: APPLICANT: Rodriguez, Moses
: APPLICANT: Miller, David J.
: APPLICANT: Asakura, Kunihiko
: TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
: TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: David A. Jackson, Esq.

```

```

STREET: 411 Hackensack Ave, Continental Plaza, 4th
: STREET: Floor
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/779,784
: FILING DATE: 07-JAN-1997
: CLASSIFICATION: 424
:
PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/692,084
: FILING DATE: 08-AUG-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/236,520
: FILING DATE: 29-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REGISTRATION NUMBER: 26,742
: REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-487-5800
: TELEFAX: 201-343-1684
:
: INFORMATION FOR SEQ ID NO: 25:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 429 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..429
:
: US-08-779-784-25
:
Query Match      63.7%; Score 235; DB 7; Length 429;
Best Local Similarity 79.4%; Pred. No. 4.9e-66;
Matches 293; Conservative 0; Mismatches 70; Indels 6; Gaps 1;

OY 1 CAGGTACAGCTGACCAATCTGGGGCTGAGTGAAGCCTGGTCTCAGTGAATAAT 60
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OY 61 TCCTGCAAGGCTTCTGGCTACACATTCACGATTAACGATTAACGATTAACAGCAG 120
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OY 121 CCTGGAATGGCCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
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Db 178 CCTGGAATGGCCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 237
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OY 181 AATCAAAAGTTCAATGGGAAGGCAACACTGCTGACAGCAAAATCCTCCAGCAGCCTAT 240
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Db 238 AATCAAAAGTTCAATGGGAAGGCAACACTGCTGACAGCAAAATCCTCCAGCAGCCTAT 297
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OY 241 ATGCACTGACAGCCTGACATCTGAGGACTCTGAGTCTATTTCTGTGCAAGAGATTGG 300
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Db 298 ATGCACTGACAGCCTGACATCTGAGGACTCTGAGTCTATTTCTGTGCAAGAGATTGG 357
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OY 301 CATTAATATAGCAGCTATATCCGTCCTTGGCTTACTGGGGCCAAAGCAGCTGTGCTACT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 CTTTACTA-----CGGTAGTAGAAGTGTGACTACTGGGGCCAAAGCAGCTGTGCTACA 411
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OY 361 GTCTCTTCA 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 412 GTCTCTTCA 420
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RESULT 8

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Db * 238 AATGAGAAATTTCAAGGAGGAGCCACACTGACAGCAACAATCTCCAGACAGCCCTAC 297
QY 241 ATGACAGTCAGACGCTTGACATCTGACGACCTCTGATTTCTGTGACAGA 294
298 ATGACAGTCAGACGCTTGACATCTGACGACCTCTGATTTCTGTGACAGA 351

RESULT 10

US-10-006-773-12
; Sequence 12, Application US/10006773
; Patent No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Jungmans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti-
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ. ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 736
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)..(430)
; OTHER INFORMATION: 4D4 Heavy chain V region, plus leader
US-10-006-773-12

Query Match 62.9%; Score 232.2; DB 12; Length 736;
Best Local Similarity 79.1%; Pred. No. 5.1e-65;
Matches 292; Conservative 0; Mismatches 68; Indels 9; Gaps 1;

QY 1 CAGGTACAGCTGACGACATCTGGGGCTGAACTAGTGAAGCCTGGCTCTCAGTGAATAATT 60
Db 71 CAGGTACAGCTGACGACATCTGGGGCTGAACTAGTGAAGCCTGGCTCTCAGTGAATAATT 130
QY 61 TCCGTGCAAGGCTTGTGCTACACATTCACCACTTATGCAATGACACTGATTAACAGCAG 120
Db 131 TCCGTGCAAGGCTTGTGCTACACATTCACCACTTATGCAATGACACTGATTAACAGCAG 190
QY 121 CCTGGAATGAGCTTGTGATGATGGGATTTATCCTGGAATGATGAATCTAAGTAC 180
Db 191 CCTGGAATGAGCTTGTGATGATGGGATTTATCCTGGAATGATGAATCTAAGTAC 250
QY 181 AATCAAAAGTTCAATGAGGAGCAACACTGACAGCAACAATCTCCAGACAGCCCTAT 240
Db 251 AATCAAAAGTTCAATGAGGAGCAACACTGACAGCAACAATCTCCAGACAGCCCTAT 310
QY 241 ATGACAGTCAGACGCTTGACATCTGACGACCTCTGATTTCTGTGCAAGGATGG 300
Db 311 ATGACAGTCAGACGCTTGACATCTGACGACCTCTGATTTCTGTGCAAGGATGG 369
QY 301 CATTACTATGACAGCTATATCCGTCCTTTCCTTACTGGGGCCAGAGCACTGTGCTACT 360
Db 370 -----TACTTCCCTTTCTTATGCTATGACTACTGGGGTCAAGGAACCTCATCTACC 421
QY 361 GTCTCTTCA 369
Db 422 GTCTCTCA 430

RESULT 11
US-09-772-120-7
; Sequence 7, Application US/09772120
; Patent No. US20010014328A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; Graziano, Robert
; Keler, Tibor
; TITLE OF INVENTION: Therapeutic Multispecific Compounds

Comprising of Anti-PC
(SYMBOL 97 \F "Symbol") Receptor Antibodies

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/772,120
FILING DATE: 26-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,011
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MXI-064CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..426
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-772-120-7

Query Match 62.9%; Score 232; DB 10; Length 426;
Best Local Similarity 76.9%; Pred. No. 4.5e-65;
Matches 283; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 2 AGTACAGCTGAGCAATCTGGGGCTGAACCTAGTGAAGCCTGGCTCTCAGTGAATAATT 61
Db 59 AGTACAGCTGAGCAATCTGGGGCTGAACCTAGTGAAGCCTGGCTCTCAGTGAATAATT 118
QY 62 CCTGCAAGGCTTGTGCTACACATTCACCACTTATGCAATGACACTGATTAACAGCAGC 121
Db 119 CCTGCAAGGCTTGTGCTACACATTCACCACTTATGCAATGACACTGATTAACAGCAGC 178
QY 122 CTGGAATGAGCTTGTGATGATGGGATTTATCCTGGAATGATGAATCTAAGTAC 181
Db 179 ATGGAAGAAGCCTTGTGATGATGGGATTTATCCTGGAATGATGAATCTAAGTAC 238
QY 182 ATCAAAAGTTCAATGAGGAGCAACACTGACAGCAACAATCTCCAGACAGCCCTATA 241
Db 239 ATCTGAGATTCAAGGAGCAACACTGACAGCAACAATCTCCAGACAGCCCTATA 298
QY 242 TGCAGCTCAGACGCTTGACATCTGACGACCTCTGATTTCTGTGCAAGGATGGC 301
Db 299 TGCAGCTCAGACGCTTGACATCTGACGACCTCTGATTTCTGTGCAAGGATGGC 358
QY 302 ATTACTATGACAGCTATATCCGTCCTTTCCTTACTGGGGCCAGAGCACTGTGCTACTG 361
Db 359 ATTACTATGACAGCTATATCCGTCCTTTCCTTACTGGGGCCAGAGCACTGTGCTACTG 418
QY 362 TCTCTTCA 369
Db 419 TCTCTCA 426

RESULT 12
US-09-897-006-11
; Sequence 11, Application US/09897006
; Patent No. US20020106729A1
; GENERAL INFORMATION:
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Expression Vectors
; FILE REFERENCE: GALA-06415
; CURRENT APPLICATION NUMBER: US/09/897,006
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,851
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 5691
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-006-11

Query Match 62.3%; Score 229.8; DB 10; Length 5691;
Best Local Similarity 84.8%; Pred. No. 8.2e-64;
Matches 238; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 CAGTACAGCTGACGACATCTGGGCTGAACCTAGTGAAGCGTGGCTCAGTGAATAATT 60
DB 2460 CAGTCCAACTGACGAGCTGTGGGCTGAGCTGTGAAGCTGGGACTTCAGTGAAGATA 2519
QY 61 TCCTGCAAGCTTCTGGCTACACATTCACAGTTACGATATGACATGGAATAAAGCAGAG 120
DB 2520 TCCTGCAAGCTTCTGGCTACACATTCACAGTTACGATATGAGGTGAAGCAGAG 2579
QY 121 CCTGGAAGTGGCTGTGAGTGGATTGGGTGATTCCTGGAATAGTAACTAGTAC 180
DB 2580 CCTGGAAGTGGCTGTGAGTGGATTGGGTGATTCCTGGAATAGTAACTAGTAC 2639
QY 181 AATCAAAAGTTCAATGGAGGCAACACTGACAGCAAAATCCTCCAGCAGGCTAT 240
DB 2640 AATGAGAAGTTCAAGGCAAGGCGCACACTGACAGCAAAATCCTCCAGCAGGCTAT 2699
QY 241 ATGACAGCTCAGCAGGCTGACATCTGAGACTCTGCGCTCTATTCTGTGCAAGAGATTGG 300
DB 2700 ATGACAGCTCAGCAGGCTGACATCTGAGACTCTGCGCTCTATTCTGTGCAAGGCTGAC 2759
QY 301 CATTA 305
DB 2760 CATGA 2764

RESULT 13
US-09-905-243-75
; Sequence 75, Application US/09905243
; Patent No. US2002006209A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS

; LOCATION: (1)...(360)
US-09-905-243-75

Query Match 61.3%; Score 226.2; DB 10; Length 360;
Best Local Similarity 78.3%; Pred. No. 3.1e-63;
Matches 289; Conservative 0; Mismatches 68; Indels 12; Gaps 1;

QY 1 CAGTACAGCTGACGACATCTGGGCTGAACCTAGTGAAGCGTGGCTCAGTGAATAATT 60
DB 1 CAGTCCAACTGACGAGCTGTGGGCTGAGCTGTGAAGCTGGGACTTCAGTGAAGATA 60
QY 61 TCCTGCAAGCTTCTGGCTACACATTCACAGTTACGATATGACATGGAATAAAGCAGAG 120
DB 61 TCCTGCAAGCTTCTGGCTACACATTCACAGTTACGATATGAGGTGAAGCAGAG 120
QY 121 CCTGGAAGTGGCTGTGAGTGGATTGGGTGATTCCTGGAATAGTAACTAGTAC 180
DB 121 CCTGGAAGTGGCTGTGAGTGGATTGGGTGATTCCTGGAATAGTAACTAGTAC 180
QY 181 AATCAAAAGTTCAATGGAGGCAACACTGACAGCAAAATCCTCCAGCAGGCTAT 240
DB 181 AATGAGAAGTTCAAGGCAAGGCGCACACTGACAGCAAAATCCTCCAGCAGGCTAT 240
QY 241 ATGACAGCTCAGCAGGCTGACATCTGAGACTCTGCGCTCTATTCTGTGCAAGAGATTGG 300
DB 241 ATGACAGCTCAGCAGGCTGACATCTGAGACTCTGCGCTCTATTCTGTGCAAGAG 295
QY 301 CATTAATGAGTATATCCGCTTCTGCTTACTGAGGCGCAAGCAGCTCTGCTACT 360
DB 296 -----AGACCTACTATGATTCCTGTTTCTTACTGAGGCGCAAGGAGCTCTGCTACT 348
QY 361 GTCTCTTCA 369
DB 349 GTCTCTGCA 357

RESULT 14
US-10-237-667-17
; Sequence 17, Application US/10237667
; Publication No. US20030022308A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES.
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,667
FILING DATE: 10-Sep-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992

FIELD OF INVENTION: NOVEL BIODEGRADABLE ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: Rhône-Poulenc Rorer Inc.
STREET: 500 Atcoia Road, 3C43
CITY: Collegeville

Qy	358	ACGTCCTCTTCA	369
Db	372	ACCGTCCTCTCA	383

Sat Mar 1 08:16:03 2003

us-09-743-482a-13.rnpb

Page 10

Search completed: February 28, 2003, 23:58:06
Job time : 101 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 18:40:08 : Search time 222 Seconds

(without alignments)
3743.186 Million cell updates/sec

Title: US-09-743-482A-13

Perfect score: 369

Sequence: 1 cagctacagctgcagcattc.....ctctgctactgtctctca 369

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	369	21	AAZ88323
2	364.8	98.9	1637	21	AAZ88358
3	252.8	68.5	1925	21	AAAI5019
4	251	68.0	363	18	AAI43806
5	246.6	66.8	831	15	AAOG2957
6	246.4	66.8	368	13	AAO32778
7	243.4	66.0	458	10	AAAG1146
8	243.4	66.0	459	20	AAV82357
9	243.4	66.0	459	22	AAH22070

10	243.4	66.0	491	18	AAI70868	2H7 heavy chain va
11	243.4	66.0	491	19	AAV18557	Mouse 2H7 antibody
12	243.4	66.0	491	19	AAV03926	Mouse 2H7 antibody
13	243.4	66.0	491	19	AAV18593	Mouse 2H7 antibody
14	243.4	66.0	518	18	AAI76316	2H7 antibody heavy
15	243.4	66.0	520	18	AAI751042	Coding sequence fo
16	242.6	65.7	470	17	AAI75134	B-cell lymphoma CH
17	242.6	65.7	470	17	AAI758327	Ber-H2 heavy gamma
18	242.6	65.7	598	17	AAI758328	Ber-H2 heavy gamma
19	242.4	65.7	372	24	ABK24404	Heavy chain DNA fr
20	241.8	65.5	459	8	AAV70971	2H7 VH sequence wh
21	241.8	65.5	1296	15	AAO70660	SCFV PRAS109 and p
22	241	65.3	366	20	AAI82028	Anti-STX1 heavy ch
23	240.2	65.1	423	21	AAO1263	Mouse monoclonal a
24	240.2	65.1	858	15	AAO64817	PRAS11 between H1
25	240.2	65.1	858	15	AAO70658	SCFV PRAS107 and p
26	240.2	65.1	1257	15	AAO70661	SCFV PRAS110 and p
27	240.2	65.1	1259	15	AAO70662	SCFV-BRNase fusio
28	240.2	65.1	1284	18	AAI77139	Single chain antiq
29	240.2	65.1	1356	15	AAO70659	SCFV PRAS108 and p
30	240.2	65.1	1648	15	AAO70665	SCFV-DnaseI fusion
31	240.2	65.1	3058	18	AAI77137	Single chain antiq
32	238.6	64.7	499	17	AAI78509	Heavy chain coding
33	238.2	64.6	1413	21	AAI63531	DNA encoding a dim
34	238.2	64.6	9208	15	AAO65629	Vector contg. TCAR
35	238.2	64.6	19001	12	AAV61793	Traget plasmid Mol
36	237	64.2	458	12	AAO15164	VH186 region of an
37	236.6	64.1	420	15	AAO65631	Murine variable re
38	236.6	64.1	1392	19	AAV70129	Anti-Fas MAb HFE7A
39	236.6	64.1	1392	21	AAV72108	cDNA encoding mous
40	236.6	64.1	1392	21	AAI1546	Murine anti-Fas an
41	236.6	64.1	1392	24	ABIA5925	Mouse humanised an
42	236.6	64.1	1392	24	ABIA8668	Humanised anti-Fas
43	236.2	64.0	416	18	AAI85854	Anti-HMG MAb CTMO
44	236.2	64.0	416	21	AAI26912	MAb CT-M-01 heavy
45	235.6	63.8	363	16	AAO90419	DNA encoding Immun

ALIGNMENTS

RESULT 1	
AAZ88323	AAZ88323 standard; DNA; 369 BP.
XX	XX
AC	AAZ88323:
XX	XX
DT	04-MAY-2000 (First entry)
XX	XX
DE	Anti-zeta-chain antibody 2-B-5 VH-region nucleotide sequence.
XX	XX
KW	Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
KW	complementary determining region; CD8; autoimmunity disease; cytotoxic;
KW	immune deficiency; T-cell malignancy; infectious disease; antiviral;
KW	immunosuppressive; antimicrobial; immune response modulator; NK-cell; ds.
OS	Rattus norvegicus.
XX	XX
PN	WO200003016-A1.
XX	XX
PD	20-JAN-2000.
XX	XX
PF	09-JUL-1999; 99WO-EP04838.
XX	XX
PR	10-JUL-1998; 98EP-0112867.
XX	XX
PA	(CONN-) CONNEX GMBH.
XX	XX
PI	Reiter C;
XX	XX
DR	WPI: 2000-160926/14.
XX	XX
DR	P-PSDB: AAV78325.
XX	XX

ID	Sequence	Score	DB	Length
Db	CACTACTATAGACAGCATATACCGTCCCTTGGTTATGCGGACCAAGCACTCTGGTACCT	79.3	NCBI	792
Qy	361 GCTCTCTC 368			
Db	793 GCTCTCTC 800			
<p>RESULT 3</p> <p>AAA15019 standard: DNA; 1925 BP.</p>				
XX	AAA15019;			
AC	21-Aug-2000 (first entry)			
XX	DNA encoding a CD-20 specific chimeric receptor.			
XX	CD20-specific receptor; CD-20 specific redirected T cell; leukemia;			
KW	CD20+ malignancy; non-Hodgkin's lymphoma; myeloblastic chemotherapy;			
KW	stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis; ss.			
OS	Synthetic.			
OS	Mus sp.			
FT	Key	Location/Qualifiers		
FT	CDS	27..1928		
FT	/*tag=	a		
PN	MO200023573-A2.			
XX	27-Apr-2000.			
PD	20-OCT-1999;	99WO-US24484.		
XX	20-OCT-1998;	98US-0105014.		
PR	(CITY) CITY OF HOPE.			
XX	Raubitschek A, Jensen MC, Wu AM;			
PI	WPI; 2000-339676/29.			
DR	P-PSDB; AAY84965.			
XX	Genetically engineered CD20-specific redirected T cells useful for			
PT	treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+			
PT	acute or chronic leukemia, and autoimmune disease -			
XX	Example 1: Page 50-53; 58pp; English.			
XX	The present sequence encodes a synthetic CD20-specific chimeric			
CC	receptor. The specification describes CD-20 specific redirected T cells			
CC	which express and bear on the cell surface membrane a CD20-chimeric			
CC	receptor comprising an intracellular signaling domain, a transmembrane			
CC	domain and an extracellular domain, the extracellular domain comprising			
CC	a CD20-specific receptor. The genetically engineered CD20-specific			
CC	redirected T cells are useful for treating a CD20+ malignancy, such			
CC	as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, in a			
CC	human patient having previously undergone myelosablative chemotherapy and			
CC	stem cell rescue. The genetically engineered CD20-specific redirected			
CC	T cells are also useful for abrogating an untoward B cell function, such			
CC	as autoimmune disease (lupus or rheumatoid arthritis) in a patient.			
XX	Sequence 1925 BP; 471 A; 554 C; 541 G; 359 T; 0 other;			
SO	Query Match	68.5%; Score 252.8; DB 21; Length 1925;		
	Best Local Similarity	82.3%; Pred. No. 1.2e-64;		
	Matches 303; Conservative 0; Mismatches 62; Indels 3; Gaps 1;			
QY	2 AGGTACACGCTCAGCAATCTGGGCTGAAGTGAAGCTGGCTTCAGTGAATAATTT 61			
Db	460 AGGTACACGCTCAGCAAGTCTGGGCTGAAGTGTGAACCTTGGGGCTTCAGTGAAGATGT 519			
Yy	62 CCTGCAAGGCTTCTGCGCTACACATTTACCAAGTTACGATATATGACGTGATTAACAAGCAGC 121			

Dd			
Oy	520	CCTGCAAGGCTTCTGGCTACACATTTACCACTTACAATATGCACATCGGTAAAGCAGCAC	579
Dd	122	CTGGAAAATGGCCCTTGAGTAGATTGGGTGGATTTATTCCTGGAAAAATGTAATACTAAGTACA	181
Oy	560	CTGGACACAGGCCCTGGAATAGATTGGAGCTATTATTCCAAGAAAATGTGATTACTTCTTACA	639
Oy	132	ATCAAAAGTTCATATGGAGAAGSCAACACTCACTGACAGACAATAATCCCTCAGCAGACCCATA	241
Dd	640	ATCAAAAGTTCATTAAGAGGCGCAGGCCCCCATTTGATCGACAGCAAATCTCCAGCAGACCTTACA	699
Oy	242	TGCACCTGACGAGCGCTGACATCTGAGGACCTGACGCTATTTCTGTGCAAGAGATTGGC	301
Dd	700	TGCAGCTAGACAGCCCTGACATCTTACGAGACTCTGCGACTATTACTGTGCAAGAGCTAATT	759
Oy	302	ATTACTATAGCAGCTATATATCCGTCCTTTGGCTACTGCGGCGCAAGGCACACTCTGGTCACTG	361
Dd	760	ATTACGAGTAGTAGCTA--CTGGTTCTTCGATGTCTGTGGGGCGACGAGGACCAGCGTACCG	816
Oy	362	TCTCTTCA 369	
Dd	817	TCTCCTCA 824	
 RESULT 4 AAT43806 ID AAT43806 standard; cDNA: 363 BP.			
Xx	AAT43806;		
Xx	12-AUG-1997 (first entry)		
Xx	Anti-DNA antibody 4b2 group heavy chain variable region cDNA.		
DE	Heavy chain; variable region; anti-DNA; monoclonal; antibody;		
Kw	4b2 group; hairpin; diagnosis; inflammatory glomerulonephritis;		
Kw	systemic lupus erythematosus; screening; treatment; prevention;		
SLE; disease; consensus; putative; ss.			
Xx	Synthetic.		
OS			
Xx	Key	Location/Qualifiers	
FT	CDS	1..363	
FT		/*lag= a	
FT		/note= "no stop codon given"	
Pn	WO9636361-A1.		
Xx	21-NOV-1996.		
Xx	16-MAY-1996;	96MO-US07113.	
Pf	18-MAY-1995;	95US-0443540.	
Xx	(UNMI) UNIV MICHIGAN.		
Xa	Glick GD, Swanson PC;		
Pi	WPI: 1997-011854/01.		
DR	P-PSDB; AAM07437.		
Xx	Anti-DNA antibody which specifically binds DNA hairpin - useful to		
PT	develop prods. for diagnosis and treatment of disorders, e.g.		
PT	glomerulonephritis or systemic lupus erythematosus		
CC	Example; Fig 9; 10zpp; English.		
CC	The present sequence encodes the heavy chain variable region of the		
CC	group 4b2 putative consensus anti-DNA monoclonal antibody (Mab),		
CC	which has a high affinity for single stranded DNA, low or no		
CC	affinity for double stranded DNA and specifically binds a DNA		
CC	hairpin. The Mab can be used diagnose disorders associated with the		
CC	pathological complexation of DNA, e.g. inflammatory		

CC glomerulonephritis and systemic lupus erythematosus. It can also be
 CC used to generate reagents to screen for pharmaceutical agents, and
 CC treat and/or prevent an above disorder.
 CC The sequence was derived by aligning homologous anti-DNA MAb cDNA,
 CC whose sequences have been published, as well as several MAb of
 CC other specificities obtained from a database search.

XX Sequence 363 BP; 89 A; 89 C; 99 G; 86 T; 0 other:

Query Match 68.0%; Score 251; DB 18; Length 363;

Best Local Similarity 82.1%; Pred. No. 2.4e-64;
 Matches 303; Conservative 0; Mismatches 60; Indels 6; Gaps 1;

QY 1 CAGGTACAGCTGACGCAATCTGGGCTGACCTGATGAGGCTGGCTCTGAGTGAATTT 60
 DB 1 CAGGTACAGCTGACGCAATCTGGGCTGACCTGATGAGGCTGGCTCTGAGTGAATTT 60
 QY 61 TCCGTGCAAGGCTTCTGGCTACACATTCACCAATTACGACTGATGAATGAACAGCAG 120
 DB 61 TCCGTGCAAGGCTTCTGGCTACACATTCACCAATTACGACTGATGAATGAACAGCAG 120
 QY 121 CCTGGAATGAGCTTGTGATGATGGTGGATTTATCTGGAATGTAATACTAAGTAC 180
 DB 121 ACTGACAGGCGCTGTGATGATGGATGATTTATCTGGAATGTAATACTAAGTAC 180
 QY 181 AATCAAAAGTTCAATGGAGGCAACACATCAGACGCAAAATCTCCAGACAGCCTAT 240
 DB 181 AATGAGAGATTCAAGGCAAGGCAACACATCAGACGCAAAATCTCCAGACAGCCTAT 240
 QY 241 ATGCAGCTCAGACAGCTGACATCTGAGAGCTCTGCACTATTTCTGCAAGAGATTGG 300
 DB 241 ATGCAGCTCAGACAGCTGACATCTGAGAGCTCTGCACTATTTCTGCAAGAGATTGG 300
 QY 301 CATTACTATAGCAGCTATATCCCTCTTGTCTACTGCGGCAAGGACATCTGTCACT 360
 DB 301 CATTACTATAGCAGCTATATCCCTCTTGTCTACTGCGGCAAGGACATCTGTCACT 360
 QY 295 CAGTCTACTATAGTACTACTCTCTGCTTGTCTACTGCGGCAAGGACATCTGTCACT 354
 DB 295 CAGTCTACTATAGTACTACTCTCTGCTTGTCTACTGCGGCAAGGACATCTGTCACT 354
 QY 361 GTCCTCTCA 369
 DB 361 GTCCTCTCA 369
 QY 355 GTCCTCTCA 363
 DB 355 GTCCTCTCA 363

RESULT 5

AA062957 standard; DNA: 831 BP.

XX AA062957;

XX 09-SEP-1994 (first entry)

XX Anti-Influenza N10 scfv.

XX Monoclonal antibody N10; target binding polypeptide: scfv;

XX scfv; single chain antibody; protein secretion: FLAG;

XX Escherichia coli; antibody engineering: humanized antibody;

XX Influenza virus; neuraminidase; ss.

XX Not specified.

XX Key Location/Qualifiers

XX sig-peptide 1..66

XX 14-APR-1994.

XX 24-SEP-1993; 93WO-AU00491.

XX 25-SEP-1992; 92AU-0004973.

XX (CSIR), COMMONWEALTH SCI & IND RES ORG.

XX Atwell JL, Colman PM, Hudson PJ, Irving RA, Kortt A;
 PI Lah M, Malbyrl, Power BE;

XX WPI: 1994-135515/16.

XX P-PSDB: AAR52865.

XX New target-binding polypeptide(s) used for diagnosis, etc.

XX having a stable core polypeptide region with at least one

XX target-binding region covalently attached, opt. mutated to alter

XX specificity, etc.

XX Disclosure: Page 41; 67pp; English.

XX An scfv fragment of NC10 (a monoclonal antibody that recognises

XX Influenza virus N9 neuraminidase) was expressed in Escherichia

XX coli. The N-terminal pelb signal peptide directed the scfv

XX fragment into the periplasm where it became associated with the

XX the C-terminus of scfv and used to monitor scfv during

XX purification.

XX Sequence 831 BP; 220 A; 197 C; 214 G; 200 T; 0 other:

Query Match 66.8%; Score 246.6; DB 15; Length 831;

Best Local Similarity 81.6%; Pred. No. 6.1e-63;

Matches 298; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 1 CAGGTACAGCTGACGCAATCTGGGCTGACCTGATGAGGCTGGCTCTGAGTGAATTT 60
 DB 67 CAGGTACAGCTGACGCAATCTGGGCTGACCTGATGAGGCTGGCTCTGAGTGAATTT 60
 QY 61 TCCGTGCAAGGCTTCTGGCTACACATTCACCAATTACGACTGATGAATGAACAGCAG 120
 DB 61 TCCGTGCAAGGCTTCTGGCTACACATTCACCAATTACGACTGATGAATGAACAGCAG 120
 QY 127 TCCGTGCAAGGCTTCTGGCTACACATTCACCAATTACGACTGATGAATGAACAGCAG 186
 DB 127 TCCGTGCAAGGCTTCTGGCTACACATTCACCAATTACGACTGATGAATGAACAGCAG 186
 QY 121 CCTGGAATGAGCTTGTGATGATGGTGGATTTATCTGGAATGTAATACTAAGTAC 180
 DB 121 CCTGGAATGAGCTTGTGATGATGGTGGATTTATCTGGAATGTAATACTAAGTAC 180
 QY 187 CCGTACAGGCGCTGTGATGATGGATGATTTATCTGGAATGTAATACTAAGTAC 246
 DB 187 CCGTACAGGCGCTGTGATGATGGATGATTTATCTGGAATGTAATACTAAGTAC 246
 QY 241 AATCAAAAGTTCAATGGAGGCAACACATCAGACGCAAAATCTCCAGACAGCCTAT 240
 DB 241 AATCAAAAGTTCAATGGAGGCAACACATCAGACGCAAAATCTCCAGACAGCCTAT 240
 QY 301 CATTACTATAGCAGCTATATCCCTCTTGTCTACTGCGGCAAGGACATCTGTCACT 360
 DB 301 CATTACTATAGCAGCTATATCCCTCTTGTCTACTGCGGCAAGGACATCTGTCACT 360
 QY 361 GTCCTCTCA 365
 DB 361 GTCCTCTCA 365
 QY 424 GTCCTCTCA 428
 DB 424 GTCCTCTCA 428

RESULT 6

AA032778 standard; DNA: 368 BP.

XX AA032778;

XX 29-APR-1993 (first entry)

XX Heavy chain variable region of anti-p24 Ab.

XX MAb: monoclonal antibody; AIDS; HIV; infection; disease; immunos assay;

XX p24; antibody-dependent cell-mediated cytotoxicity; macrophages;

XX lymphoid cells.

XX Chimeric; Homo sapiens; Mus musculus.

FH Key Location/Qualifiers
 FT CDS 90..104
 FT /tag= a
 FT /product= CDR7H
 FT 147..197
 FT CDS /tag= b
 FT /product= CDR8H
 FT 294..335
 FT CDS /tag= c
 FT /product= CDR9H
 FT 7..358
 FT /tag= d
 FT /product= "Heavy chain variable region of anti-p24 Ab"
 FT /note= "Heavy chain variable region of anti-p24 Ab"
 EP519866-A.
 PD 23-DEC-1992.
 XX 10-JUN-1993; 93EP-0810445.
 XX 18-JUN-1991; 91EP-0810468.
 XX (CIBA) CIBA GEIGY AG.
 PA
 PI WESTAN J, LAZDINS JK, WOODS-COOK KA, HARDMAN N, HOCHKEPPEL H;
 DR WPI: 1992-426048/52.
 DR P-PSDB: AAR30014.
 PT Monoclonal antibody specific for HIV core protein p24 - mediate
 PT antibody-dependent cell-mediated cytotoxicity, for treating,
 PT preventing and diagnosing HIV infection.
 XX
 PS Example 4: Page 37; 44pp; English.
 CC This sequence represents the heavy chain variable region of
 CC anti-p24 Ab. The coding sequence was isolated by PCR as detailed in
 CC AAQ32769-73, and then sequenced. The rearrangement seen uses the JH3
 CC H-chain J-mingene joining exon (beginning at nucleotide 286) and
 CC includes a continuous ORF encoding a polypeptide sequence formed by
 CC V-D-J exon fusion, characteristic of a functional Ig H-chain gene
 CC rearrangement.
 CC
 XX
 SQ Sequence 368 BP; 97 A; 94 C; 94 G; 83 T; 0 other;
 Query Match 66.8%; Score 246.4; DB 13; Length 368;
 Best Local Similarity 79.3%; Pred. No. 5.4e-63;
 Matches 292; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
 QY 2 AGGTACAGCTGACCAATCTGGGGCTGAACTGAAAGCCCTGGCTCTCAGTGAATAATT 61
 DB 1 AGGTGACAGCTGACCAATCTGGGGCTGAACTGAAAGCCCTGGCTCTCAGTGAATAATT 60
 QY 62 CCTGCAAGGCTTGGCTGACATTCACCACTTACAGATATGACATGATTAATAACAGCAGC 121
 DB 61 CCTGCAAGGCTTGGCTGACATTCACCACTTACAGATATGACATGATTAATAACAGCAGC 120
 QY 122 CTGGAATATGAGTCTGAGTATGGTGGATTTATCTGGAATATGATTAATCTAGTACA 181
 DB 121 CTGGAATATGAGTCTGAGTATGGTGGATTTATCTGGAATATGATTAATCTAGTACA 180
 QY 182 ATCAAAAGTTCATATGGAAGCAACACTGACCTGAGACAAATCTCCAGCAGAGCTTATA 241
 DB 181 ATCAAAAGTTCATATGGAAGCAACACTGACCTGAGACAAATCTCCAGCAGAGCTTATA 240
 QY 242 TGCAGCTCAGAGCTGACATCTGAGACCTGAGATATTTCTGTCAAGAGATTGGC 301
 DB 241 TGCAGCTCAGAGCTGACATCTGAGACCTGAGATATTTCTGTCAAGAGATTGGC 300
 QY 302 ATTACTATAGAGCTTATATCCCTTGGTCTACTGGGCGCAAGGACACTGCTGCTCATG 361
 DB 301 ATTACTATAGAGCTTATATCCCTTGGTCTACTGGGCGCAAGGACACTGCTGCTCATG 360

QY 362 TCTCTTCA 369
 DB 361 TCTCTTCA 368
 RESULT 7
 AAN91146
 ID AAN91146 standard; DNA; 458 BP.
 XX
 AC AAN91146;
 XX
 DT 06-JUL-1990 (first entry)
 XX
 DE 2H7 Vh sequence.
 XX
 KM Antibodies; passive immunisation; pH3-6a; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 39..458
 FT /tag= a
 FT /tag= b
 FT /note= "Sequence homologous to DSP.2"
 FT /tag= c
 FT /note= "JH1 region"
 W08900999-A.
 PD 09-FEB-1989.
 XX 25-JUL-1988; 88WO-US02514.
 XX 24-JUL-1987; 87US-0077528.
 XX (ITGE-) INT GENETIC ENG INC.
 PA
 PI Robinson RR, Liu AY, Horwitz AH, Wall R, Better M;
 DR WPI: 1989-061144/08.
 DR P-PSDB: AAP94780.
 PT Polynucleotide(s) encoding Immunoglobulin molecules -
 PT used for efficient prodn. of chimeric human or non-human or
 PT class switched antibodies.
 XX
 PS Disclosure: ; 7pp; English.
 CC Sequence carries 2H7 Vh region of the chimeric immunoglobulin sequence.
 CC The antibodies are useful in passive immunisation avoiding negative
 CC immune reactions. They are also useful in assaying and in vitro imaging.
 CC
 XX
 SQ Sequence 458 BP; 113 A; 120 C; 112 G; 113 T; 0 other;
 Query Match 66.0%; Score 243.4; DB 10; Length 458;
 Best Local Similarity 81.1%; Pred. No. 4.5e-62;
 Matches 296; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
 QY 1 CAGGTACAGCTGACCAATCTGGGGCTGAACTGAAAGCCCTGGCTCTCAGTGAATAATT 60
 DB 96 CAGGTATATCTACACACACTGCTGGGCTGAGCTGAGAGGCTCGGCTCAGTGAAGATG 155
 QY 61 TCTGCAAGGCTTGGCTGACATTCACCACTTACAGATATGACATGATTAATAACAGCAG 120
 DB 156 TCTGCAAGGCTTGGCTGACATTCACCACTTACAGATATGACATGATTAATAACAGCAG 120
 QY 121 CTGGAATATGAGTCTGAGTATGGTGGATTTATCTGGAATATGATTAATCTAGTACA 180
 DB 216 CTGGAATATGAGTCTGAGTATGGTGGATTTATCTGGAATATGATTAATCTAGTACA 180

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QY 181 AATCAAAAGTTCAATGGGAGGCAACACATCTGACAGACAATTCCTCCAGCAGCCTAT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 276 AATCAGAGAAGTTCAAGGCAAGGCAACACATCTGACAGACAATTCCTCCAGCAGCCTAC 335
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 ATGCAGCTCAGCAGCCTGACATCTGAGAGCTCTGACATCTATTTCTGTGCAAGATTGG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 336 ATGCAGCTCAGCAGCCTGACATCTGAGAGCTCTGAGAGCTCTATTTCTGTGCAAGAG--TG 392
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 CATTACTATATGACATCTATTCCTCCCTTTGCTTACTGAGGCGCAAGCAGCTGTGCTACT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 393 GTGTACTATATGATTAATCTTACTGTGATCTGATGTCTGAGGCGCAAGCAGCAGCTGACC 452
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 GTCTC 365
    |||||
DB 453 GTCTC 457

RESULT 8
AAV82357
ID AAV82357 standard; DNA: 459 BP.
XX
AC AAV82357;
XX
DT 30-MAR-1999 (first entry)
XX
DE Mouse antibody 2H7 heavy chain variable region encoding sequence.
XX
KM pelB pectate lyase; secretion signal; chimeric antibody;
KW heavy chain; B-cell antigen; antibody 2H7; ss.
XX
OS Mus sp.
XX
FH Key 40..459
FT CDS /*tag= a
FT /note= "partial CDS"
XX
XX US846818-A.
XX
PN 08-DEC-1998.
XX
PD 06-JUN-1995; 95US-0472696.
XX
PF 29-MAR-1990; 90US-0501092.
XX
PR 01-NOV-1985; 85US-0793980.
XX
PR 24-JUL-1987; 87US-0077528.
XX
PR 11-JAN-1988; 88US-0142039.
XX
PR 08-DEC-1992; 92US-0987555.
XX
PR 22-FEB-1993; 93US-0020671.
XX
PR 09-DEC-1994; 94US-0357234.
XX
PR 06-JUN-1995; 95US-0472696.
XX
PA (XOMA ) XOMA CORP.
XX
PI Better M, Horowitz AH, Lei S, Liu AY, Robinson RR;
PI Wall R, Wilcox GL;
XX
XX WPI: 1999-059072/05.
XX
DR P-PSDB: AAB89540.
XX
XX
XX pelB pectate lyase signal sequence - and vector for expression of
PT secreted proteins in Gram-negative bacteria
XX
XX Example 4; Fig 21; 98pp; English.
XX
XX The present sequence encodes the mouse antibody 2H7 heavy chain
XX variable region. Antibody 2H7 is specific for human B-cell antigen. The
XX antibody sequence was used to construct a chimeric human-mouse antibody,
XX in the course of the invention. The chimeric antibody is expressed in a
XX secretion vector comprising a pelB pectate lyase secretion signal
XX peptide. The pelB pectate lyase secretion sequence is useful for
XX producing a protein such as a chimeric antibody in a bacterial host.
XX

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SQ Sequence 459 BP; 113 A; 121 C; 112 G; 113 T; 0 other:
Query Match 66.0%; Score 243.4; DB 20; Length 459;
Best Local Similarity 81.1%; Pred. No. 4.5e-62;
Matches 296; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 CAGGTACAGCTGACGATCTGGGGCTGAACTAGTGAAGCCTGGCTCAGTGAATAAT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 97 CAGGCTTATCTACAGCAGCTGCGGGCTGAGCTGTGAGGCTCGGGGCTGATGAATG 156
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 TCCTGCAAGGCTTCTGGCTACACATTTCACAGCTTATGATATGCTGATTAACAGCAG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 157 TCCTGCAAGGCTTCTGGCTACACATTTCACAGCTTATGATATGCTGATTAACAGCAG 216
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CCTGGAATGGCTTGTGATGGATTGATTTATCTGGAATGTAATACTAAGTAC 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 217 CCTGACAGAGGCTTGTGATGGATTGATTTATCTGGAATGTAATACTAAGTAC 276
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 AATCAAAAGTTCAATGGGAGGCAACACATCTGACAGACAATTCCTCCAGCAGCCTAT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 277 AATCAGAGAAGTTCAAGGCAAGGCAACACATCTGACAGACAATTCCTCCAGCAGCCTAC 336
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 ATGCAGCTCAGCAGCCTGACATCTGAGAGCTCTGACATCTATTTCTGTGCAAGATTGG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 337 ATGCAGCTCAGCAGCCTGACATCTGAGAGCTCTGAGAGCTCTATTTCTGTGCAAGAG--TG 393
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 CATTACTATATGACATCTATTCCTCCCTTTGCTTACTGAGGCGCAAGCAGCTGTGCTACT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 394 GTGTACTATATGATTAATCTTACTGTGATCTGATGTCTGAGGCGCAAGCAGCAGCTGACC 453
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 GTCTC 365
    |||||
DB 454 GTCTC 458

RESULT 9
AAH22070
ID AAH22070 standard; DNA: 459 BP.
XX
XX AAH22070;
XX
AC 17-AUG-2001 (first entry)
XX
DT 2H7 heavy chain variable region gene sequence.
XX
DE Human; mouse; chimeric immunoglobulin; chimeric antibody;
KW genetic engineering; primer; ss.
XX
XX Homo sapiens.
XX
OS Mus sp.
XX
XX US6204023-B1.
XX
PN 20-MAR-2001.
XX
PD 06-JUN-1995; 95US-0472691.
XX
PF 18-AUG-1994; 94US-0299085.
XX
PR 29-MAR-1990; 90US-0501092.
XX
PR 08-DEC-1992; 92US-0987555.
XX
PR 25-MAY-1995; 95US-0450731.
XX
PR 01-NOV-1985; 85US-0793980.
XX
PR 27-OCT-1986; 86WO-US02269.
XX
PR 24-JUL-1987; 87US-0077528.
XX
PA (XOMA ) XOMA LTD.
XX
PI Robinson RR, Liu AY, Horwitz AH, Better M, Wall R, Lei S;
PI Wilcox GL;
XX
XX WPI: 2001-289514/30.
XX
DR P-PSDB: AAB96092.
XX
XX

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PT Preparing immunoglobulins or genetically engineered antibodies for the
 PT large scale production of antibodies involves modular assembly of
 PT antibodies through cloning and expression of light and heavy chains
 XX
 XX
 PS Example 4; Fig 21; 100pp; English.

CC The present invention describes a method for preparing an immunoglobulin
 CC that is capable of binding antigen and expression of light and heavy
 CC antibodies through gene cloning and expression of light and heavy
 CC chains. The cloned immunoglobulin gene can be produced by expression in
 CC genetically engineered organisms. The method comprises: (a) expressing,
 CC in a bacterial cell, of a first nucleic acid that encodes a bacterial
 CC signal sequence operably linked to either the heavy chain or heavy chain
 CC fragment, and a second nucleic acid that encodes a bacterial signal
 CC sequence operably linked to either the light chain or light chain
 CC fragment, and obtaining the immunoglobulin from the periplasmic space or
 CC culture medium; or (b) operably linking a nucleic acid encoding a
 CC bacterial signal sequence to a nucleic acid encoding the heavy chain
 CC variable region or the light chain variable region or both of the
 CC variable regions, and obtaining the immunoglobulin from the periplasmic
 CC space or culture medium. The bacterial signal sequences bring about the
 CC transport of the heavy chain or heavy chain fragment, and the light chain
 CC or light chain fragment, or the variable regions through the cytoplasmic
 CC membrane of a bacterial cell. The immunoglobulin comprises: (a) a heavy
 CC chain or heavy chain fragment, and a light chain or light chain fragment;
 CC or (b) a heavy chain variable region and a light chain variable region.
 CC The method is useful for producing genetically engineered antibodies of
 CC desired variable region specificity and constant region properties. The
 CC method is also useful large scale production of human antibodies.
 CC AAH21985 to AAH22082 and AAB98085 to AAB98097 represent sequences used in
 CC the exemplification of the present invention.

XX Sequence 459 BP; 113 A; 121 C; 112 G; 113 T; 0 other;

Query Match 66.0%; Score 243.4; DB 22; Length 459;
 Best Local Similarity 81.1%; Pred. No. 4.5e-62;
 Matches 296; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

OY 1 CAGGTACAGCTGCAGCAATCTGGGCTGACACTAGTGAAGCCCTGGCTCCTCAATGAATTT 60
 DB 97 CAGGCTTATCTACACAGCACTCTGGGCTGAGCTGGAGCGGCGCTCAATGAAGATG 156
 OY 61 TCCTGCAAGGCTTGGCTGACATTTCAACAGTTAGTATGCTGTAAGAGCAG 120
 DB 157 TCCTGCAAGGCTTGGCTGACATTTCAACAGTTAGTATGCTGTAAGAGCAG 216
 OY 121 CCTGCAAGGCTTGGCTGACATTTCAACAGTTAGTATGCTGTAAGAGCAG 180
 DB 217 CTTAGACAGGCTTGGCTGACATTTCAACAGTTAGTATGCTGTAAGAGCAG 276
 OY 181 AATCAAGTTCATAGGAGGACACACTGACAGCAATCTCCGACAGCAGCTTAT 240
 DB 277 AATCAAGTTCATAGGAGGACACACTGACAGCAATCTCCGACAGCAGCTTAT 336
 OY 241 ATGCACTCAGAGCTGACATCTGAGAGCTGCAAGTCTATTTCTGTCAGAGATTGG 300
 DB 337 ATGCACTCAGAGCTGACATCTGAGAGCTGCAAGTCTATTTCTGTCAGAGATTGG 393
 OY 301 CATTACTATAGCAGTATATCCCTGCTTACTGGGGCAGAGCAGCTGCTGCTACT 360
 DB 394 GTGTACTATAGTACTTACTGATGCTGCTGAGGAGCAGGAGCAGGAGCAGC 453
 OY 361 GTCTC 365
 DB 454 GTCTC 458

RESULT 10
 AAT70868
 ID AAT70868 standard: cDNA; 491 BP.
 XX
 AC
 AC AAT70868;
 XX

DT 04-SEP-1997 (first entry)
 XX
 DE 2H7 heavy chain variable sequence.
 XX
 KW Antibody engineering; heavy chain; light chain; chimeric antibody;
 KW passive immunisation; diagnosis; hybridoma; monoclonal antibody;
 KW 2H7; B-cell antigen; Bp35; ss.
 XX
 OS Mus sp.

XX Key Location/Qualifiers
 FH sig_peptide 72..128
 FT /tag= a 129..491
 FT mat_peptide 129..491
 FT /tag= b 393..439
 FT misc_feature 393..439
 FT /tag= c
 FT /note= "JH1 sequence element"
 FT 429..439
 FT /tag= d
 FT /note= "DSP.2 sequence element"
 FT 469..490
 FT /tag= e
 FT /note= "primer JHBSTETI"

PD US5618920-A.

XX 08-APR-1997.

XX 01-NOV-1985; 85US-0793980.

XX 29-MAR-1990; 90US-0501092.

XX 01-NOV-1985; 85US-0793980.

XX 27-OCT-1986; 86MO-US02269.

XX 24-OUL-1987; 87US-0077528.

XX 11-JAN-1988; 88US-0142039.

XX 17-APR-1992; 92US-0870404.

XX 29-APR-1994; 94US-0235225.

XX (XOMA) XOMA CORP.

PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
 PI Wall R, Wilcox GL;

DR WPI: 1997-225473/20.

DR P-PSDB: AAT16343.

XX Secretable immunoglobulin heavy and light chain fragments - capable
 XX of assembling into chimeric antibodies, useful for e.g. passive
 XX immunisation, diagnosis, etc

PS Example 4; Fig 21; 96pp; English.

XX A cDNA clone (AAT70868) codes for the heavy chain variable region
 XX (AAH16343) of the 2H7 mouse monoclonal antibody, which recognises
 XX human B-cell surface antigen Bp35. The sequence was isolated from
 XX a 2H7 cell line cDNA library by PCR amplification. The 2H7 light
 XX chain variable sequence (AAT60869) has also been isolated. The
 XX sequences have been used to construct a human-mouse chimeric
 XX antibody with specificity for the human B-cell antigen.

Sequence 491 BP; 113 A; 153 C; 112 G; 113 T; 0 other;

Query Match 66.0%; Score 243.4; DB 18; Length 491;
 Best Local Similarity 81.1%; Pred. No. 4.6e-62;
 Matches 296; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

OY 1 CAGGTACAGCTGCAGCAATCTGGGCTGACACTAGTGAAGCCCTGGCTCCTCAATGAATTT 60
 DB 129 CAGGCTTATCTACACAGCACTCTGGGCTGAGCTGGAGCGGCGCTCAATGAAGATG 188
 OY 61 TCCTGCAAGGCTTGGCTGACATTTCAACAGTTAGTATGCTGTAAGAGCAG 120
 DB 157 TCCTGCAAGGCTTGGCTGACATTTCAACAGTTAGTATGCTGTAAGAGCAG 216
 OY 121 CCTGCAAGGCTTGGCTGACATTTCAACAGTTAGTATGCTGTAAGAGCAG 180
 DB 217 CTTAGACAGGCTTGGCTGACATTTCAACAGTTAGTATGCTGTAAGAGCAG 276
 OY 181 AATCAAGTTCATAGGAGGACACACTGACAGCAATCTCCGACAGCAGCTTAT 240
 DB 277 AATCAAGTTCATAGGAGGACACACTGACAGCAATCTCCGACAGCAGCTTAT 336
 OY 241 ATGCACTCAGAGCTGACATCTGAGAGCTGCAAGTCTATTTCTGTCAGAGATTGG 300
 DB 337 ATGCACTCAGAGCTGACATCTGAGAGCTGCAAGTCTATTTCTGTCAGAGATTGG 393
 OY 301 CATTACTATAGCAGTATATCCCTGCTTACTGGGGCAGAGCAGCTGCTGCTACT 360
 DB 394 GTGTACTATAGTACTTACTGATGCTGCTGAGGAGCAGGAGCAGGAGCAGC 453
 OY 361 GTCTC 365
 DB 454 GTCTC 458

Db 189 TCCTGCAAGGCTTCTGGCTACACATTTACCAATATGCACTGGGTAAAGCAGACA 248
 QY 121 CCTGGAATGGCCCTTGATGGATTGGTGGATTATCCGGAATGATATAGTAC 180
 Db 249 CCTGAGACAGGCGCTGGATGGATTGGAGCTATTATCCAGGAATGGTATCTCTAC 308
 QY 181 AATCAAAAGTTCAATGGGAAGGCAACACTGACAGCAAAATCCTCCAGCAGCCTAT 240
 Db 309 AATCAGAAAGTTCAAGGGCAGGCGCACACTGATAGACAAATCCTCCAGCAGCCTAC 368
 QY 241 ATGAGCTCAGCAGCCCTGACATCTGAGAGATCTGCACTATTTCTGTGCAAGATTGG 300
 Db 369 ATGAGCTCAGCAGCCCTGACATCTGAGAGATCTGCGCTATTTCTGTGCAAGAG--TG 425
 QY 301 CATTAATATGACAGCTATATCCCTGCTTCTTACTGGGCGCAAGCAGCAGCTGCTAC 360
 Db 426 GTGACTATATGTAACCTTACTGCTGCTGATGTCTGGGCGACAGGAGCAGCGTAC 485
 QY 361 GTCTC 365
 Db 486 GTCTC 490
 RESULT 11
 ID AAV18557 standard; cDNA; 491 BP.
 AC AAV18557;
 DT 05-JUN-1998 (first entry)
 DE Mouse 2H7 antibody heavy chain variable region cDNA.
 KW Mouse; murine; heavy chain; variable region;
 KM immunoglobulin fragment production; Ig fragment production;
 OS monoclonal antibody 2H7; human B-cell surface antigen; ss.
 XX Mus sp.
 XX Key Location/Qualifiers
 FT sig-peptide 72..128
 FT mat-peptide /*tag= a
 FT /129..491
 FT /*tag= b
 XX US5698435-A.
 PD 16-DEC-1997.
 PF 06-JUN-1995; 95US-0467140.
 XX 29-MAR-1990; 90US-0501092.
 PR 01-NOV-1985; 85US-0793980.
 PR 27-OCT-1986; 86WO-US02269.
 PR 24-JUL-1987; 87US-0077528.
 PR 11-JAN-1988; 88US-0142039.
 PR 08-DEC-1992; 92US-0987555.
 PR 18-AUG-1994; 94US-0299085.
 PR 06-JUN-1995; 95US-0467140.
 XX (XOMA) XOMA CORP.
 XX PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
 PI Wall R, Wilcox GL;
 XX MPI: 1998-051492/05.
 DR P-PSDB; AAW47513.
 PT DN4 encoding secretable immunoglobulin fragments - comprising at
 XX least the variable regions of light or heavy chains
 XX Example IV: Fig 21; 98pp: English.
 XX

CC The present sequence was used in the development of a novel method
 CC for the production of an immunoglobulin (Ig) fragment capable of
 CC binding an antigen. The method comprises culturing an E. coli host
 CC that has been transformed with a nucleic acid molecule encoding the
 CC Ig fragment, under conditions so that the Ig fragment is produced
 CC and secreted. The nucleic acid molecule comprises DNA sequences
 CC encoding: (a) pectate lyase secretion signal sequence operably
 CC linked to a DNA sequence encoding at least the variable region of
 CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
 CC operably linked to a DNA sequence encoding at least the variable
 CC region of an Ig light chain, where (a) and (b) are operably linked
 CC to a single prokaryotic promoter to form a chimeric Fab
 CC transcription unit. The method is used to produce chimeric Fab
 CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
 CC against human B-cell surface antigen. The invention provides a
 CC novel approach for producing genetically engineered antibodies of
 CC desired variable region specificity and constant region
 CC properties. The cloned Ig gene products can be produced by
 CC expression in genetically engineered organisms. The application of
 CC chemical gene synthesis, recombinant DNA cloning and production of
 CC specific Ig chains in various organisms provides an effective
 CC solution for the efficient large scale production of human
 CC monoclonal antibodies. The invention also provides a solution to
 CC the problem of class switching antibody molecules.
 CC
 SQ Sequence 491 BP; 113 A; 152 C; 113 G; 113 T; 0 other;

Query Match 66.0%; Score 243.4; DB 19; Length 491;
 Best Local Similarity 81.1%; Pred. No. 4.6e-62;
 Matches 296; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 CAGTACAGCTGACAGCAATCTGGGCTGAGTACAGAGCCTGGGCTCAGTAAATTT 60
 Db 129 CAGGCTTTATCTACACAGCTCTGGGCTGAGCTGGGAGCCTGGGCTCAGTAAATTT 188
 QY 61 TCCTGCAAGGCTTCTGGCTTACACATTTCCAGTTACGATATGCACTGGATAAACAGCAG 120
 Db 189 TCCTGCAAGGCTTCTGGCTTACACATTTCCAGTTACGATATGCACTGGATAAACAGCAG 248
 QY 121 CCTGGAATGGCTTGGATGGGCTGATTTATCCTGGAATGTAATCTAATATAC 180
 Db 249 CCTGAGACAGGCGCTGGATGGATTTGAGCTATTATCCAGAAATGGTGAATCTTGTCTAC 308
 QY 181 AATCAAAAGTTCAATGGGAAGGCAACACTGACAGCAAAATCCTCCAGCAGCCTAT 240
 Db 309 AATCAGAAAGTTCAAGGGCAGGCGCACACTGATAGACAAATCCTCCAGCAGCCTAC 368
 QY 241 ATGAGCTCAGCAGCCCTGACATCTGAGAGATCTGCACTATTTCTGTGCAAGATTGG 300
 Db 369 ATGAGCTCAGCAGCCCTGACATCTGAGAGATCTGCGCTATTTCTGTGCAAGAG--TG 425
 QY 301 CATTAATATGACAGCTATATCCCTGCTTCTTACTGGGCGCAAGCAGCAGCTGCTAC 360
 Db 426 GTGACTATATGTAACCTTACTGCTGCTGATGTCTGGGCGACAGGAGCAGCGTAC 485
 QY 361 GTCTC 365
 Db 486 GTCTC 490

RESULT 12
 ID AAV03926
 AC AAV03926;
 DT 01-JUN-1998 (first entry)
 DE Mouse 2H7 antibody heavy chain variable region cDNA.
 KW Mouse; murine; heavy chain; variable region;
 KM immunoglobulin fragment production; Ig fragment production;
 OS monoclonal antibody 2H7; human B-cell surface antigen; ss.
 XX

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XX  Mus sp.
OS  Key
FH  sig_peptide
FT  72..128
FT  /tag= a
FT  mat_peptide 129..491
FT  /*tag= b
XX  US5693493-A.
PN  02-DEC-1997.
PD  25-MAY-1995;
PE  95US-0450731.
PF  29-MAR-1990;
PR  01-NOV-1985;
PR  27-OCT-1986;
PR  24-JUL-1987;
PR  11-JAN-1988;
PR  08-DEC-1992;
PR  18-AUG-1994;
PR  25-MAY-1995;
XX  95US-0450731.
PA  (XOMA ) XOMA CORP.
PI  Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
PI  Wall R, Wilcox GL;
XX  WPI: 1998-031749/03.
XX  P-PSDB: AAW41070.
PT  Production of chimeric antibody fragments - by culturing E. coli
PT  transformed with dicistronic expression cassette
XX  Example IV; Fig 21; 98pp; English.
XX  The present sequence was used in the development of a novel method
XX  for the production of an immunoglobulin (Ig) fragment capable of
XX  binding an antigen. The method comprises culturing an E. coli host
XX  cell that has been transformed with a nucleic acid molecule encoding the
XX  Ig fragment, under conditions so that the Ig fragment is produced
XX  and secreted. The nucleic acid molecule comprises DNA sequences
XX  encoding: (a) pectate lyase secretion signal sequence operably
XX  linked to a DNA sequence encoding at least the variable region of
XX  an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
XX  operably linked to a DNA sequence encoding at least the variable
XX  region of an Ig light chain, where (a) and (b) are operably linked
XX  to a single prokaryotic promoter to form a dicistronic
XX  transcription unit. The method is used to produce chimeric Fab
XX  molecules, e.g. derived from murine monoclonal antibody 2H7 raised
XX  against human B-cell surface antigen. The invention provides a
XX  novel approach for producing genetically engineered antibodies of
XX  desired variable region specificity and constant region
XX  properties. The cloned Ig gene products can be produced by
XX  expression in genetically engineered organisms. The application of
XX  chemical gene synthesis, recombinant DNA cloning and production of
XX  specific Ig chains in various organisms provides an effective
XX  solution for the efficient large scale production of human
XX  monoclonal antibodies. The invention also provides a solution to
XX  the problem of class switching antibody molecules.
XX  Sequence 491 BP; 113 A; 152 C; 113 G; 113 T; 0 other;
XX  Query Match 66.0%; Score 243.4; DB 19; Length 491;
XX  Best Local Similarity 81.1%; Pred. No. 4,6e-62;
XX  Matches 296; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
QY  1 CAGGTACAGTGCAGCAATCTGGCGCTGAGCTAGTGAAGCTGGCTCCTCAGTGAATAATT 60
DB  129 CAGGCTTATCTACAGCAGCTGCTGGCGCTGAGCTAGTGAAGCTGGCTCCTCAGTGAATAATT 188
QY  61 TCCTGCAAGGCTTCTGCTACACATTCACCACTTACGATATGCAATGAATGAACAGCAG 120

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DB  189 TCTGCAAGGCTTCTGCTACACATTCACCACTTACGATATGCAATGAATGAACAGCAG 248
QY  121 CCTGGAATGAGCCTTGAGTGGATTTGATTTATCCCTGGAATGATTAAGTAC 180
DB  249 CCTAGACAGGCGCTGGAATGATTTGAGCTATTTATCCAGGAATGATGATTAAGTAC 308
QY  181 AATCAAAAGTTCAATGGGAAGCAACACCTGACAGCAAAATCCCTCAGCAGCCTAT 240
DB  309 AATCAGAAGTTCAAGGCGCAGCCACACTGACTGTAGACAAATCCCTCAGCAGCCTAC 368
QY  241 ATGAGCTCAGAGCCGATGATCTGAGACTCTGCACTATTTCTGTGCAAGATTG 300
DB  369 ATGAGCTCAGAGCCGATGATCTGAGACTCTGCACTATTTCTGTGCAAGATTG 425
QY  301 CATTAATATGACAGCTATATCCCTTCTGCTTACTGAGGCAACAGCAGTGTAC 360
DB  426 GTGACTATAGTAACTCTTACTGTACTGTCTGATGCTGTGGGCAAGGACAGCGTAC 485
QY  361 GTCTC 365
DB  486 GTCTC 490

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RESULT 13

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AAV18593
ID  AAV18593 standard; cDNA; 491 BP.
XX
XX  AAV18593;
AC  AAV18593;
XX
DT  05-JUN-1998 (first entry)
XX
DE  Mouse 2H7 antibody heavy chain variable region cDNA.
XX
KW  Mouse; murine; heavy chain; variable region;
KW  immunoglobulin fragment production; Ig fragment production;
KW  monoclonal antibody 2H7; human B-cell surface antigen; ss.
XX
OS  Mus sp.
XX
XX  Key
XX  sig_peptide 72..128
XX  mat_peptide 129..491
XX  /*tag= a
XX  /*tag= b
XX
PN  US5698417-A.
XX
PD  16-DEC-1997.
XX
PF  06-JUN-1995;
XX  95US-0466203.
PR  29-MAR-1990;
PR  01-NOV-1985;
PR  27-OCT-1986;
PR  24-JUL-1987;
PR  11-JAN-1988;
PR  08-DEC-1992;
PR  18-AUG-1994;
PR  25-MAY-1995;
PR  06-JUN-1995;
XX  95US-0466203.
XX
PA  (XOMA ) XOMA CORP.
PI  Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
PI  Wall R, Wilcox GL;
XX  WPI: 1998-051487/05.
XX  P-PSDB: AAW47520.
PT  Production of recombinant immunoglobulin fragment - comprising Fd
PT  molecule and light chain
XX

```

PS Example IV; Fig 21; 98pp; English.

CC The present sequence was used in the development of a novel method
 CC for the production of an immunoglobulin (Ig) fragment capable of
 CC binding an antigen. The method comprises culturing an E. coli host
 CC that has been transformed with a nucleic acid molecule encoding the
 CC Ig fragment, under conditions so that the Ig fragment is produced
 CC and secreted. The nucleic acid molecule comprises DNA sequences
 CC encoding: (a) pectate lyase secretion signal sequence operably
 CC linked to a DNA sequence encoding at least the variable region of
 CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
 CC operably linked to a DNA sequence encoding at least the variable
 CC region of an Ig light chain, where (a) and (b) are operably linked
 CC to a single prokaryotic promoter to form a dicistronic
 CC transcription unit. The method is used to produce chimeric Fab
 CC molecules, e.g., derived from murine monoclonal antibody 2H7 raised
 CC against human B-cell surface antigen. The invention provides a
 CC novel approach for producing genetically engineered antibodies of
 CC desired variable region specificity and constant region
 CC properties. The cloned Ig gene products can be produced by
 CC expression in genetically engineered organisms. The application of
 CC chemical gene synthesis, recombinant DNA cloning and production of
 CC specific Ig chains in various organisms provides an effective
 CC solution for the efficient large scale production of human
 CC monoclonal antibodies. The invention also provides a solution to
 CC the problem of class switching antibody molecules.

XX Sequence 491 BP; 113 A; 152 C; 113 G; 113 T; 0 other;

XX Query Match

Best Local Similarity 66.0%; Score 243.4; DB 19; Length 491;
 Matches 296; Conservative 81.1%; Pred. No. 4.6e-62;

Mismatches 296; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 CAGGTACAGCTGACAGCAATCTGGGCGCTGAACTAGTGAAGCCTGGCTCCTAGTGAATTT 60
 DB 129 CAGGCTTATCTACAGAGCTGTGGGCTGAGAGCTGCTGGGCGCTGAGGAAGTG 188
 QY 61 TCCGTGAAGGCTTCTGGCTACATTCACAGTTAGCATATGAGATGAATGAACAGAG 120
 DB 189 TCCGTGAAGGCTTCTGGCTACATTCACAGTTAGCATATGAGATGAATGAACAGAG 248
 QY 121 CCTGGAAGTGGCTTGAATGATTTGGTGGATTTATCTCGGAATGTAATTAAGTAC 180
 DB 249 CCTGGAAGTGGCTTGAATGATTTGGTGGATTTATCTCGGAATGTAATTAAGTAC 308
 QY 181 AATGAAGTTCATGGAAGGAGCAACCTGACAGCAAAATCCTGACAGAGCTAT 240
 DB 309 AATGAAGTTCATGGAAGGAGCAACCTGACAGCAAAATCCTGACAGAGCTAT 368
 QY 241 ATGAGCTGACAGCTGACATCTGAGAGACTTGCAGTCTATTTCTGCAAGAGATTGG 300
 DB 369 ATGAGCTGACAGCTGACATCTGAGAGACTTGCAGTCTATTTCTGCAAGAGATTGG 425
 QY 301 CATTACTATAGACCTATATTCCTGCTTCTGCTTCTGCTGAGGAGCAAGCACTGGTCACT 360
 DB 426 GTGTACTATATGATTAATCTGCTTCTGCTTCTGCTGAGGAGCAAGCAAGCAAGTCAAC 485
 QY 361 GTCTC 365
 DB 486 GTCTC 490

RESULT 14

AAT36316

ID AAT36316 standard; cDNA; 518 BP.

XX AAT36316;

XX 21-OCT-1997 (first entry)

XX 2H7 antibody heavy chain variable region cDNA.
 XX Immunoglobulin G; IgG; heavy chain; recombinant production;

KW antibody; passive immunisation; serum sickness; anaphylactic shock;
 KW immunoassay; imaging; reagent; complement mediated lysis;
 KW therapy; variable region; ss.

OS Mus spp.

FI Key Location/Qualifiers

FT sig-peptide 71..127

FT mat-peptide 128..490

FT /tag= a

FT /tag= b

US5595989-A.

21-JAN-1997.

01-NOV-1985; 85US-0793980.

29-MAR-1990; 90US-0501092.

01-NOV-1985; 85US-0793980.

27-OCT-1986; 86MO-US02269.

24-JUL-1987; 87US-0077528.

11-JAN-1988; 88US-0142039.

08-DEC-1992; 92US-0967535.

18-AUG-1994; 94US-0299085.

(XOMA) XOMA CORP.

Belter M, Horwitz AH, Lei S, Liu AY, Robinson RR;

Wall R, Wilcox GL;

WPI; 1997-107579/10.

P-PSDB; AAM10588.

Nucleic acid encoding immunoglobulin fragment - comprising

dicistronic transcription unit with pectate lyase signal sequences

Example; Fig 21; 95pp; English.

The present sequence encodes the heavy chain variable region of

a novel polynucleotide molecule encoding an Ig fragment. The DNA

molecule comprises 2 DNA sequences encoding a pectate lyase

secretion signal sequences respectively linked to a DNA sequence

encoding an Ig Fd molecule or Ig light chain, operably linked to a

single prokaryotic promoter so as to form a dicistronic

transcription unit, provided that the Ig fragment can bind an

antigen and is produced and secreted by an E. coli host cell when

the nucleic acid molecule is expressed in the host cell.

The polynucleotide molecule is used for the production of

recombinant antibodies, which can be used for passive immunisation

CC without negative immune reactions (e.g. serum sickness and

anaphylactic shock), in labelled forms as immunoassay or imaging

CC reagents, in complement mediated lysis and for therapeutic

CC purposes when coupled to a toxin or other therapeutic agent.

Sequence 518 BP; 113 A; 152 C; 140 G; 113 T; 0 other;

XX Query Match

Best Local Similarity 66.0%; Score 243.4; DB 18; Length 518;
 Matches 296; Conservative 81.1%; Pred. No. 4.6e-62;

Mismatches 296; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 CAGGTACAGCTGACAGCAATCTGGGCGCTGAACTAGTGAAGCCTGGCTCCTAGTGAATTT 60
 DB 128 CAGGCTTATCTACAGAGCTGTGGGCTGAGAGCTGCTGGGCGCTGAGGAAGTG 187
 QY 61 TCCGTGAAGGCTTCTGGCTACATTCACAGTTAGCATATGAGATGAATGAACAGAG 120
 DB 188 TCCGTGAAGGCTTCTGGCTACATTCACAGTTAGCATATGAGATGAATGAACAGAG 247
 QY 121 CCTGGAAGTGGCTTGAATGATTTGGTGGATTTATCTCGGAATGTAATTAAGTAC 180
 DB 248 CCTGGAAGTGGCTTGAATGATTTGGTGGATTTATCTCGGAATGTAATTAAGTAC 307

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OY 181 AATCAAAAGTTCAATGGGAGGCAACACTCACTGACAGCAAAATCCCTCCAGCAGCCAT 240
DB 308 AATCAGAGTTCAAGGGGCAAGGCAACACTGACTGTAGAAATCTCCAGCAGCAGCTAC 367
OY 241 ATGCAGCTCAGACAGCTGACATCTGAGAGCTCTGCAGTCTATTCTGTGCAAGAGATTGG 300
DB 368 ATGCAGCTCAGACAGCTGACATCTGAGAGCTCTGCAGTCTATTCTGTGCAAGAG---TG 424
OY 301 CATTAATATAGCAGCTATATCCGCTTCTGCTTACTGGGGGCAAGGCACTCTGGTCACT 360
DB 425 GTGTACTATATAGTAACTCTTACTGACTGTGATCTTGATGCTGTGGGCAAGGCAAGGCTGACC 484
OY 361 GTCTC 365
DB 485 GTCTC 489

RESULT 15
AAT51042
ID AAT51042 standard; cDNA; 520 BP.
AC AAT51042;
DT 06-AUG-1997 (first entry)
DE Coding sequence for heavy chain variable region of 2H7.
KW Pectate lyase; signal sequence; Gram-negative bacterium; immunoglobulin;
KW protein production; human; constant region; passive immunisation; toxin;
KW serum sickness; anaphylaxis; sweetener; thaumatin; cytoplasm; periplasm;
KW antibody; Ig; heavy chain; hepatitis; mouse; lung carcinoma; cancer;
KW myeloma cell; B-cell antigen; ss.
OS Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 71..490
XX FT /*tag= a
XX FT /product= heavy chain variable region of 2H7
XX FT /note= "no stop codon given"
XX
XX US5576195-A.
XX PD 19-NOV-1996.
XX
XX PF 01-NOV-1985; 85US-0793980.
XX
XX PR 29-MAR-1990; 90US-0501092.
XX PR 01-NOV-1985; 85US-0793980.
XX PR 27-OCT-1986; 86WO-US02289.
XX PR 24-JUL-1987; 87US-0077528.
XX PR 11-JAN-1988; 88US-0142039.
XX PR 08-DEC-1992; 92US-0987555.
XX PR 22-FEB-1993; 93US-0020671.
XX PR 09-DEC-1994; 94US-0357234.
XX
XX (XOMA ) XOMA CORP.
XX
XX PI Better M, Lei S, Robinson RR, Wilcox GL.
XX WPI: 1997-011254/01.
XX DR P-PSDB; AAM12042.
XX
XX PT Improved prodn. of protein in Gram -ve bacteria using signal
XX PT sequence - from pectate lyase to ensure transport of protein from
XX PT the cytoplasm, esp. for prodn. of antibodies
XX
XX PS Example 4; Flg 21; 86pp; English.
XX
CC This sequence represents the coding sequence for the heavy chain
CC variable region of the 2H7 mouse monoclonal antibody. The 2H7 antibody
CC recognises the human B-cell surface antigen Bp35, which plays a role in

```

```

CC B-cell activation. This sequence was used in a human-mouse chimeric
CC antibody with human B-cell antigen specificity, that was produced using
CC the method of the invention. The method of the invention is for the
CC production of a protein in a Gram-negative bacterium. The method improves
CC on current techniques, by using a vector including DNA encoding the
CC pectate lyase signal sequence (see AAT51042), attached to the sequence
CC encoding the protein for production. The method is especially used to
CC make immunoglobulins (Ig), particularly those with a human constant
CC region, suitable for passive immunisation (without risk of serum sickness
CC or anaphylaxis) or for in vivo/in vitro diagnosis and imaging. The Ig
CC may also be used therapeutically, optionally coupled to toxins, etc.
CC Alternatively the protein to be produced is the sweetener thaumatin. The
CC presence of this signal sequence means that the protein is exported from
CC the cytoplasm and can be recovered from the culture medium or periplasm,
CC in active and correctly folded form. The method allows the class of any
CC antibody to be switched, e.g. most human-human Ig are of M class, easily
CC reduced and aggregated, and these can now be changed to G, A or E
CC classes.
XX
XX Sequence 520 BP; 113 A; 153 C; 141 G; 113 T; 0 other:

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Query Match 66.0%; Score 243.4; DB 18; Length 520;
Best Local Similarity 81.1%; Pred. No. 4,6e-62;
Matches 296; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

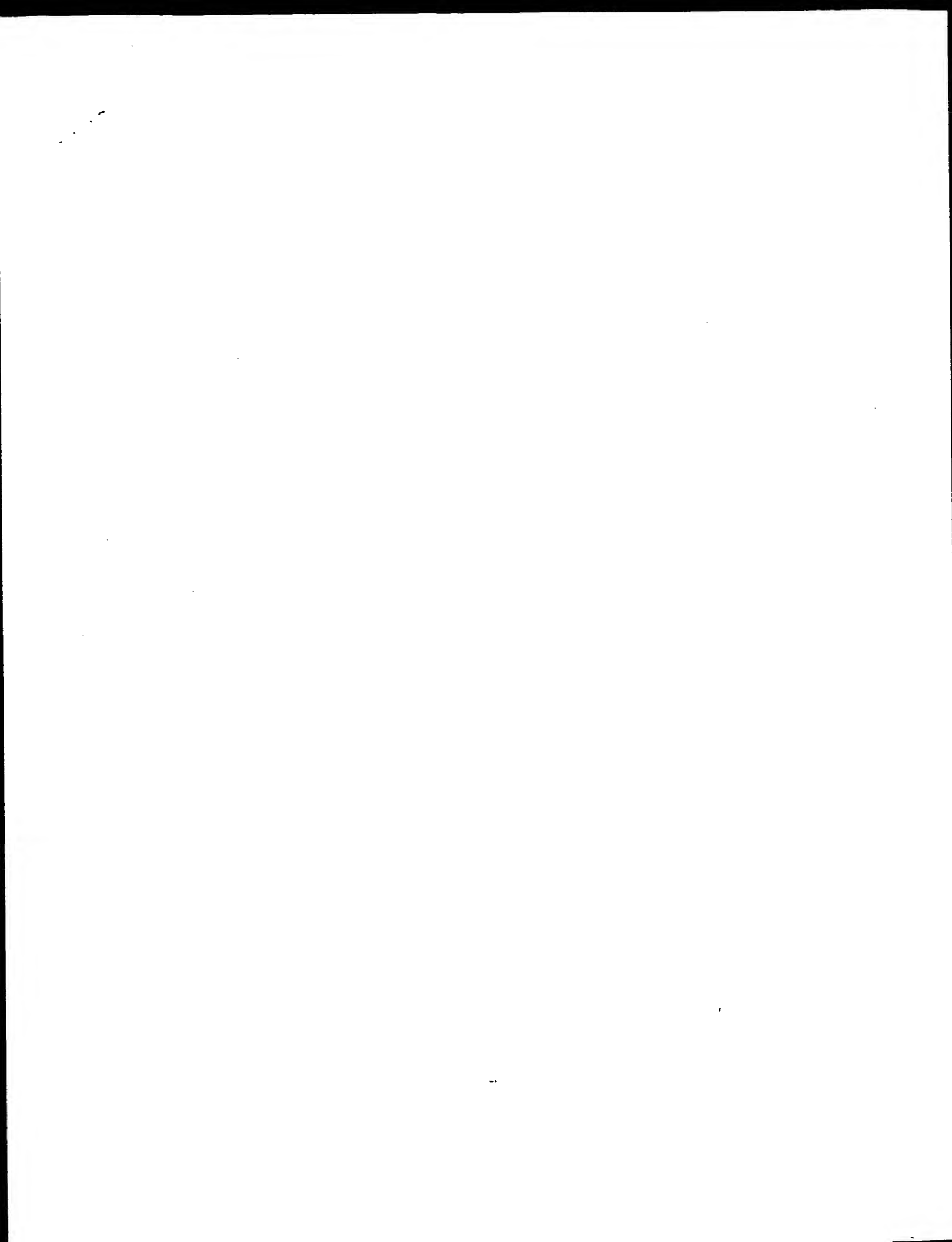
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OY 1 CAGGTACAGCTGCGAGCAATCTGGGGCTGAACTGAGAGCTGGCTCTAGTGAATAT 60
DB 129 CAGGCTTATCTACAGAGCTGTGGGGCTGAGAGCTGGGCTCTCAGTGAAGATG 188
OY 61 TCCTGCAAGGCTTCTGTGCTACACATTCACCAGTATGAGTATGAGTGAATGAAGCAG 120
DB 189 TCCTGCAAGGCTTCTGTGCTACACATTCACCAGTATGAGTATGAGTGAATGAAGCAG 248
OY 121 CCTGGAATGCGCTTGAAGTATGGGATTTATCTGGAATGTAATTAAGTAC 180
DB 249 CTTAGACAGGCGCTGGAATGATTTGAGCTATTTATCCAGAAATGATGATCTTCTAC 308
OY 181 AATCAAAAGTTCAATGGGAGGCAACACTGACAGCAAAATCCCTCCAGCAGCCTAT 240
DB 309 AATCAGAGTTCAAGGGGCAAGGCAACACTGAGTGAACAAATCTCCAGCAGCCTAC 368
OY 241 ATGCAGCTCAGACAGCTGACATCTGAGAGCTCTGCAGTCTATTCTGTGCAAGAGATTGG 300
DB 369 ATGCAGCTCAGACAGCTGACATCTGAGAGCTCTGCAGTCTATTCTGTGCAAGAG---TG 425
OY 301 CATTAATATAGCAGCTATATCCGCTTCTGCTTACTGGGGCAAGCAGCTGTGCTACT 360
DB 426 GTGTACTATATAGTAACTCTTACTGACTGTGAGGCAAGGCAAGGCTGACCC 485
OY 361 GTCTC 365
DB 486 GTCTC 490

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Search completed: February 28, 2003, 22:22:33
 Job time : 226 secs



GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 22:11:14 : Search time 1464 Seconds
(Without alignments)
4082.059 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
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6: em_estpl:*
7: em_estro:*
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9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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21: em_gss_vrt:*
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24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	338.6	91.8	517	12	BF545108 UI-R-C2P-
2	251.8	68.2	794	13	B1150371 602915205
3	246.2	66.7	896	13	B1149320 602848859
4	245.4	66.5	1575	11	AK007918 Mus muscu
5	238.2	64.6	724	13	BC962137 602826902
6	235.4	63.8	672	12	BF580337 602097080

Result No.	Score	Query Match	Length	ID	Description
7	234.8	63.6	896	13	BC963760 602831408
8	233.4	63.3	916	12	BF136295 601781413
9	233.4	63.1	941	12	BF138189 601781314
10	233	63.1	745	12	BC871607 602790090
11	232.6	63.0	920	13	B1647308 603279436
12	232.2	62.9	849	12	BF582051 602099230
13	231.2	62.7	921	14	BO959119 AGENCOURT
14	230.6	62.5	1524	11	AK007826 Mus muscu
15	230.4	62.4	934	12	BF139595 601785525
16	230.2	62.4	358	12	BE850886 uw89h05.y
17	229.4	62.2	406	12	BF016722 uc34h12.y
18	228.8	62.0	689	11	AK007163 Mus muscu
19	227.2	61.6	607	9	AV259014 AV259014
20	227	61.5	739	10	BE284158 601099428
21	226.4	61.4	379	10	AW908776 u157d02.y
22	226.4	61.4	698	12	BF584024 602096264
23	226	61.2	507	12	BF015548 uy23a08.y
24	226	61.2	861	13	BC962366 602827176
25	224.2	60.8	702	13	BC966479 602832989
26	224	60.7	598	13	B1104341 602889919
27	223.8	60.7	723	13	BC969577 602837386
28	223.8	60.7	760	12	BF180474 601805266
29	223	60.4	581	14	BO264833 NISC_ff01
30	223	60.4	596	10	BE310080 601091549
31	222	60.2	700	12	BE540088 602050325
32	221.6	60.1	512	12	BF023434 ux08b04.y
33	221.6	60.1	644	10	BE281961 601099518
34	221.4	60.0	439	10	BE136816 u956b01.y
35	221.2	59.9	793	12	BF136093 601783539
36	221	59.9	933	14	BO929209 AGENCOURT
37	220.8	59.8	685	12	BF136104 601783550
38	220	59.6	464	10	BE368025 601221914
39	219.8	59.6	729	13	B1100304 602885769
40	219.8	59.6	935	12	BO947728 AGENCOURT
41	219.4	59.5	891	12	BF138460 601782916
42	219.2	59.4	670	12	BF141092 601776180
43	219	59.3	847	12	BF165486 601777393
44	218.6	59.2	865	13	BC964435 602832080
45	218.6	59.2	910	14	BO952357 AGENCOURT

ALIGNMENTS

RESULT 1
LOCUS BF545108 517 bp mRNA linear EST 11-DEC-2000
DEFINITION UI-R-C2P-gt-h-03-0-UI.r1 UI-R-C2P Rattus norvegicus cDNA clone
ACCESSION BF545108
VERSION BF545108.1 GI:11636215
KEYWORDS EST.

SOURCE

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

1 (bases 1 to 517)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)

JOURNAL

MEDLINE
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

Email: msocares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at

LN.L. (info@image.llnl.gov). IMAGE ID= 1789298
Seq primer: M13 Forward.

FEATURES

Location/Qualifiers
1..517

/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C2p-gt-h-03-0-UI"
/clone_lib="UI-R-C2p"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pUT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2p) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3' ESTs had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonaldi, Lennon and Soares, Genome Research 6:
791-806, 1996)."

BASE COUNT 142 a 133 c 122 g 120 t
ORIGIN

Query Match 91.8%; Score 338.6; DB 12; Length 517;
Best Local Similarity 96.7%; Pred. No. 1.2e-98;
Matches 357; Conservative 0; Mismatches 9; Indels 3; Gaps 1;

QY 1 CAGGTACAGCTGCAGCAATCTGGGCTGAGTGAAGCTGGTCTCAGTGAATTT 60
DB 83 CAGGTACAGCTGCAGCAATCTGGGCTGAGTGAAGCTGGTCTCAGTGAATTT 142
QY 61 TCCGCAAGGCTTGGCTACATTCACAGTTACGATTCAGTGAATTAACAGCAG 120
DB 143 TCCGCAAGGCTTGGCTACATTCACAGTTACGATTCAGTGAATTAACAGCAG 202
QY 121 CCTGCAAGGCTTGGCTACATTCACAGTTACGATTCAGTGAATTAACAGCAG 180
DB 203 CCTGCAAGGCTTGGCTACATTCACAGTTACGATTCAGTGAATTAACAGCAG 262
QY 181 AATCAAAAGTTCAATGGGAAGCAACACTCAGCAAGCAATCTCCAGACAGCCAT 240
DB 263 AATCAAAAGTTCAATGGGAAGCAACACTCAGCAAGCAATCTCCAGACAGCCAT 322
QY 241 ATGCAAGCTCAGCAGCTGAGACATCTGAGACATCTGAGACATCTGAGACATCT 300
DB 323 ATGCAAGCTCAGCAGCTGAGACATCTGAGACATCTGAGACATCTGAGACATCT 382
QY 301 CATTACTATAGACATATATCCCTTGGCTTACTGAGGCAAGGCACTCTGGTCACT 360
DB 383 TATTACTATAGACATATATCCCTTGGCTTACTGAGGCAAGGCACTCTGGTCACT 439
QY 361 GTCTCTTCA 369
DB 440 GTCTCTTCA 448

RESULT 2
B1150371 794 bp mRNA linear EST 05-JUL-2001
LOCUS B1150371

DEFINITION 602915205F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5065801 5',
mRNA sequence.
ACCESSION B1150371
VERSION B1150371.1 GI:14610372
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerogasthi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 794)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: gcapsb@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LN.L)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LN.L at:
http://image.llnl.gov
plate: L1AM1177 row: 1 column: 02
High quality sequence stop: 794.

FEATURES
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Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5065801"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."
/lab_host="DH10B"
/note="Organ: Lung; Vector: pCMV-Sport6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 185 a 229 c 200 g 180 t
ORIGIN

Query Match 68.2%; Score 251.8; DB 13; Length 794;
Best Local Similarity 82.7%; Pred. No. 2.3e-70;
Matches 305; Conservative 0; Mismatches 52; Indels 12; Gaps 1;

QY 1 CAGGTACAGCTGCAGCAATCTGGGCTGAGTGAAGCTGGTCTCAGTGAATTT 60
DB 99 CAGGTACAGCTGCAGCAATCTGGGCTGAGTGAAGCTGGTCTCAGTGAATTT 158
QY 61 TCCGCAAGGCTTGGCTACATTCACAGTTACGATTCAGTGAATTAACAGCAG 120
DB 159 TCCGCAAGGCTTGGCTACATTCACAGTTACGATTCAGTGAATTAACAGCAG 218
QY 121 CCTGCAAGGCTTGGCTACATTCACAGTTACGATTCAGTGAATTAACAGCAG 180
DB 219 CCTGCAAGGCTTGGCTACATTCACAGTTACGATTCAGTGAATTAACAGCAG 278
QY 219 AATCAAAAGTTCAATGGGAAGCAACACTCAGCAAGCAATCTCCAGACAGCCAT 240
DB 279 AATCAAAAGTTCAATGGGAAGCAACACTCAGCAAGCAATCTCCAGACAGCCAT 338
QY 241 ATGCAAGCTCAGCAGCTGAGACATCTGAGACATCTGAGACATCTGAGACATCT 300
DB 339 ATGCAAGCTCAGCAGCTGAGACATCTGAGACATCTGAGACATCTGAGACATCT 398
QY 301 CATTACTATAGACATATATCCCTTGGCTTACTGAGGCAAGGCACTCTGGTCACT 360
DB 399 TATTACTATAGACATATATCCCTTGGCTTACTGAGGCAAGGCACTCTGGTCACT 446
QY 361 GTCTCTTCA 369
DB 447 GTCTCTTCA 455


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High quality sequence stop: 796.
location/Qualifiers
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BASE COUNT	214 a	262 c	230 g	214 t
ORIGIN				

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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LBNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LBNL at:
http://image.lbl.gov
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High quality sequence stop: 732.
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/organism="Mus musculus"
FEATURES
SOURCE
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BASE COUNT	215 a	226 c	209 g	199 t
ORIGIN				

RESULT	12
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DEFINITION	mRNA sequence.
ACCESSION	BF582051
VERSION	BF582051.1 GI:11655763
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE 1 (bases 1 to 849)
 AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC).
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.

RESULT 13	
B0959119	
LOCUS	
DEFINITION	B0959119 921 bp mRNA linear EST 21-AUG-2002
ACCESSION	AGNCOURT_8953364 NC1_CGAP_Go24 Mus musculus cDNA clone
VERSION	B0959119 IMAGE:6477382 5', mRNA sequence.
KEYWORDS	B0959119.1 GI:22374597
SOURCE	EST. house mouse.
ORGANISM	Mus musculus

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 921)	NIH-MGC	http://mgc.ncbi.nlm.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	
		Unpublished (1999)		
	Contact: Robert Strusberg, Ph.D.	Email: cgabbs@nhi.nih.gov		
	Tissue: Procurement: The Cepko Laboratory			
	cDNA Library Preparation: Life Technologies, Inc.			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MCC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LNA14019 row: d column: 23
 High quality sequence stop: 646.
 Location/Qualifiers

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 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone_image="6477382"
 /clone_id="NCI_CGAP_C024"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: colon; Vector: PCW-SpORF6; Site: 1; NCI;
 Site-2: Salt; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT
 214 a 266 c 219 g 217 t 5 others

Query Match 62.7% Score 231.2; DB 14; Length 921;
 Best Local Similarity 78.2%; Pred. No. 1.2e-63;
 Matches 291; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

QY 1 CAGGTACAGCTGACGCAATCTGGGCTGAACTAGTACAGCTGGCTCCTCAGTGAATTT 60
 DB 58 CAGGTACAGCTGACGCAATCTGGGCTGAACTAGTACAGCTGGCTCCTCAGTGAATTT 117
 QY 61 TCCTCCAGGCTTGGCTGACATTCACGCTTACGATATGACCTGGATTAACAGCAG 120
 DB 118 TCCTCCAGGCTTGGCTGACATTCACGCTTACGATATGACCTGGATTAACAGCAG 177
 QY 121 CCTGGAATGGCTTGAATGATGGGCTGATTTATCTGGAATGGTAACTAAGTAC 180
 DB 178 CCTGGAATGGCTTGAATGATGGGCTGATTTATCTGGAATGGTAACTAAGTAC 237
 QY 181 AATCAAAAGTTCATGGAAGGCAACACTCTGACGCAACAATCCTCCAGCAGCCTAT 240
 DB 238 AATGAATTTTCAGGCTGAAAGCCACACTGACGACATCTCCTCAGCAGCCTAT 297
 QY 241 ATGACGCTGACGCTGACATCTGAGAGCTGACGCTGATTTCTGTGCAAGAGATTGG 300
 DB 298 GTGATCTTACGACGCTGACATCTGAGAGCTGACGCTGATTTCTGTGCAAGAGATTGG 357
 QY 301 CATT---ACTATGACGCTGATATCTGCTTCTTCTTACTGAGGCAAGCAGCTGCTG 357
 DB 358 TATTACAACGATGATACCTCTTCTTCTTACTGAGGCAAGCAGCAGCTGCTG 417
 QY 358 ACTGCTCTTCA 369
 DB 418 ACAGCTCTCTCA 429

RESULT 14
 AK007826
 LOCUS 1524 bp mRNA linear HTC 19-JAN-2002
 DEFINITION Mus musculus 10 day old male pancreas cDNA, RIKEN full-length
 (J558 family), full insert sequence.
 ACCESSION AK007826
 VERSION AK007826.1 GI:12841627
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (strain: C57BL/6J) 10 day old male pancreas cDNA to
 mRNA, clone_id: RIKEN full-length enriched mouse cDNA library
 clone:1810048H17.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 Carninci, P. and Hayashizaki, Y.
 AUTHORS High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
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 AUTHORS

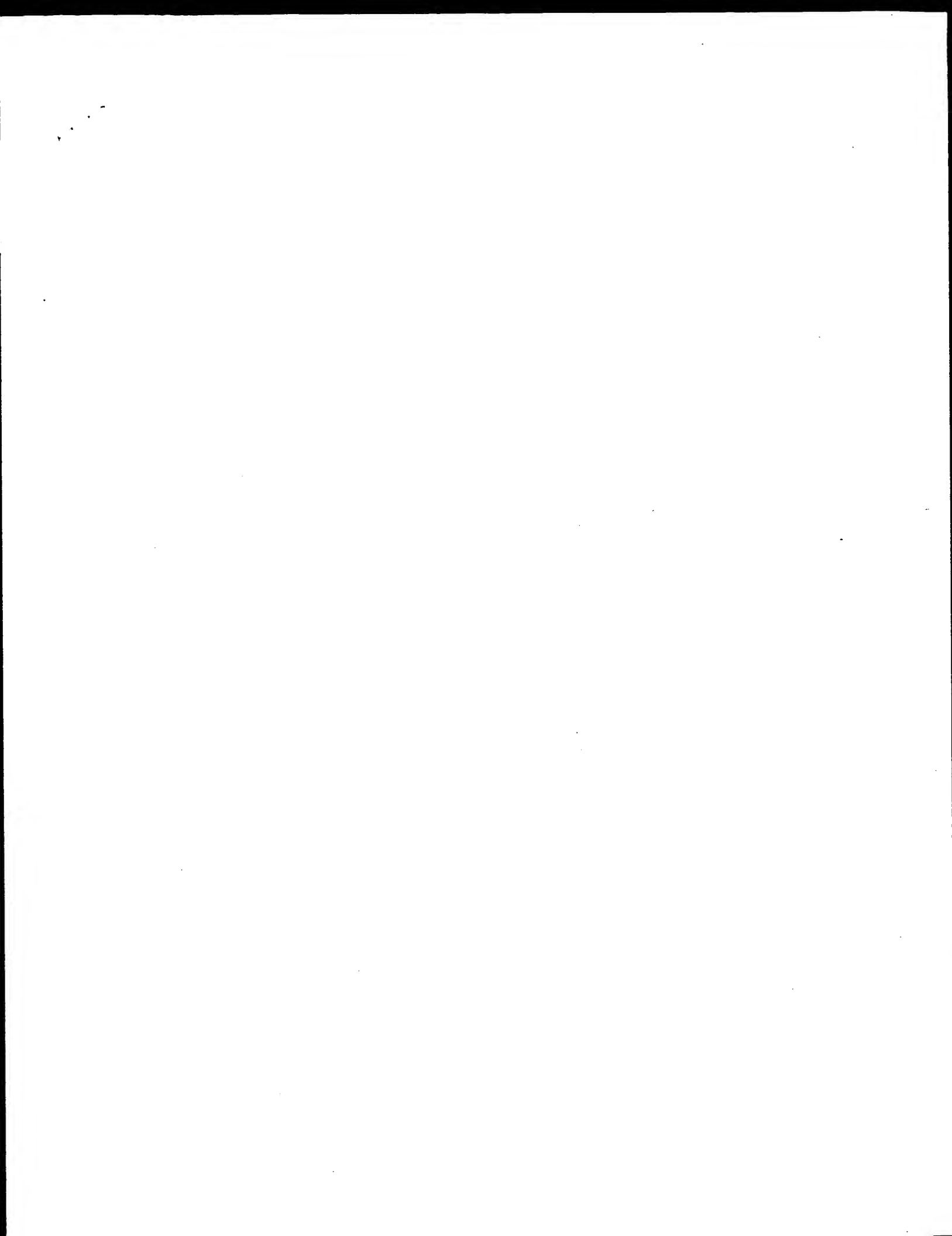
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 AUTHORS

Sat Mar 1 08:16:06 2003

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Page 11

Job time : 1473 secs



GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-743-482a-13

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

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14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

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19: em_mu:*

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22: em_ov:*

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29: em_vl:*

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32: em_hlg_other:*

33: em_hlg_mus:*

34: em_hlg_pln:*

35: em_hlg_rtd:*

36: em_hlg_man:*

37: em_hlg_vrl:*

38: em_sy:*

39: em_hgo_hum:*

40: em_hgo_mus:*

41: em_hgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	369	6 AX006746	AX006746 Sequence
2	364.8	98.9	1637	6 AX006750	AX006750 Sequence
3	300	81.3	377	10 R18GM01	X78893 R.norvegicus
4	294.4	79.8	158266	2 AC109704	AC109704 Rattus no
5	294.4	79.8	160122	2 AC097697	AC097697 Rattus no
6	278	75.3	336	10 R18GM01	X78893 R.norvegicus
7	265.8	72.0	293	10 R18GM01	X78893 R.norvegicus
8	257	69.6	738	10 MMU0581	U40581 Mus musculus
9	255.4	69.2	387	10 AY058907	AY058907 Mus musculus
10	251.8	68.2	497	10 S73918	S73918 Igm-mu heav
11	251.8	68.2	592	10 AF439575	AF439575 Mus muscu
12	251.8	68.2	3260	10 MMSB6718	MMSB6718 Mouse reart
13	250.2	67.8	592	10 AF439570	AF439570 Mus muscu
14	250.2	67.8	592	10 AF439571	AF439571 Mus muscu
15	250.2	67.8	592	10 AF439572	AF439572 Mus muscu
16	250.2	67.8	592	10 AF439573	AF439573 Mus muscu
17	250.2	67.8	592	10 AF439574	AF439574 Mus muscu
18	250.2	67.8	593	10 AF439565	AF439565 Mus muscu
19	249.6	67.6	369	10 AF163742	AF163742 Mus muscu
20	249	67.5	369	10 MMV20552B	MMV20552B Sequence
21	249	67.5	387	10 AB057945	AB057945 Mus muscu
22	248.8	67.4	592	10 AF316522	AF316522 Mus muscu
23	248.6	67.4	592	10 AF439566	AF439566 Mus muscu
24	248.6	67.4	592	10 AF439567	AF439567 Mus muscu
25	248.6	67.4	592	10 AF439568	AF439568 Mus muscu
26	248.6	67.4	592	10 AF439573	AF439573 Mus muscu
27	248.6	67.4	592	10 AF439574	AF439574 Mus muscu
28	248.2	67.3	369	10 MMV20302A	MMV20302A Sequence
29	247.8	67.2	363	6 AR100552	AR100552 Sequence
30	247.6	67.1	382	10 AF434687	AF434687 Mus muscu
31	247.4	67.0	369	10 MMV20512B	MMV20512B Sequence
32	246.6	66.8	831	6 AR063209	AR063209 Sequence
33	246.6	66.8	831	6 MMU10410	MMU10410 Mus musculu
34	246.4	66.8	368	6 A22588	A22588 M.musculus
35	246.2	66.7	352	10 MMU26465	MMU26465 Mus musculu
36	245.8	66.6	369	10 MMV20652B	MMV20652B Mus muscu
37	245.8	66.6	450	10 AF029236	AF029236 Mus muscu
38	245.6	66.6	351	10 AF316523	AF316523 Mus muscu
39	245.6	66.6	360	10 MMHCVR1	X75095 M.musculus
40	245.2	66.4	363	10 MDIGMVAR	MDIGMVAR M.domesticu
41	245	66.4	369	10 MDIGMVAR	MDIGMVAR M.domesticu
42	244.8	66.3	366	10 MIGHPS6A	X68122 M.musculus
43	244.8	66.3	369	10 AF321931	AF321931 Mus muscu
44	244.8	66.3	369	10 MMU59154	MMU59154 Mus musculu
45	244.8	66.3	1075	10 M05IGHYIE	L09596 Mouse (hybr

ALIGNMENTS

RESULT 1

AX006746

LOCUS AX006746

DEFINITION Sequence 13 from Patent WO0003016.

ACCESSION AX006746

VERSION AX006746.1 GI:9994789

KEYWORDS

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 369)

REITER,C.

AUTHORS Immunological reagent specifically interacting with the

TITLE

extracellular domain of the human zeta chain
Patent: WO 0003016-A 13 20-JAN-2000;
CONNEX GMBH (DE); REITER CHRISTIAN (DE)

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ORIGIN				

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Matches 369; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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121 CCTGGAATGGCCTTGAGTGGATTGCGGTGGATTATCCTGGAATGGTAATACTAAGTAC 180

101 AA1CAGAGG11CA1GGGAAAGGCAACAC1CAC1GGAGACAAAC1CCAGGACAGCC1AT 24

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db 301 CATTACTATAGCAGCTATATCCGTCCTTTGCTTACTGGGGCCAAAGGCACTGTGTCCT 36

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AX006750	AX006750	1637 bp	DNA	118833	DATE 06-SEP-2000
LOCUS					

BASE COUNT ,	398 a	404 c	436 g	399 t
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ORIGIN

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Best Local Similarity	99.5%;	Pred. No. 4.4e-108;		
Matches 366;	Conservative	0;	Mismatches 2;	Indels 0;
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Db 433 CAGGTACAGCTGCAGCAATCTGGAGCTGAGCTAGTGAAGCCTGGGTCCTCAGTGAATAAT 499

433 1C1GCAAGG11C1GG1ACACAA1CACCG1AACCA1A1GCA1GGAA1AAAACAGGCG 22

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241 ATGCAGCTCAGCAGCTGACATCTGAGGACTCTGAGTCTATTCTGTGCAAGAGATTGG 30

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Db 1 CTGACGAGATCAGGACTGAAGTGTGAGAGCTGCTGCTCAGTGAATAATTCCTGCAAG 60
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QY 70 GCTTCTGGTACACATTCACCAAGTTAGCATATGCACTGGATGAACACAGCCTGGAAAT 129
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Db 61 GCTTCTGGTACACCTTCACCAAGTTAGCATATGCACTGGATGAACACAGCCTGGAAAT 120
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QY 130 GGGCTTGGATGGATGGTGGATTTATCTCTGGAATGGTATACTAATACATCAAAAG 189
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QY 250 AGCAGCTGACATCTGAGAGCTCTGACGTATTTCTGTGCAAGATTTGCAATTACTAT 309
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QY 310 AGCAGTATATATCCCTCTGCTTACCTGAGGAGGCAAGGCACTGCTGCTCTCTCA 369
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RESULT 4
AC109704/c 158266 bp DNA linear HTG 13-JUL-2002
LOCUS      Rattus norvegicus clone CH230-210K20, *** SEQUENCING IN PROGRESS
DEFINITION
AC109704 158266 bp DNA linear HTG 13-JUL-2002
AC109704.3 GI:21738017
VERSION    HTG: HTGS PHASE1.
KEYWORDS   Norway rat.
SOURCE     Rattus norvegicus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
1 (bases 1 to 158266)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Aldbrooks,S.L., Amaralunga,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbier,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
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DeLahey,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
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Earnhardt,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabriel,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,

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TITLE
JOURNAL
REFERENCE
AUTHORS
Worley,K.C.
Direct Submission
Submitted (07-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 158266)
Worley,K.C.
Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:18864930.
----- genome center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GOCX
Center clone name: CH230-210K20
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 93498 bases at least Q40
Consensus quality: 101443 bases at least Q30
Consensus quality: 109649 bases at least Q20
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a working draft sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1445: contig of 1445 bp in length
* 1446: gap of unknown length
* 1546: contig of 1228 bp in length
* 2774: gap of unknown length
* 2874: contig of 1276 bp in length
* 4150: gap of unknown length
* 4250: contig of 1191 bp in length

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5441 5540: gap of unknown length
5541 6829: contig of 1289 bp in length
6830 6830: gap of unknown length
6830 8474: contig of 1545 bp in length
8475 8574: gap of unknown length
8574 10438: contig of 1864 bp in length
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18852 20057: contig of 1206 bp in length
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20158 21818: contig of 1661 bp in length
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21919 22934: contig of 1016 bp in length
22935 23034: gap of unknown length
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24858 26326: contig of 1469 bp in length
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26427 28255: contig of 1829 bp in length
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30801 32191: contig of 1391 bp in length
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32292 33413: contig of 1122 bp in length
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33515 36255: contig of 2742 bp in length
36256 36355: gap of unknown length
36356 37528: contig of 1173 bp in length
37529 37628: gap of unknown length
37629 38806: contig of 1178 bp in length
38807 38906: gap of unknown length
38907 41001: contig of 2095 bp in length
41002 41101: gap of unknown length
41102 42809: contig of 1708 bp in length
42810 42909: gap of unknown length
42910 44991: contig of 2082 bp in length
44992 45091: gap of unknown length
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47375 47474: gap of unknown length
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58732 61059: contig of 2328 bp in length
61060 61159: gap of unknown length
61160 64177: contig of 3018 bp in length
64178 64277: gap of unknown length
64279 68019: contig of 3742 bp in length
68020 68120: gap of unknown length
68120 70558: contig of 2439 bp in length
70559 70658: gap of unknown length
70659 72237: contig of 1579 bp in length
72238 72337: gap of unknown length
72338 74896: contig of 2559 bp in length
74897 74996: gap of unknown length

74997 78107: contig of 3111 bp in length
78108 78207: gap of unknown length
78208 81500: contig of 3293 bp in length
81501 81600: gap of unknown length
81601 83452: contig of 1852 bp in length
83453 83552: gap of unknown length
83553 86622: contig of 3070 bp in length
86623 86722: gap of unknown length
86723 89627: contig of 2905 bp in length
89628 89727: gap of unknown length
89728 93306: contig of 3579 bp in length
93307 93406: gap of unknown length
93407 95904: contig of 2498 bp in length
95905 96004: gap of unknown length
96005 99160: contig of 3156 bp in length
99161 99260: gap of unknown length
99261 102393: contig of 3133 bp in length
102394 102493: gap of unknown length
102494 106532: contig of 4039 bp in length
106533 106632: gap of unknown length
106633 108992: contig of 2360 bp in length
108993 109093: gap of unknown length
109093 113971: contig of 4879 bp in length
113972 114071: gap of unknown length
114072 117449: contig of 3378 bp in length
117450 117549: gap of unknown length
117550 123298: contig of 5749 bp in length

Query Match 79.88; Score 294.4; DB 2; Length 158266;
Best Local Similarity 99.7%; Pred. No. 7.2e-85;
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGTACAGCGGCAATCTGGGGCTGAAGTGAAGCTGGGTCTCGTAATTT 60
Db 86482 CAGGTACAGCGGCAATCTGGGGCTGAAGTGAAGCTGGGTCTCGTAATTT 86423
QY 61 TCCTGCAAGGCTTGGCTACACATTCACAGTTAGTATGATGATTAACAGCAG 120
Db 86422 TCCTGCAAGGCTTGGCTACACATTCACAGTTAGTATGATGATTAACAGCAG 86363
QY 121 CCTGCAAGTGGCTTGGCTACATTCACAGTTAGTATGATGATTAACAGCAG 180
Db 86362 CCTGCAAGTGGCTTGGCTACATTCACAGTTAGTATGATGATTAACAGCAG 86303
QY 181 AATCAAAAGTTCATGGGAAGCAACACTCAGTCAAGCAATCTCAGCAGACGCTAT 240
Db 86302 AATCAAAAGTTCATGGGAAGCAACACTCAGTCAAGCAATCTCAGCAGACGCTAT 86243
QY 241 ATGCAGCTCAGCAGCTGACATCTGAGAGCTCTGAGTATTTCTGTGCAAGAGA 296
Db 86242 ATGCAGCTCAGCAGCTGACATCTGAGAGCTCTGAGTATTTCTGTGCAAGAGA 86187

RESULT 5
AC097697
LOCUS
DEFINITION
Rattus norvegicus clone CH230-144016, *** SEQUENCING IN PROGRESS
*** 68 unordered pieces.

AC097697 160122 bp DNA linear HTG 12-JUL-2002
AC097697.4 GI:21729830
AC097697
VERSION
KEYWORDS
HTG: HTGS_PHASE1.
SOURCE
Norway rat.
ORGANISM
Rattus norvegicus

REFERENCE
AUTHORS
1 (bases 1 to 160122)
Mazny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralunga,H.C., Are,J.R., Ayale,M., Banks,T.,
Barberia,J., Benton,J., Bimaye,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brileva,M., Brown,M., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,

Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthett, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsl, F., Howard, S., Huber, J., Hui, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Louised, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, U., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenko, S., Ogih, M., Okunolu, G., Orangunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojurokan, I., Rolfe, M., Ruiz, S., Savary, G., Scheraga, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, I., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wleczky, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.

Unpublished
Direct Submission
2 (bases 1 to 160122)
Worley, K.C.
Submitted (21-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 160122)
Worley, K.C.
Direct Submission
Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:17973776.

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GIKY
Center clone name: CH230-144016
Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 102481 bases at least Q40
Consensus quality: 108188 bases at least Q30
Consensus quality: 112424 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
* consists of 68 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
* be preserved.

1	1055:	contig of 1055 bp in length
*	1056	1155: gap of unknown length
*	1156	2674: contig of 1519 bp in length
*	2675	2774: gap of unknown length
*	2775	3972: contig of 1198 bp in length
*	3973	4072: gap of unknown length
*	4073	5115: contig of 1043 bp in length
*	5116	5215: gap of unknown length
*	5216	6238: contig of 1023 bp in length
*	6239	6338: gap of unknown length
*	6339	7600: contig of 1262 bp in length ;
*	7601	7700: gap of unknown length
*	7701	9411: contig of 1711 bp in length
*	9412	9511: gap of unknown length
*	9512	10678: contig of 1167 bp in length
*	10679	10778: gap of unknown length
*	10779	12569: contig of 1791 bp in length
*	12570	12659: gap of unknown length
*	12670	13842: contig of 1173 bp in length
*	13843	13942: gap of unknown length
*	13943	15522: contig of 1580 bp in length
*	15523	15622: gap of unknown length
*	15623	16787: contig of 1165 bp in length
*	16788	16887: gap of unknown length
*	16888	17882: contig of 1005 bp in length
*	17893	17992: gap of unknown length
*	17993	19386: contig of 1294 bp in length
*	19287	19386: gap of unknown length
*	19387	20471: contig of 1085 bp in length
*	20472	20571: gap of unknown length
*	20572	22163: contig of 1552 bp in length
*	22164	22263: gap of unknown length
*	22264	23959: contig of 1696 bp in length
*	23960	24059: gap of unknown length
*	24060	25526: contig of 1467 bp in length
*	25527	25626: gap of unknown length
*	25627	27102: contig of 1476 bp in length
*	27103	27202: gap of unknown length
*	27203	29010: contig of 1808 bp in length
*	29011	29110: gap of unknown length
*	29111	30538: contig of 1428 bp in length
*	30539	30638: gap of unknown length
*	30639	32068: contig of 1430 bp in length
*	32069	32168: gap of unknown length
*	32169	34195: contig of 2027 bp in length
*	34196	34295: gap of unknown length
*	34296	36002: contig of 1707 bp in length
*	36003	36102: gap of unknown length
*	36103	38000: contig of 1898 bp in length
*	38001	38100: gap of unknown length
*	38101	39690: contig of 1590 bp in length
*	39691	39790: gap of unknown length
*	39791	41112: contig of 1322 bp in length
*	41113	41212: gap of unknown length
*	41213	42629: contig of 1417 bp in length
*	42630	42729: gap of unknown length
*	42730	43961: contig of 1232 bp in length
*	43962	44061: gap of unknown length
*	44062	45620: contig of 1559 bp in length
*	45621	45720: gap of unknown length
*	45721	47099: contig of 1379 bp in length
*	47100	47199: gap of unknown length
*	47200	48664: contig of 1465 bp in length
*	48665	48764: gap of unknown length
*	48765	50564: contig of 1800 bp in length
*	50565	50664: gap of unknown length
*	50665	52073: contig of 1409 bp in length
*	52074	52173: gap of unknown length
*	52174	53561: contig of 1388 bp in length
*	53562	53661: gap of unknown length
*	53662	55202: contig of 1541 bp in length

* 55303 55302: gap of unknown length
 * 55303 57116: contig of 1814 bp in length
 * 57117 57216: gap of unknown length
 * 57217 59380: contig of 2164 bp in length
 * 59381 59480: gap of unknown length
 * 59481 62511: contig of 3031 bp in length
 * 62512 62512: gap of unknown length
 * 62612 64588: contig of 2247 bp in length
 * 64589 65058: gap of unknown length
 * 65059 67458: contig of 2400 bp in length
 * 67459 67558: gap of unknown length
 * 67559 69016: contig of 1458 bp in length
 * 69017 69116: gap of unknown length
 * 69117 71787: contig of 2671 bp in length
 * 71788 71887: gap of unknown length
 * 71888 74420: contig of 2533 bp in length
 * 74421 74520: gap of unknown length
 * 74521 76340: contig of 1820 bp in length
 * 76341 76440: gap of unknown length
 * 76441 78440: contig of 2000 bp in length
 * 78441 78540: gap of unknown length
 * 78541 80615: contig of 2075 bp in length
 * 80616 80715: gap of unknown length
 * 80716 83350: contig of 2635 bp in length
 * 83351 83450: gap of unknown length
 * 83451 86241: contig of 2791 bp in length
 * 86242 86341: gap of unknown length
 * 86342 88765: contig of 2424 bp in length
 * 88766 88865: gap of unknown length
 * 88866 91115: contig of 2250 bp in length
 * 91116 91215: gap of unknown length
 * 91216 94444: contig of 3229 bp in length
 * 94445 94544: gap of unknown length
 * 94545 97016: contig of 2472 bp in length
 * 97017 97117: gap of unknown length
 * 97117 100199: contig of 3083 bp in length

Query Match
 Best Local Similarity 99.7%; Score 294.4; DB 2; Length 160122;
 Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CAGGTACAGCTGCAGCAATATGGGGCTGAACTAGTGAAGCTGGCTCCAGTGAATAAT 60
 Db 54735 CAGGTACAGCTGCAGCAATATGGGGCTGAACTAGTGAAGCTGGCTCCAGTGAATAAT 54794
 Oy 61 TCCTGCAAGGCTTCTGCTACATTCACCACTTACAGATATGCACTGATTAATAACAGCAG 120
 Db 54795 TCCTGCAAGGCTTCTGCTACATTCACCACTTACAGATATGCACTGATTAATAACAGCAG 54854
 Oy 121 CCTGGAATGGCTTGGATGGATTTGATTCCTGGAATGTAATTAAGTAC 180
 Db 54855 CCTGGAATGGCTTGGATGGATTTGATTCCTGGAATGTAATTAAGTAC 54914
 Oy 181 AATCAAAAGTTCAATGGGAAGGCAACCTCAGTGCAGACAATAATCCTCCAGCAGCCTAT 240
 Db 54915 AATCAAAAGTTCAATGGGAAGGCAACCTCAGTGCAGACAATAATCCTCCAGCAGCCTAT 54974
 Oy 241 ATGCAGCTCAGACGCTGACATCTGAGAGCTTGCAGCTATTTCTGTGCAAGAGA 296
 Db 54975 ATGCAGCTCAGACGCTGACATCTGAGAGCTTGCAGCTATTTCTGTGCAAGAGA 55030

RESULT 6
 RN293359 336 bp mRNA linear ROD 26-SEP-1997
 LOCUS R.norvegicus mRNA for immunoglobulin variable region (clone
 DEFNITION ERF2.13).
 ACCESSION Z93359
 VERSION Z93359.1 GI:1911150
 KEYWORDS Immunoglobulin; immunoglobulin heavy chain; immunoglobulin
 superfamily; joining region; variable region.
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 336)
 REFERENCE
 AUTHORS Dammers, P.M.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAR-1997) Dammers P. M., University of Groningen,
 Histology and Cell Biology, Oostersingel 69-1, Groningen,
 Groningen, The Netherlands, NL-9713 EZ
 2 (bases 1 to 336)
 REFERENCE
 AUTHORS Vermeer, L.A., Dammers, P.M., Rajewsky, K., Bos, N.A. and Kroese, F.G.M.
 TITLE A non-random Vh gene family usage in a peripheral subpopulation of
 recently generated B cells
 JOURNAL Unpublished
 FEATURES
 SOURCE Location/Qualifiers
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 /organism="Rattus norvegicus"
 /strain="PVG/E"
 /db_xref="taxon:10116"
 /clone="ERF2.13"
 /cell_type="B cell"
 /tissue_type="spleen"
 /dev_stage="adult"
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 /product="Immunoglobulin variable region"
 /note="J558 Vh gene family"
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 /product="Immunoglobulin joining region"
 /note="Jh2 or Jh3"

V-segment
 J-segment
 BASE COUNT 91 a 78 c 84 g 83 t
 ORIGIN

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 Matches 284; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 1 CAGGTACAGCTGCAGCAATATGGGGCTGAACTAGTGAAGCTGGGGTCTCAGTGAATAAT 60
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 Oy 61 TCCTGCAAGGCTTCTGCTACATTCACCACTTACAGATATGCACTGATTAATAACAGCAG 120
 Db 61 TCCTGCAAGGCTTCTGCTACATTCACCACTTACAGATATGCACTGATTAATAACAGCAG 120
 Oy 121 CCTGGAATGGCTTGGATGGATTTGATTCCTGGAATGTAATTAAGTAC 180
 Db 121 CCTGGAATGGCTTGGATGGATTTGATTCCTGGAATGTAATTAAGTAC 180
 Oy 181 AATCAAAAGTTCAATGGGAAGGCAACCTCAGTGCAGACAATAATCCTCCAGCAGCCTAT 240
 Db 181 AATCAAAAGTTCAATGGGAAGGCAACCTCAGTGCAGACAATAATCCTCCAGCAGCCTAT 240
 Oy 241 ATGCAGCTCAGACGCTGACATCTGAGAGCTTGCAGCTATTTCTGTGCAAGAGA 294
 Db 241 ATGCAGCTCAGACGCTGACATCTGAGAGCTTGCAGCTATTTCTGTGCAAGAGA 294

RESULT 7
 RN293359 293 bp DNA linear ROD 04-MAY-1995
 LOCUS R.norvegicus (GLVH18 isolate) J558 gene.
 DEFINITION X86663
 ACCESSION X86663
 VERSION X86663.1 GI:798856
 KEYWORDS Ig heavy chain variable region; V region.
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 293)
 REFERENCE
 AUTHORS Vermeer, L.A., Dammers, P.M., De Vries, A.F. and Bos, N.A.
 TITLE The rat and mouse J558 and PC7183 Vh gene families show different
 evolutionary dispersion patterns which correlate with the inherent

ORIGINATOR Phas, Muculata
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus
AUTHORS 1 (bases 1 to 387)
TITLE Dechant,M., Glennie,M.J. and Valerius,T.
JOURNAL Direct Submission
DATE Submitted (09-07-2001) Department of Medicine, UT
UNIVERSITY University of

FEATURES
source
location/Qualifiers
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/note="TNP-specific hybridoma"
misc_feature
complement(<1..352)
/note="nonfunctional immunoglobulin heavy chain variable
VDJ region due to somatic hypermutation"
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Best Local Similarity 82.7%; Pred. No. 4.1e-71;
Matches 305; Conservative 0; Mismatches 52; Indels 12; Gaps 1;
QY 1 CAGGTACAGCTGCAGCAATCTGGGGCTGAGTACTGATGAGCTGGGCTGCTGAGTGAATAT 60
DB 204 CAGGTACAGCTGCAGCAATCTGGGGCTGAGTACTGATGAGCTGGGCTGCTGAGTGAATAT 263
QY 61 TCCTGCAAGGCTTCTGGCTACACATTCACCAAGTACAGATGAGCTGATGAGTGAATAT 120
DB 264 TCCTGCAAGGCTTCTGGCTACACATTCACCAAGTACAGATGAGCTGATGAGTGAATAT 323
QY 121 CCGGAATGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 324 CCGGAATGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 383
QY 181 AATCAAAAGTTCAATGAGGAGCAACACTGACAGCAATCTGCAAGAGCTTAT 240
DB 384 AATCAAAAGTTCAATGAGGAGCAACACTGACAGCAATCTGCAAGAGCTTAT 443
QY 241 ATGACAGCTGACAGCTGACATCTGAGAGCTGACAGCTTATGTCGACAGAGATTGG 300
DB 444 ATGACAGCTGACAGCTGACATCTGAGAGCTGACAGCTTATGTCGACAGAGATTGG 501
QY 301 CATTAATATGAGCTATATCCGCTTGTGCTTACAGGGGAGCAAGGAGCTGCTGACCT 360
DB 502 -----ACGCTAGTACTGAGGAGCTTGTGCTTACAGGGGAGCAAGGAGCTGCTGACCT 551
QY 361 GTCTCTTCA 369
DB 552 GTCTCTGCA 560
RESULT 12
MMSp6718 3260 bp DNA linear ROD 25-NOV-1996
LOCUS
DEFINITION
MMSp6718 3260 bp DNA linear ROD 25-NOV-1996
Mouse rearranged Sp6-718 gene for Ig mu (5) heavy chain variable
region (VH1 subgroup, anti TNP antibody).
ACCESSION
X56936
VERSION
X56936.1 GI:54163
KEYWORDS
Ig heavy chain; IgM heavy chain; variable region.
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
Ostermayer, M.
Direct Submissions
Submitted (14-JAN-1991) M. Ostermayer, BIOZENTRUM, UNIVERSITAET
BASEL, KLINGELBERGSTR 70, CH-4056 BASEL, SWITZERLAND
JOURNAL
2 (bases 1 to 1365)
REFERENCE
Ostermayer, M., Black, C.H., Trautwein, A. and Koehler, G.
TITLE
Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu
heavy chain gene and its upstream region
JOURNAL
See also M12827, V01523 & J00440.
COMMENT
Location/Qualifiers

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misc_signal
679..689
/note="octamer"
TATA_signal
705..710
gene
727..3260
/gene="Sp6-718"
prim_transcript
727..3260
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/evidence=experimental
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/evidence=experimental
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/translation="MGSRITFLFLITIAAGHCYQYQAOQSPPELVKPGASVIRISCKAS
GYTFSTYIHWKORPGGGLGIMWITIPGNVNTYNEKFKATLADKSSSTAYMOL
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/db_xref="GI:54164"
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exon
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/note="VDJ region"
/number=2
misc_signal
2802..2812
/gene="Sp6-718"
BASE COUNT 934 a 639 c 703 g 984 t
ORIGIN
Query Match 68.2% Score 251.8; DB 10; Length 3260;
Best Local Similarity 82.7%; Pred. No. 4.7e-71;
Matches 305; Conservative 0; Mismatches 52; Indels 12; Gaps 1;
QY 1 CAGGTACAGCTGCAGCAATCTGGGGCTGAGTACTGATGAGCTGGGCTGCTGAGTGAATAT 60
DB 928 CAGGTACAGCTGCAGCAATCTGGGGCTGAGTACTGATGAGCTGGGCTGCTGAGTGAATAT 987
QY 61 TCCTGCAAGGCTTCTGGCTACACATTCACCAAGTACAGATGAGCTGATGAGTGAATAT 120
DB 988 TCCTGCAAGGCTTCTGGCTACACATTCACCAAGTACAGATGAGCTGATGAGTGAATAT 1047
QY 121 CCGGAATGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 1048 CCGGAATGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1107
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DB 1108 AATCAAAAGTTCAATGAGGAGCAACACTGACAGCAATCTGCAAGAGCTTAT 1167
QY 241 ATGACAGCTGACAGCTGACATCTGAGAGCTGACAGCTTATGTCGACAGAGATTGG 300
DB 1168 ATGACAGCTGACAGCTGACATCTGAGAGCTGACAGCTTATGTCGACAGAGATTGG 1225
QY 301 CATTAATATGAGCTATATCCGCTTGTGCTTACAGGGGAGCAAGGAGCTGCTGACCT 360
DB 1226 -----ACGCTAGTACTGAGGAGCTTGTGCTTACAGGGGAGCAAGGAGCTGCTGACCT 1275
QY 361 GTCTCTTCA 369

QY 361 GTCTCTTCA 369
| | | | |
Db 41 GTCTCTGCA 33

RESULT 15

AF439571

DEFINITION Mus musculus clone 7 nonfunctional immunoglobulin heavy chain

AF439571 592 bp DNA linear ROD 06-MAR-2002

ACCESSION AF439571

VERSION AF439571.1 GI:19171886

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL Nature 415 (6873), 802-806 (2002)

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. 592

/organism="Mus musculus"

/strain="BALB/c"

/isolate="1797_A09_MS-127742-065.ab1"

/db_xref="taxon:10090"

/clone="7"

/cell_type="N114 hybridoma"

/note="TNP-specific hybridoma"

/note="nonfunctional immunoglobulin heavy chain variable

VDJ region due to somatic hypermutation"

BASE COUNT 151 a 153 c 144 g 144 t

ORIGIN

Query Match

Best Local Similarity 82.4%; Score 250.2; DB 10; Length 592;

Matches 304; Conservative 0; Mismatches 53; Indels 12; Gaps 1;

QY 1 CAGGTACAGCTGACGATCTGGGGCTGAGTGAAGCTGGGCTCTCAGTGAATTT 60

Db 204 CAGGTACAGCTGACGATCTGGGGCTGAGTGAAGCTGGGCTCTCAGTGAATTT 263

QY 61 TCCTGCAAGGCTCTGCTGACATTCACATTCACAGTTCAGTATGATGATGAATGAACACAG 120

Db 264 TCCTGCAAGGCTCTGCTGACATTCACATTCACAGTTCAGTATGATGATGAATGAACAG 323

QY 121 CTTGGAATGGCTTGTGATGATGGTGGATTTATCTGGAATGTAATTAAGTAC 180

Db 324 CTTGGAATGGCTTGTGATGATGGTGGATTTATCTGGAATGTAATTAAGTAC 383

QY 181 AATCAAAAGTTCAATGGAGGCAACACATTCAGTGAAGCAAAATCTCAGCAGCCTAT 240

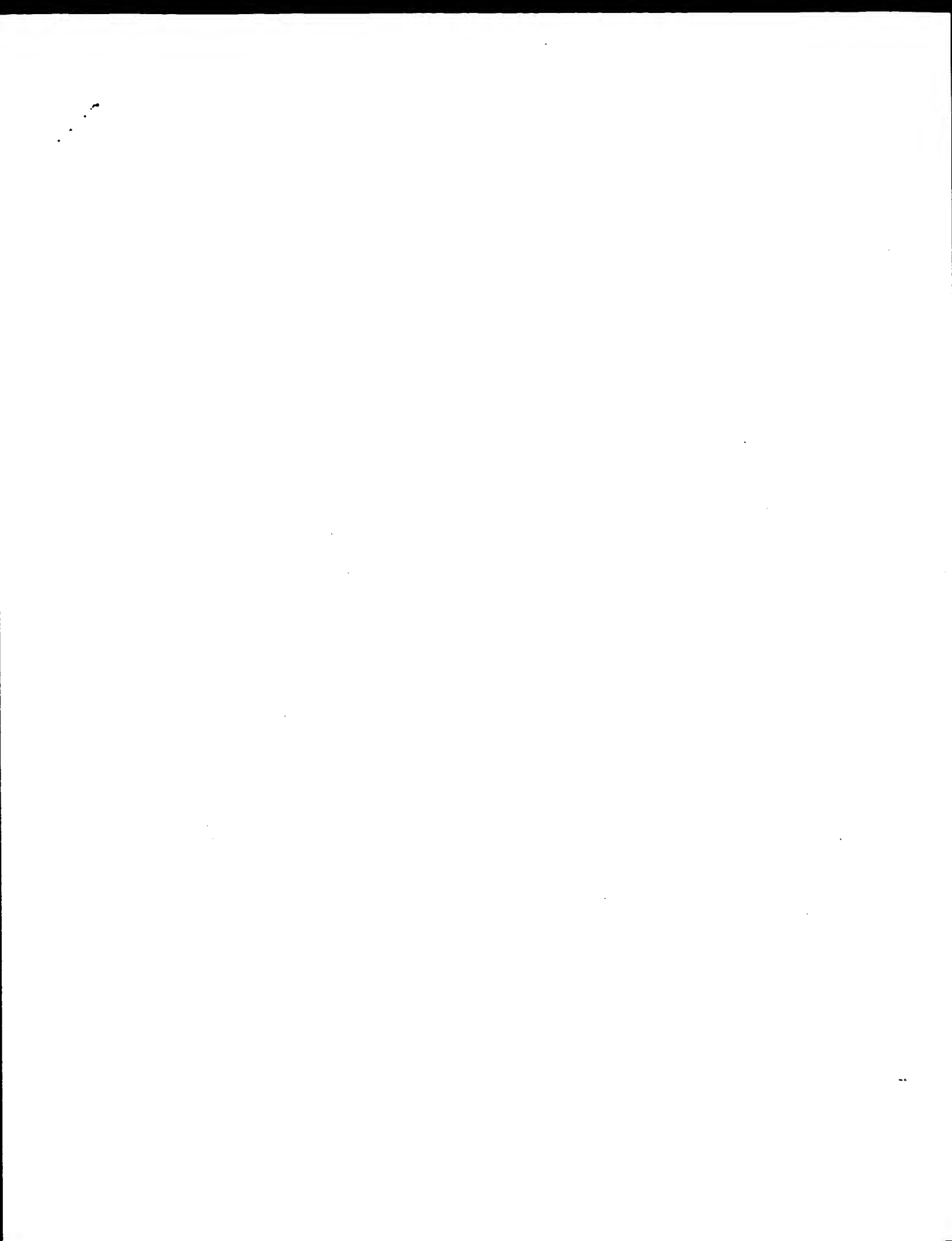
Db 384 AATCAAAAGTTCAATGGAGGCAACACATTCAGTGAAGCAAAATCTCAGCAGCCTAT 443

QY 241 ATGAGCTCAGCAGCTGACATCTGAGAGCTCTGACATCTATTTCTGCAAGAGATTGG 300

Db 444 ATGAGCTCAGCAGCTGACATCTGAGAGCTCTGACATCTATTTCTGCAAGAGATTGG 501

Db 502 -----ACGGTAGTACTAGGGGCTTGTACTGGGGCCAGAGGACTGTGTACT 551
QY 361 GTCTCTTCA 369
| | | | |
Db 552 GTCTCTGCA 560

Search completed: February 28, 2003, 22:46:35
Job time: 1433 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 : Search time 1.22833 Seconds
(without alignments)
263,489 Million cell updates/sec

Title: US-09-743-482A-2
Perfect score: 59
Sequence: 1 QASODIGMFLA 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/laa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/laa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/laa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/laa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/laa/PTUTS-COMB.pep.*
6: /cgn2_6/ptodata/1/laa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	79.7	105	1	US-08-276-852-89
2	47	79.7	105	1	US-08-889-575-89
3	47	79.7	105	1	US-08-899-575-89
4	47	79.7	105	5	PCT-US95-08743-89
5	41	69.5	98	1	US-08-401-908-2
6	40.5	68.6	534	2	US-08-356-786-10
7	40	67.8	19	1	US-07-805-437-5
8	40	67.8	76	4	US-08-851-362D-20
9	40	67.8	105	4	US-08-851-362D-24
10	40	67.8	105	4	US-08-851-362D-28
11	40	67.8	105	4	US-08-851-362D-34
12	40	67.8	105	4	US-08-851-362D-38
13	40	67.8	120	4	US-09-621-625A-23
14	40	67.8	197	4	US-09-621-625A-25
15	40	67.8	215	4	US-09-621-625A-21
16	40	67.8	232	6	US-09-621-625A-17
17	40	67.8	257	6	US-09-621-625A-17
18	40	67.8	258	6	US-09-621-625A-17
19	40	67.8	275	1	US-08-589-446-4
20	40	67.8	275	1	US-08-444-882-4
21	40	67.8	275	2	US-08-389-459A-4
22	40	67.8	275	3	US-08-389-459A-4
23	40	67.8	283	6	US-08-987-867A-4
24	40	67.8	292	4	US-09-621-625A-2
25	40	67.8	292	4	US-09-621-625A-2
26	40	67.8	294	4	US-09-370-368-3
27	40	67.8	333	6	US-08-276-852-89

28	40	67.8	337	1	US-07-648-796A-1	Sequence 1, Appl1
29	40	67.8	363	2	US-08-850-049-130	Sequence 130, App
30	40	67.8	363	2	US-08-050-478-130	Sequence 130, App
31	40	67.8	363	4	US-09-414-117-130	Sequence 130, App
32	40	67.8	363	4	US-09-678-437-130	Sequence 130, App
33	40	67.8	437	3	US-08-392-794A-2	Sequence 2, Appl1
34	40	67.8	458	1	US-07-648-796A-3	Sequence 2, Appl1
35	40	67.8	478	1	US-08-127-499A-11	Sequence 11, Appl1
36	40	67.8	478	1	US-08-482-847-11	Sequence 11, Appl1
37	40	67.8	500	1	US-08-375-510-1	Sequence 1, Appl1
38	40	67.8	500	2	US-08-487-657-1	Sequence 1, Appl1
39	40	67.8	500	2	US-08-816-155B-45	Sequence 45, Appl1
40	40	67.8	500	4	US-09-879-587-45	Sequence 45, Appl1
41	40	67.8	500	4	US-09-309-572-16	Sequence 16, Appl1
42	40	67.8	512	3	US-08-463-210-8	Sequence 8, Appl1
43	40	67.8	512	4	US-09-124-900-2	Sequence 2, Appl1
44	40	67.8	770	1	US-07-648-796A-8	Sequence 8, Appl1
45	40	67.8	799	1	US-07-648-796A-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-08-276-852-89
Sequence 89, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESSES:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-89

Query Match 79.7%; Score 47; DB 1; Length 105;
Best Local Similarity 81.8%; Pred. No. 0.4;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNMILA 11
:|||||
Db 22 RASODIHNMILA 32

RESULT 2
US-08-899-575-89

; Sequence 89, Application US/08899575
; Patent No. 5770440

; GENERAL INFORMATION:

; APPLICANT: Burton, Dennis R

; APPLICANT: Barbas, Carlos F

; APPLICANT: Lerner, Richard A

; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

; NUMBER OF SEQUENCES: 170

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

; ADDRESSEE: Patent Counsel

; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,

; STREET: Mail Drop TPC8

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/899,575

; FILING DATE: 24-JUL-1997

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/276,852

; FILING DATE: 18-JUL-1994

; APPLICATION NUMBER: US 08/178,302

; FILING DATE: 30-SEP-1993

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 07/954,148

; FILING DATE: 30-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitting, Thomas

; REGISTRATION NUMBER: 34,163

; REFERENCE/DOCKET NUMBER: SCR1452P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-554-2937

; TELEFAX: 619-554-6312

; INFORMATION FOR SEQ ID NO: 89:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 105 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-899-575-89

Query Match 79.7%; Score 47; DB 1; Length 105;
Best Local Similarity 81.8%; Pred. No. 0.4;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNMILA 11
:|||||
Db 22 RASODIHNMILA 32

RESULT 3
US-08-899-575-89

; Sequence 89, Application US/08899575

; Patent No. 5804440

; GENERAL INFORMATION:

; APPLICANT: Burton, Dennis R

; APPLICANT: Barbas, Carlos F

; APPLICANT: Lerner, Richard A

; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

; NUMBER OF SEQUENCES: 170

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

; ADDRESSEE: Patent Counsel

; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,

; STREET: Mail Drop TPC8

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/899,575

; FILING DATE: 24-JUL-1997

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/276,852

; FILING DATE: 18-JUL-1994

; APPLICATION NUMBER: US 08/178,302

; FILING DATE: 30-SEP-1993

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 07/954,148

; FILING DATE: 30-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitting, Thomas

; REGISTRATION NUMBER: 34,163

; REFERENCE/DOCKET NUMBER: SCR1452P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-554-2937

; TELEFAX: 619-554-6312

; INFORMATION FOR SEQ ID NO: 89:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 105 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-899-575-89

Query Match 79.7%; Score 47; DB 1; Length 105;
Best Local Similarity 81.8%; Pred. No. 0.4;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNMILA 11
:|||||
Db 22 RASODIHNMILA 32

RESULT 4
PCT-US95-08743-89

; Sequence 89, Application PC/TUS9508743

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

; NUMBER OF SEQUENCES: 170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/08743

FILING DATE: 11-JUL-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/276,852
 FILING DATE: 18-JUL-1994
 INFORMATION FOR SEQ ID NO: 89:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 105 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-08743-89

Query Match 79.7%; Score 47; DB 5; Length 105;
 Best Local Similarity 81.8%; Pred. No. 0.4;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASODIGNWLA 11
 :|||||
 DB 22 RASODIGNWLA 32

RESULT 5

US-08-401-908-2
 Sequence 2, Application US/08401908
 Patent No. 5684146
 GENERAL INFORMATION:
 APPLICANT: Yoshinobu OKUNO et al.
 TITLE OF INVENTION: A DNA WHICH CODES FOR THE VARIABLE REGION OF
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wenderoth, Lind & Ponack
 STREET: 805 Fifteenth Street, N.W., #700
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/401,908
 FILING DATE: March 10, 1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-8850
 TELEFAX:
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 98
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-401-908-2

Query Match 69.5%; Score 41; DB 1; Length 98;
 Best Local Similarity 80.0%; Pred. No. 3.8;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASODIGNWLA 11
 :|||||
 DB 25 ASQITIGWLA 34

RESULT 6

US-08-356-786-10
 Sequence 10, Application US/08356786
 Patent No. 5877305
 GENERAL INFORMATION:
 APPLICANT: Huston, James S.
 APPLICANT: Oppermann, Hermann
 APPLICANT: Houston, L. L.
 APPLICANT: Ring, David B.
 TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
 STREET: Exchange Place, 53 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/356,786
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/831,967
 FILING DATE: 06-FEB-1992

ATTORNEY/AGENT INFORMATION:
 NAME: Pitcher, Edmund R.
 REGISTRATION NUMBER: 27,829
 REFERENCE/DOCKET NUMBER: CRP-053
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 248-7000
 TELEFAX: (617) 248-7100
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 534 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-356-786-10

Query Match 68.6%; Score 40.5; DB 2; Length 534;
 Best Local Similarity 64.3%; Pred. No. 27;
 Matches 9; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 1 QASODIGN--WLA 11
 :|||||
 DB 448 RASODIGNSLTWLS 461

RESULT 7

US-07-805-437-5
 Sequence 5, Application US/07805437
 Patent No. 5364757
 GENERAL INFORMATION:
 APPLICANT: Garry, R.F. et al.
 TITLE OF INVENTION: Association Between A Human
 TITLE OF INVENTION: Immunodeficiency Virus-Related Retrovirus And Autoimmune
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penile & Edmonds
 STREET: 1155 Avenue of Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/805,437
FILING DATE: 19911211
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18, 872
REFERENCE/DOCKET NUMBER: 5113-034
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-805-437-5

Query Match 67.8%; Score 40; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 1;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNML 10
|||||:|:
DB 7 QASQEVKNM 16

RESULT 8
US-08-851-362D-20
Sequence 20, Application US/08851362D
Patent No. 6235883
GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851,362D
CURRENT FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 76
TYPE: PRT
ORGANISM: human
US-08-851-362D-20

Query Match 67.8%; Score 40; DB 4; Length 76;
Best Local Similarity 80.0%; Pred. No. 4.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNML 10
|||||:|:
DB 5 QASQDISNML 14

RESULT 9
US-08-851-362D-24
Sequence 24, Application US/08851362D
Patent No. 6235883
GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya

APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851,362D
CURRENT FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 105
TYPE: PRT
ORGANISM: human
US-08-851-362D-24

Query Match 67.8%; Score 40; DB 4; Length 105;
Best Local Similarity 80.0%; Pred. No. 6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNML 10
|||||:|:
DB 5 QASQDINNML 14

RESULT 10
US-08-851-362D-28
Sequence 28, Application US/08851362D
Patent No. 6235883
GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851,362D
CURRENT FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 105
TYPE: PRT
ORGANISM: human
US-08-851-362D-28

Query Match 67.8%; Score 40; DB 4; Length 105;
Best Local Similarity 80.0%; Pred. No. 6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNML 10
|||||:|:
DB 5 QASQDISNML 14

RESULT 11
US-08-851-362D-34
Sequence 34, Application US/08851362D
Patent No. 6235883
GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851,362D
CURRENT FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34

LENGTH: 105
TYPE: PRT
ORGANISM: human
US-08-851-362D-34

Query Match 67.8%; Score 40; DB 4; Length 105;
Best Local Similarity 80.0%; Pred. No. 6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWL 10
|||||
Db 5 QASODISNYL 14

RESULT 12
US-08-851-362D-38
Sequence 38, Application US/08851362D

PATENT NO. 6235883
GENERAL INFORMATION:
APPLICANT: JAKOBOVITS, AYA
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-CH
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851.362D
CURRENT FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 38
LENGTH: 105
TYPE: PRT
ORGANISM: human
US-08-851-362D-38

Query Match 67.8%; Score 40; DB 4; Length 105;
Best Local Similarity 80.0%; Pred. No. 6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWL 10
|||||
Db 5 QASODISNYL 14

RESULT 13
US-09-621-625A-23
Sequence 23, Application US/09621625A

PATENT NO. 6432633
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: YOSHIOKI, Akemi
APPLICANT: MATSUI, Toshio
APPLICANT: UMETANI, Atsushi
TITLE OF INVENTION: Immunoassay Method of HIV-1p24 Antigen and Reagent Therefor
FILE REFERENCE: 1121-0111P
CURRENT APPLICATION NUMBER: US/09/621.625A
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: Japan 11-213224
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0

SEQ ID NO 23
LENGTH: 120
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-621-625A-23

Query Match 67.8%; Score 40; DB 4; Length 120;
Best Local Similarity 60.0%; Pred. No. 6.9;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASODIGNWL 10

Db 69 QASQEVKNWM 78
|||||

RESULT 14
US-09-621-625A-25
Sequence 25, Application US/09621625A
PATENT NO. 6432633
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: YOSHIOKI, Akemi
APPLICANT: MATSUI, Toshio
APPLICANT: UMETANI, Atsushi
TITLE OF INVENTION: Immunoassay Method of HIV-1p24 Antigen and Reagent Therefor
FILE REFERENCE: 1121-0111P
CURRENT APPLICATION NUMBER: US/09/621.625A
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: Japan 11-213224
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0

SEQ ID NO 25
LENGTH: 197
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-621-625A-25

Query Match 67.8%; Score 40; DB 4; Length 197;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASQDIGNWL 10
|||||
Db 69 QASQEVKNWM 78

RESULT 15
US-09-621-625A-21
Sequence 21, Application US/09621625A
PATENT NO. 6432633
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: YOSHIOKI, Akemi
APPLICANT: MATSUI, Toshio
APPLICANT: UMETANI, Atsushi
TITLE OF INVENTION: Immunoassay Method of HIV-1p24 Antigen and Reagent Therefor
FILE REFERENCE: 1121-0111P
CURRENT APPLICATION NUMBER: US/09/621.625A
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: Japan 11-213224
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0

SEQ ID NO 21
LENGTH: 215
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-621-625A-21

Query Match 67.8%; Score 40; DB 4; Length 215;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASQDIGNWL 10
|||||
Db 164 QASQEVKNWM 173

Search completed: February 25, 2003, 10:38:39
Job time : 2.22833 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 0.886667 Seconds
(without alignments)
758.956 Million cell updates/sec

Title: US-09-743-482a-4
Sequence: 1 SATSLAD 7

Scoring table: BLOSUM62
Gap 10.0, Capext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.73:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	1106	2 T40931	nad-specific gluta
2	29	93.5	473	2 AH0887	probable exported
3	28	90.3	66	2 T35489	hypothetical prote
4	28	90.3	101	2 B37262	Ig kappa chain V r
5	28	90.3	175	2 AC2648	conserved hypothet
6	28	90.3	185	2 B97430	hypothetical prote
7	28	90.3	326	2 S36705	dmp diphosphatase
8	28	90.3	433	2 G64594	hemolysin secretio
9	28	90.3	433	2 H71917	methyl-accepting c
10	28	90.3	511	2 T43282	alp21 protein - fl
11	28	90.3	535	2 H88039	protein F47F6.7 (1
12	28	90.3	703	2 T41065	RNA binding protei
13	28	90.3	851	2 D87252	Tomb-dependent rec
14	28	90.3	1148	2 T13347	Cnn protein - fru
15	28	90.3	1215	2 E70614	hypothetical prote
16	27	87.1	75	2 H90913	hypothetical prote
17	27	87.1	101	2 S13701	Ig kappa chain V r
18	27	87.1	103	2 S13703	Ig kappa chain V r
19	27	87.1	104	2 S13700	Ig kappa chain V r
20	27	87.1	211	2 AF0644	probable MetR-fam
21	27	87.1	217	2 AH0561	potential acraB op
22	27	87.1	231	2 T50853	response regulator
23	27	87.1	236	2 A90815	hypothetical prote
24	27	87.1	236	2 E85674	hypothetical prote
25	27	87.1	236	2 D64855	probable transcrip
26	27	87.1	430	1 E69559	molybdopterin bios
27	27	87.1	541	1 E69559	PEP112 protein - Y
28	27	87.1	553	1 C84920	hypothetical prote
29	27	87.1	578	2 E70645	hypothetical prote

30	27	87.1	709	2 T32089	hypothetical prote
31	27	87.1	757	2 T02884	D-(L)-3-hydroxybut
32	27	87.1	884	2 E89010	protein R08F11.1 (
33	27	87.1	918	2 T02759	hypothetical prote
34	27	87.1	2420	2 A84652	hypothetical prote
35	26	83.9	91	2 T17521	hypothetical prote
36	26	83.9	355	2 F70983	probable serine pr
37	26	83.9	369	2 J02278	hydroxymethylbilan
38	26	83.9	403	2 T06631	pollen surface pro
39	26	83.9	417	2 S68151	phosphoglycerate k
40	26	83.9	503	2 S63257	probable membrane
41	26	83.9	506	2 A11521	flagellar hook-ass
42	26	83.9	564	2 T12550	hypothetical prote
43	26	83.9	596	2 S58106	hypothetical 65.9
44	26	83.9	640	2 T41977	hypothetical prote
45	26	83.9	675	2 AF0185	methionine-tRNA II

ALIGNMENTS

RESULT 1

T40931
nad-specific glutamate dehydrogenase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T40931
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Aert, R.; Volkhardt, G.
submitted to the EMBL Data Library, October 1999
A:Reference number: 221958
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1106 <LYN>
A:Cross-References: EMBL:AL121807; PIDN:CA58131.1; GSPDB:GN00068; SPDB:SPCC132.04C
A:Experimental source: strain 972h.; cosmid c132
C:Genetics:
A:Gene: SPDB:SPCC132.04c
A:Map position: 3
C:Superfamily: glutamate dehydrogenase

Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 1106;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7

DB 507 SATSLAD 513

RESULT 2

AH0887
probable exported protein STY3343 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C:Species: Salmonella enterica subsp. enterica serovar Typhimurium
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AH0887
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church, T.; Connerton, P.; Croft, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr, S.; Mout, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A.; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium
A:Reference number: AB0502; PMID:11677608
A:Accession: AH0887
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-473 <PAR>
A:Cross-References: GB:AL513382; PIDN:CAD03000.1; PID:G16504246; GSPDB:GN00176
C:Genetics:
A:Gene: STY3343

Query Match

93.5%; Score 29; DB 2; Length 473;

Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 SATSLAD 7
:|||||
Db 182 SATSLAD 188

RESULT 3
T35489
hypothetical protein SC6E10.02 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T35489
R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A:Reference number: 221580
A:Accession: T35489
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-66 <SEE>
A:Cross-references: EMBL:AL109661; PIDN:CAB51956.1; GSPDB:GN00070; SC6E10.02
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SC6E10.02

Query Match
Best Local Similarity 85.7%; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
:|||||
Db 47 SATSLAD 53

RESULT 4
B37262
Ig kappa chain V region (IG1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C:Accession: B37262
R:Goshorn, S.C.; Retzel, E.; Jemerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: B37262
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-101 <GOS>
A:Cross-references: GB:M57988; NID:9196421; PIDN:AAA63368.1; PID:9196422
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
P:8-82/Domain: Immunoglobulin homology <IMM>

Query Match
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
:|||||
Db 42 SATSLAD 48

RESULT 5
AC2648
conserved hypothetical protein Atu0584 [Imported] - Agrobacterium tumefaciens (strain C5
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AC2648
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, D.
erage, G.; Miller, M.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
sier, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AC2648
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-175 <KUR>
A:Cross-references: GB:AE008688; PIDN:AA141601.1; PID:917738938; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0584
A:Map position: circular chromosome

Query Match
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
:|||||
Db 27 SATSLAD 33

RESULT 6
B97430
hypothetical protein AGR_C_1032 [Imported] - Agrobacterium tumefaciens (strain C58, C
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: B97430
R:Goodner, B.; Hinkle, G.; Gatlung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A:Reference number: A97359; PMID:11743194
A:Accession: B97430
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-185 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK86395.1; PID:91515525; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_1032
A:Map position: circular chromosome

Query Match
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
:|||||
Db 37 SATSLAD 43

RESULT 7
S36705
dmp dihydrophosphate (EC 3.6.1.23) - equine herpesvirus 4
C:Species: equine herpesvirus 4
C:Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 03-Jun-2002
C:Accession: S36705
R:Rigdio, P.
submitted to the EMBL Data Library, November 1989
A:Reference number: S36703
A:Accession: S36705
A:Molecule type: DNA
A:Residues: 1-326 <RIG>
A:Cross-references: EMBL:X17684; NID:9312459; PIDN:CAA3671.1; PID:959218
C:Superfamily: herpesvirus dmp pyrophosphatase
C:Keywords: hydrolase

Query Match
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7

Db 3 SATSLAD 9

RESULT 8

hemolysin secretion protein precursor - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C:Accession: G64594

R:Tombs, J.F.; White, O.; Kellavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodex, A.; McKen-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Feldman, J.M.; Fujii, C.; Bowman, C.; Watney, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: G64594

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-433 <TOM>

A:Cross-references: GB:AE000573; GB:AE000511; NID:92313712; PIDN:AD067662.1; PID:9231371

Query Match

Best Local Similarity 90.3%; Score 28; DB 2; Length 433;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7

Db 175 NATSLAD 181

RESULT 9

methyl-accepting chemotaxis protein (MCP) - Helicobacter pylori (strain J99)

C:Species: Helicobacter pylori

C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999

C:Accession: H71917

R:Alm, R.A.; Ling, L.S.L.; Mofr, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

Ires, C.; Gibson, R.; Metberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Voyis, G.F.;

Nature 397, 176-180, 1999

A>Title: Genome sequence comparison of two unrelated isolates of the human gastric path

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: H71917

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-433 <ARN>

A:Cross-references: GB:AE001487; GB:AE001439; NID:94155086; PIDN:AD06131.1; PID:9415509

A:Experimental source: strain J99

C:Genetics:

A:Gene: jhp0546

Query Match

Best Local Similarity 90.3%; Score 28; DB 2; Length 433;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7

Db 175 NATSLAD 181

RESULT 10

alp21 protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000

C:Accession: T43282; T38213

R:Radcliffe, P.A.; Toda, T.

submitted to the EMBL Data Library, November 1997

A:Description: Alp21 homologue of cofactor E required for microtubule function.

A:Reference number: T22391

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-511 <RAD>

A:Cross-references: EMBL:AB008749; PIDN:BA23374.1

R:Grishchuk, K.; McInosh, J.R.; Devlin, K.; Churcher, C.; Barrell, B.G.; Rajandream,

submitted to the EMBL Data Library, February 1996

A:Reference number: T21778

A:Accession: T38213

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-511 <DEV>

A:Cross-references: EMBL:Z69730; PIDN:CA93613.1; GSPDB:GN00066; SPDB:SPAC22H10.10

A:Experimental source: strain 972h-; cosmid c22H10

C:Genetics: <RAD1>

A:Gene: alp21

A:Map position: 1

A:Introns: 52/3; 142/1; 175/2; 267/3

C:Genetics: <DEV1>

A:Gene: SPAC22H10.10

A:Map position: 1

A:Introns: 52/2; 142/1; 175/2; 267/2

Query Match

Best Local Similarity 90.3%; Score 28; DB 2; Length 511;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7

Db 274 SSTSAD 280

RESULT 11

protein F47F6.7 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: H88039

R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A>Title: Genome sequence of the nematode C. elegans: a platform for investigating bio

A:Reference number: A75000; MUID:99069613; PMID:9851916

A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_

A:Accession: H88039

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-535 <STO>

A:Cross-references: GB:chr_II; PIDN:AC71116.1; PID:91707164; GSPDB:GN00020; CESP:F47F

C:Genetics:

A:Gene: F47F6.7

A:Map position: 2

Query Match

Best Local Similarity 90.3%; Score 28; DB 2; Length 535;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7

Db 89 SATSLAD 95

RESULT 12

RNA binding protein, pumilio-family - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T41065

R:Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, September 1998

A:Reference number: T21968

A:Accession: T41065

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-703 <MUR>
 A:Cross-references: EMBL:AL031525; PIDN:CAA20674.1; GSPDB:GN00068; SPDB:SPCC1682.08c
 A:Experimental source: strain 972h-; cosmid c1682
 C:Genetics:
 A:Gene: SPDB:SPCC1682.08c
 A:Map position: 3

Query Match 90.3%; Score 28; DB 2; Length 703;
 Best Local Similarity 85.7%; Pred. No. 89;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
 1111111
 DB 142 SATSLAD 148

RESULT 13

DB87252
 TonB-dependent receptor [Imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 14-Sep-2001

C:Accession: DB87252
 R:Neiman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: DB87252
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-851 <STO>
 A:Cross-references: GB:AE005673; NID:g13421118; PIDN:AAK22016.1; GSPDB:GN00148
 C:Genetics:

A:Gene: CC0028
 C:Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homo

Query Match 90.3%; Score 28; DB 2; Length 851;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
 1111111
 DB 174 SATSLAD 180

RESULT 14

Cnn proteain - fruit fly (Drosophila melanogaster)
 N:Alternate names: centrosomin
 C:Species: Drosophila melanogaster
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: T13347
 R:Heuer, J.G.; Li, K.; Kaufman, T.C.
 Development 121, 3861-3876, 1995
 A:Title: The Drosophila homeotic target gene centrosomin (cnn) encodes a novel centrosom

A:Reference number: Z17655; MUID:96102828; PMID:8582295
 A:Accession: T13347
 A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA
 A:Residues: 1-1148 <HEU>
 A:Cross-references: EMBL:U05621; NID:g2570233; PID:g2570234; PIDN:AAB82065.1
 A:Experimental source: strain Oregon R

C:Genetics:

A:Gene: Cnn
 A:Cross-references: FlyBase:FBgn0013765
 A:Map position: 2

C:Function:

A:Description: may participate in mitotic spindle assembly and the mechanics of morphoge

C:Keyword: leucine zipper
 Query Match 90.3%; Score 28; DB 2; Length 1148;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
 1111111
 DB 581 TATSLAD 587

RESULT 15

E70614
 hypothetical protein RV0648 - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: E70614
 R:Colo, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: E70614
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1215 <COL>

A:Cross-references: GB:292772; GB:AL123456; NID:g3261722; PIDN:CAB07105.1; PID:e30667

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV0648

Query Match 90.3%; Score 28; DB 2; Length 1215;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
 1111111
 DB 118 SATSLAD 124

Search completed: February 25, 2003, 10:33:49
 Job time: 2.88667 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 0.618333 Seconds
(without alignments)
469.543 Million cell updates/sec

Title: us-09-743-482a-4
Perfect score: 31
Sequence: 1 SATSLAD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	90.3	326	1 DUT_HSV4	000030 equine hep
2	28	90.3	511	1 AL21_SCHPO	Q10303 schizosacch
3	28	90.3	1148	1 CNN_DROME	P54623 drosophila
4	27	87.1	210	1 YCRO_ECOLI	P75952 escherichia
5	27	87.1	441	1 HSB2_ASPFU	P40292 aspergillus
6	27	87.1	482	1 RNF9_HUMAN	Q9u4y6 homo sapien
7	27	87.1	489	1 RNF9_MOUSE	Q9u4h5 mus musculu
8	27	87.1	541	1 GATB_YEAST	P33893 saccharomyc
9	27	87.1	731	1 MR11_COPCI	Q9u4v9 coprinus ci
10	26	83.9	369	1 HEM3_PEA	Q43082 pisum sativ
11	26	83.9	417	1 PGK_YARLI	P29407 yarrowia li
12	26	83.9	503	1 YN23_YEAST	P09729 schizosacch
13	26	83.9	596	1 Y44C_SCHPO	P52455 human herpe
14	26	83.9	640	1 UL06_HSV7J	P61624 mus musculu
15	26	83.9	794	1 Z148_MOUSE	Q62806 rattus norv
16	26	83.9	794	1 Z148_RAT	Q62806 rattus norv
17	26	83.9	1609	1 FIG2_YEAST	P25653 saccharomyc
18	25	80.6	130	1 MINK_RABIT	Q28705 oryctolagus
19	25	80.6	242	1 CU07_HUMAN	P57077 homo sapien
20	25	80.6	303	1 PANE_HALNI	Q9hrt0 halobacteri
21	25	80.6	310	1 HKL2_ARATH	P46640 arabidopsis
22	25	80.6	326	1 LDH_TOXGO	Q27797 toxoplasma
23	25	80.6	341	1 AAP2_RHLIV	Q52812 rhizobium 1
24	25	80.6	357	1 AROB_STRPY	Q99v73 streptococc
25	25	80.6	357	1 AROB_STRPY	P00365 agrobacteri
26	25	80.6	358	1 DHIO_AGRV4	P94210 agrobacteri
27	25	80.6	364	1 DDIA_AGRVI	P23844 escherichia
28	25	80.6	367	1 RIBD_ECOLI	P25539 e riboflavi
29	25	80.6	376	1 PROB_MYCTU	P71910 mycobacteri
30	25	80.6	377	1 FLA_CLOTY	P80583 clostridium
31	25	80.6	382	1 KSEI_ECOLI	P42501 escherichia
32	25	80.6	382	1 KSEI_ECOLI	P42501 escherichia
33	25	80.6	385	1 AGAS_STRCO	O50523 streptomyce

34	25	80.6	477	1 MEI2_HUMAN	O14770 homo sapien
35	25	80.6	477	1 MEI2_MOUSE	P97367 mus musculu
36	25	80.6	509	1 PDI_RABIT	P21195 oryctolagus
37	25	80.6	522	1 YH24_CAERL	O27242 caenorhabdi
38	25	80.6	549	1 WTP7_PSEAE	P05103 pseudomonas
39	25	80.6	573	1 RCEN_TREPA	O83456 treponema p
40	25	80.6	954	1 BIR1_YEAST	P47134 saccharomyc
41	25	80.6	1034	1 PMPE_CHLTR	P38008 chlamydia t
42	25	80.6	1468	1 DPOA_YEAST	P13382 saccharomyc
43	25	80.6	2670	1 YAO5_SCHPO	Q10105 schizosacch
44	25	80.6	2842	1 APC_RAT	P70478 rattus norv
45	25	80.6	2843	1 APC_HUMAN	P25054 homo sapien

ALIGNMENTS

RESULT 1
DUT_HSV4 STANDARD: PRT; 326 AA.

AC 000030:
DT 01-DEC-1992 (rel. 24, Created)
DT 01-DEC-1992 (rel. 24, Last sequence update)
DT 15-DEC-1998 (rel. 37, Last annotation update)
DE Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)
DE (dUTPase) (dUTP pyrophosphatase).
GN 9 OR B3.

OS Equine herpesvirus type 4 (strain 1942) (EHV-4) (Equine herpesvirus type 1 subtype 2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae.
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=10333;

RA MEDLINE=91202570; PubMed=1850013;
RA Whitaker G.R., Riggo M.P., Halliburton I.W., Killington R.A.,
RA Allen G.P., Meredith D.M.;

RT Antigenic and protein sequence homology between VP13/14, a herpes simplex virus type 1 tegument protein, and gp10, a glycoprotein of equine herpesvirus 1 and 4.*
RT J. Virol. 65:2320-2326(1991).

CC FUNCTION: THIS ENZYME IS INVOLVED IN NUCLEOTIDE METABOLISM. IT PRODUCES DUMP, THE IMMEDIATE PRECURSOR OF THYMIDINE NUCLEOTIDES. AND IT DECREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT URACIL CANNOT BE INCORPORATED INTO DNA.
CC CATALYTIC ACTIVITY: dUTP + H(2)O = dUMP + diphosphate.
CC SIMILARITY: BELONGS TO THE DUTPASE FAMILY.

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DR EMBL: X17684; GAA35671.1; -
DR PIR: S36705;
DR InterPro: IPR001428; DeoxyUTPase.
DR Pfam: PF00692; dUTPase; 1
KW Hydrolase; Nucleotide metabolism
SQ SEQUENCE 326 AA; 35172 MW; C0825CB752D36D58 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 326;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
|||:||||
Db 3 SATNLAD 9

RESULT 2

AL21_SCHPO
ID AL21_SCHPO STANDARD: PRT: 511 AA.
AC Q10303;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cell polarity protein alp21.
GN ALP21 OR STOI OR SPAC22H10.10.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
ON NCBI_TaxID=4896;
RX SEQUENCE FROM N.A.
RA Radcliffe P.A., Toda T.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RC STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moutie S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Slimmons M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Wolckstein G., Aert R., Robben J., Grymopre B.,
RA Welterts I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC - FUNCTION: REQUIRED FOR MICROTUBULES FUNCTION.
CC -----
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CC -----
CC EMBL: AB008749; BAA23374.1; -
DR EMBL: Z69730; CA93613.1; -
DR InterPro: IPR001611; LRR.
DR Pfam: PF00560; LRR; 2.
KW Microtubules.
SQ SEQUENCE 511 AA: 58591 MW; B6FD84864AD648B6 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 511;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
Db 27% SATSLAD 280

RESULT 3
ID CNN_DROME STANDARD: PRT: 1148 AA.
AC P54623;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Centrosomin (arrow protein).
GN CNN OR ARR
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
ON NCBI_TaxID=7227;
RX SEQUENCE FROM N.A.
RA STRAIN=Oregon-R;
RC MEDLINE=96102828; PubMed=8582295;
RA Heuer J.G., Li K., Kaufman T.C.;
RT "The Drosophila homeotic target gene centrosomin (cn) encodes a
RT novel centrosomal protein with leucine zippers and maps to a genomic
RT region required for midgut morphogenesis.";
RL Development 121:3861-3876(1995).
RN [2]
RN REVISIONS.
RC STRAIN=Oregon-R;
RA Li K., Kaufman T.C.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=9622300; PubMed=8653793;
RA Li K., Kaufman T.C.;
RT "The homeotic target gene centrosomin encodes an essential centrosomal
RT component.";
RL Cell 85:585-596(1996).
CC - FUNCTION: MAY PARTICIPATE IN MITOTIC SPINDLE ASSEMBLY AND THE
CC MECHANICS OF MORPHOGENESIS THROUGH AN INTERACTION WITH
CC MICROTUBULES, EITHER DIRECTLY OR INDIRECTLY. CNN IS A TARGET OF
CC SEVERAL HOMEOTIC GENES.
CC - SUBUNIT: MONOMER.
CC - SUBCELLULAR LOCATION: LOCALIZED TO THE CENTROSOMES THROUGH
CC COMPLETE NUCLEAR CYCLES IN MITOTIC CELLS. REDISTRIBUTED INTO THE
CC CYTOSOL IN G2 PHASE CELLS.
CC - TISSUE SPECIFICITY: DEVELOPING VISCERAL MESODERM OF THE MIDGUT,
CC THE CENTRAL AND PERIPHERAL NERVOUS SYSTEM, AND DEVELOPING GONADS.
CC -----
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CC -----
CC EMBL: U35621; AAB82065.1; -
DR Phosphorylation: FBgn0013765; cm.
KW Phosphorylation; Developmental protein; Coiled coil.
FT DOMAIN 97 516
FT DOMAIN 626 654
FT DOMAIN 644 656
FT DOMAIN 712 983
SQ SEQUENCE 1148 AA: 129907 MW; 6C178AF7ABEC89C6 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 1148;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
Db 581 SATSLAD 587

RESULT 4

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YCFO_ECOLI STANDARD: PRT: 210 AA.
ID YCFO_ECOLI
AC P75952; Q9R7N8; Q9R7N9;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical transcriptional regulator ycfO.
GN YCFO OR B1111.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=9742617; PubMed=9278503;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RL "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Alba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horuchi T.;
RL "A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
CC -1 SIMILARITY: BELONGS TO THE TETR/ACR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
-----
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-----
CC EMBL: AE000211; AAC74195.1; ALT_INIT.
CC EMBL: D90746; BAA35926.1; ALT_INIT.
CC EMBL: D90747; BAA35931.1; ALT_INIT.
CC Ecogen: EG13435; YCFO.
DR InterPro: IPR001647; HTH_Tetr.
DR Pfam: PF00440; Tetr_1.
DR PROSITE: PS01081; HTH_TETR_FAMILY; FALSE_NEG.
KW Hypothetical protein; transcription regulation; DNA-binding;
KW Complete proteome.
FT DNA_BIND 41 60 H-T-H MOTIF (POTENTIAL);
FT SEQUENCE 210 AA; 23361 MW; 8CID525687556E2 CRC64;
SO QUERY MATCH
Query Match 87.18; Score 27; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Heat shock protein HSP1 (65 kDa IGE-binding protein) (Allergen Asp f
DE 12) (Fragment).
GN HSP1.
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurup V.P., Banerjee B.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 165-284 FROM N.A.
RC STRAIN-ATCC 4202 / AF-102;
RX MEDLINE=93260199; PubMed=8491935;
RA Kumar A., Reddy L.V., Sochanik A., Kurup V.P.;
RA "Isolation and characterization of a recombinant heat shock protein
RT of Aspergillus fumigatus.";
RL J. Allergy Clin. Immunol. 91:1024-1030(1993).
CC -1 FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
-----
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-----
CC EMBL: U92465; AAB51544.1;
DR InterPro: IPR001404; Hsp90.
DR Pfam: PF00183; HSP90_1.
DR PROSITE: PS00298; HSP90; PARTIAL.
KW Chaperone; ATP-binding; Heat shock; Allergen.
FT NON_TER 1
FT SEQUENCE 441 AA; 50523 MW; 3726AF5C8F83A4 CRC64;
SO QUERY MATCH
Query Match 87.18; Score 27; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RX MEDLINE-2123161; PubMed-11331580;
 RA Raymond A., Meroni G., Fantozzi A., Meila G., Cairo S., Luzzi L.,
 RA Rignaneli D., Zanaria E., Messali S., Calanca S., Guftanti A.,
 RA Minucci S., Pellicci P.G., Ballabio A.,
 RT "The tripartite motif family identifies cell compartments.";
 RL EMBO J. 20:2140-2151(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RA Shima S., Tamaya G., Oka A., Inoko H.,
 RT "Homo sapiens 21228,817bp genomic DNA of 6p21.3 HLA class I region.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Seems to play an important role in erythropoiesis (By similarity).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: alpha (shown here) and beta; are produced by alternative splicing.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 1 B BOX-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
 CC -----
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 CC -----
 DR EMBL: Y07829; CAB5384.1; -;
 DR EMBL: AF220122; AAG53495.1; -;
 DR EMBL: AF220123; AAG53496.1; -;
 DR EMBL: AP000517; BAB6332.1; -;
 DR Genew: HGNC:110072; TRIM10.
 DR MIM: 605701; -;
 DR Interpro: IPR001870; Gamma_carboxylase.
 DR Interpro: IPR003877; SPRY_domain.
 DR Interpro: IPR003877; SPRY_receptor.
 DR Interpro: IPR00315; ZnF_Box.
 DR Interpro: IPR001841; ZnF_Ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00643; zf-B-box; 1.
 DR Pfam: PF00643; SPRY; 2.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00449; SPRY; 1.
 DR PROSITE: PS50119; ZF_Box; 1.
 DR PROSITE: PS50158; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Zinc-finger; Coiled coil; Alternative splicing.
 FT ZN_FING 16 61
 FT ZN_FING 94 136
 FT DOMAIN 143 178
 FT DOMAIN 363 462
 FT VARSPLIC 370 482
 FT -----
 FT CONFLICT 104 105
 FT CONFLICT 104 105
 FT CONFLICT 168 168
 FT CONFLICT 337 337
 FT CONFLICT 378 378
 FT CONFLICT 378 378
 SQ SEQUENCE 482 AA: 55087 MW: 19354750602CD42C CRC64:
 Query Match 87.1%; Score 27; DB 1; Length 482;
 Best Local Similarity 85.7%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7
 ID RNF9_MOUSE STANDARD: PRT: 489 AA.
 AC Q9WH05; Q9CY03;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE RING finger protein 9 (hematopoietic RING finger 1) (Tripartite motif protein 10).
 GN TRIM10 OR RNF9 OR HERP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE-99223609; PubMed-10207104;
 RA Harada H., Harada Y., O'Brien D.P., Rice D.S., Naeve C.W.,
 RA Downing J.R.;
 RT "HERP1, a novel hematopoiesis-specific RING finger protein, is required for terminal differentiation of erythroid cells.";
 RL Mol. Cell. Biol. 19:3808-3815(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Reymond A., Meroni G.;
 RT "Deciphering the function of the tripartite motif containing proteins.";
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryonic Liver;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batool S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyshaw-Borisi A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Seems to play an important role in erythropoiesis.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 1 B BOX-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
 CC -----
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 CC -----
 DR EMBL: AF134811; AAD28534.1; -;
 DR EMBL: AF220121; AAG53494.1; -;
 DR EMBL: AK011082; BAB27386.1; -;
 DR MGD: MGI:1338757; Trim10.
 DR Interpro: IPR001870; Gamma_carboxylase.
 DR Interpro: IPR003877; SPRY_domain.
 DR Interpro: IPR003877; SPRY_receptor.

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DR InterPro: IPR000315; ZnF_Box.
DR InterPro: IPR001841; ZnF_Fing.
DR Pfam: PF00097; zf-C3HC4.1.
DR Pfam: PF00623; SPRY.1.
DR Pfam: PF00643; zf-B_box.1.
DR SMART: SM00336; BBOX.1.
DR SMART: SM00449; RING.1.
DR PROSITE: PS00119; ZF_BOX.1.
DR PROSITE: PS00518; ZF_RING.1.
DR PROSITE: PS50089; ZF_RING_2.1.
DR Zinc_Finger; Coiled coil.
FT ZN_FING 16 61 RING-TYPE.
FT ZN_FING 94 135 B_BOX-TYPE.
FT DOMAIN 144 180 COILED COIL (POTENTIAL).
FT DOMAIN 362 484 SPRY.
FT CONFLICT 133 133 R -> H (IN REF. 1).
FT CONFLICT 231 231 R -> Q (IN REF. 1).
FT CONFLICT 365 365 H -> Y (IN REF. 1).
FT CONFLICT 368 368 M -> V (IN REF. 1).
SQ SEQUENCE 489 AA; 55630 MW; AA7E26FABD120804 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 489;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SATSLAD 7
Db 6 SVTSLAD 12

RESULT 8
GATB_YEAST
ID GATB_YEAST STANDARD: PRT: 541 AA.
AC P33893;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Probable glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial
DE precursor (EC 6.3.5.-) (Glu-ADT subunit B) (Cytochrome oxidase
DE assembly factor Pmt112).
DE Pmt112 OR YBL080C OR YBL0724.
CN Saccharomyces cerevisiae (Baker's yeast).
OS Saccharomyces cerevisiae.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94363744; PubMed=8082172;
RA Mulero J.J., Rosenthal J.K., Fox T.D.;
RT "PMT112, a Saccharomyces cerevisiae nuclear gene regulated to maintain
RT rho+ mitochondrial DNA."
RL Curr. Genet. 25:299-304(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C;
RX MEDLINE=96076635; PubMed=7502586;
RA Opermeier B., Gassenhuber J., Piravandi E., Domdey H.;
RT "Sequence analysis of a 78.6 kb segment of the left end of
RT Saccharomyces cerevisiae chromosome II."
RL Yeast 11:1103-1112(1995).
CC -1- FUNCTION: FURNISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED
CC Gln-tRNA(Gln) THROUGH THE TRANSMUTATION OF MISACTYLATED Gln-
CC tRNA(Gln) IN THE MITOCHONDRIA. THE REACTION TAKES PLACE IN THE
CC PRESENCE OF GLUTAMINE AND ATP THROUGH AN ACTIVATED GAMMA-PHOSPHO-
CC Gln-tRNA(Gln) (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Mitochondrial (Probable).
CC -1- SIMILARITY: BELONGS TO THE GATB FAMILY.
CC
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CC
DR EMBL: X79489; CAA56028.1; -
DR EMBL: Z35841; CAA84901.1; -
DR EMBL: L22072; AAC37508.1; -
DR PIR: S45428; S45428.
DR SGD: S0000176; Pmt112.
DR InterPro: IPR004413; GATB.
DR InterPro: IPR003789; GATB_Yqey.
DR InterPro: IPR001773; Gln_amidtransfb.
DR Pfam: PF01162; GATB.1.
DR Pfam: PF02637; DUF166.2.
DR Pfam: PF02834; GATB_N.1.
DR TIGRFAMs: TIGR00133; gatb; 1.
DR PROSITE: PS01234; GATB; 1.
KW Protein biosynthesis; Ligase; Mitochondrion; Transl. peptide.
FT TRANSIT 1 541 MITOCHONDRION (POTENTIAL).
FT CHAIN ? 541 PROBABLE GLUTAMYL-tRNA(Gln)
FT CONFLICT 415 415 AMIDOTRANSFERASE SUBUNIT B.
SQ SEQUENCE 541 AA; 61842 MW; EE96E82F0F82BDC CRC64;

Query Match 87.1%; Score 27; DB 1; Length 541;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SATSLAD 7
Db 52 SATSLWD 58

RESULT 9
MRE11_COPCI
ID MRE11_COPCI STANDARD: PRT: 731 AA.
AC Q9UVN9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Double-strand break repair protein MRE11.
CN MRE11.
OS Coprinus cinereus (Binkley cap fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Phlebotremataceae; Coprinopsis.
OX NCBI_TaxID=5346;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Okayama-7;
RX MEDLINE=20221721; PubMed=10757758;
RA Gerecke E.E., Zolan M.E.;
RT "An mre11 mutant of Coprinus cinereus has defects in meiotic
RT chromosome pairing, condensation and synapsis."
RL Genetics 154:1125-1139(2000).
CC -1- FUNCTION: Involved in DNA double-strand break repair (DSBR).
CC Possesses single-strand endonuclease activity and double-strand-
CC specific 3'-5' exonuclease activity. Also involved in meiotic DSB
CC processing (by similarity).
CC -1- COFACTOR: Manganese (By similarity).
CC -1- SUBUNIT: FORMS A COMPLEX WITH RAD50 (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MRE11/RAD52 FAMILY.
CC
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CC
DR EMBL: AF178433; AAD55951.1; -
DR InterPro: IPR003701; DNA_repair.
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DR InterPro: IPR004843; M-peptidase.
 DR InterPro: IPR004844; S/T-phosphatase.
 DR Pfam: PF00149; Metallophos. 1.
 DR TIGRPFAMs: TIGR00583; mre11; 1.
 DR DNA repair: Hydrolyase; Nuclease; Endonuclease; Exonuclease;
 KW Nuclear protein; Manganese; Melosis.
 SQ SEQUENCE 731 AA; 80647 MW; 09281A77D69FA916 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 731;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSLAD 7
 |||||
 Db 292 ATSLAD 297

RESULT 10
 HEM3_PEA STANDARD; PRT; 369 AA.

AC Q43082;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Porphobilinogen deaminase, chloroplast precursor (EC 4.3.1.8) (PBG)
 DE (Hydroxymethylbilane synthase) (HMBs) (Pre-uroporphyrinogen synthase).
 GN HMC.
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciales; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=cv. Little Marvel; TISSUE=Leaf;
 RX MEDLINE=94269188; PubMed=7516080;
 RA Wlty M., Wallace-Cook A.D.M., Albrecht H., Spano A.J., Michel H.,
 RA Shadrinow J., Hunt D.F., Timko M.P., Smith A.G.;
 RT Structure and expression of chloroplast-localized porphobilinogen
 RT deaminase from pea (Pisum sativum L.) isolated by redundant
 RT polymerase chain reaction.";
 RT Plant Physiol. 103:139-147(1993).

CC -1- FUNCTION: TETRAPOLYMERIZATION OF THE MONOPYRROLE PBG INTO THE
 CC HYDROXYMETHYLBILANE PREUROPORPHYRINOGEN IN SEVERAL DISCRETE STEPS.
 CC -1- CATALYTIC ACTIVITY: 4 porphobilinogen + H(2)O =
 CC hydroxymethylbilane + 4 NH(3).
 CC -1- COFACTOR: COVALENTLY BINDS A DIPHROMETHANE COFACTOR TO WHICH
 CC THE PORPHOBILINOGEN SUBUNITS ARE ADDED.
 CC -1- PATHWAY: Porphyrin biosynthesis by the C5 pathway, fourth step.
 CC Involved in chlorophyll biosynthesis.
 CC -1- SIMILARITY: BELONGS TO THE HMBs FAMILY.

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CC EMBL: X73418; CA51820.1; -;
 DR HSSP: P06983; YPN.

DR InterPro: IPR000860; Porphobil_deam.
 DR Pfam: PF01379; Porphobil_deam; 1.

DR PRINTS: PR00151; PORPHBDNMAE.
 DR Prodom: PD002745; Porphobil_deam; 1.

DR TIGRPFAMs: TIGR00212; hmc1; 1.
 DR PROSITE: PS00533; PORPHOBILINOGEN_DEAM; 1.

KW Porphyrin biosynthesis; Chlorophyll biosynthesis; lyase; Chloroplast;
 KW Treasit peptide.

FT TRANSIT 1 46 CHLOROPLAST.
 FT CHAIN 47 369 PORPHOBILINOGEN DEAMINASE.

FT BINDING 303 303 PYRROMETHANE COFACTOR (BY SIMILARITY).

SQ SEQUENCE 369 AA; 39930 MW; F7660D8390894431 CRC64;

Query Match 83.9%; Score 26; DB 1; Length 369;
 Best Local Similarity 85.7%; Pred. No. 65;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SATSLAD 7
 |||||
 Db 172 SATSLAD 178

RESULT 11
 PGK_YARLI STANDARD; PRT; 417 AA.

AC P29407;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphoglycerate kinase (EC 2.7.2.3).
 GN PGK1.
 OS Yarrowia lipolytica (Candida lipolytica).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OX NCBI_TaxID=4952;
 RN [1]
 RP SEQUENCE FROM N.A. / W29;
 RC STRAIN=ATCC 20460 / W29;
 RA Le Dall M.-T., Nicaud J.-M., Tretton B.Y., Galliard C.;
 RL Submitted (XX-1992) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-
 CC phospho-D-glyceroyl phosphate.
 CC -1- PATHWAY: Second phase of glycolysis; second step.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.

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CC EMBL: M91598; AAC37504.1; -;
 DR HSSP: P00560; IOPG.

DR InterPro: IPR001576; PGK.
 DR Pfam: PF00162; PGK; 1.

DR PRINTS: PR00477; PHGICKINASE.
 DR PROSITE: PS00111; PGKICERATE_KINASE; 1.

KW Transferase; Kinase; Glycolysis.
 SQ SEQUENCE 417 AA; 44772 MW; 3F308467FCC730BF CRC64;

Query Match 83.9%; Score 26; DB 1; Length 417;
 Best Local Similarity 85.7%; Pred. No. 75;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SATSLAD 7
 |||||
 Db 152 SATSLAD 158

RESULT 12
 YN3_YEAST STANDARD; PRT; 503 AA.

AC P53832;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Hypothetical 52.3 kDa protein in MRPL10-ERG24 intergenic region
 DE precursor.

GN YNL283C OR N0583.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

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OC Saccharomycetales; Saccharomycetales; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Messenguy F., Dubois E., Vierendeels F., Scherens B., Pierard A.,
RA Glansdorff N.;
RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO S.POMBE SPBC3D5.14C.
CC -----
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CC -----
DR EMBL: Z71559; CA96195.1; -
DR SGD: S0005227; INL283C.
DR InterPro: IPR002889; WSC.
DR Pfam: PF01822; WSC. 1.
DR SMART: SM00321; WSC. 1.
KW Hypothetical protein; Transmembrane; Signal.
FT SIGNAL 1 23
FT CHAIN 24 503
FT TRANSMEM 61 81
FT TRANSMEM 326 346
FT CARBOHYD 394 394
FT CARBOHYD 429 429
FT CARBOHYD 475 475
FT CARBOHYD 483 483
FT CARBOHYD 498 498
FT CARBOHYD 499 499
SQ SEQUENCE 503 AA; 52292 MW; F2392A73C5CBAB50 CRC64;

Query Match      83.9%; Score 26; DB 1; Length 503;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SATSLAD 7
Db 455 SATSLAD 461

RESULT 13
YAC_SCHPO STANDARD; PRT; 596 AA.
ID YAC_SCHPO
AC 009729;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C31A2.12 in chromosome I.
GN SPAC31A2.12.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetales;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RC MEDLINE=21848401; Pubmed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Soudous J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moutle S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

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RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckert G., Aert R., Robben J., Gymnopoulos B.,
RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer C., Holzer D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambui R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motlier S.,
RA Gilbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet X., Gallard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Cerretti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
RA Sipakvski G.V., Uesery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: TO S.POMBE SPAC8A.13C AND TO YEAST ROD1, YFR022W AND
CC YGR068C.
CC -----
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CC -----
DR EMBL: Z50113; CA90470.1; -
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 194 211
FT DOMAIN 532 537
SQ SEQUENCE 596 AA; 65902 MW; C93B9FA55688E7B1 CRC64;

Query Match      83.9%; Score 26; DB 1; Length 596;
Best Local Similarity 85.7%; Pred. No. 11e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SATSLAD 7
Db 449 SETSLAD 455

RESULT 14
UL06_HSV7J STANDARD; PRT; 640 AA.
ID UL06_HSV7J
AC P52455;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Varion protein U76.
GN U76.
OS Human herpesvirus (type 7 / strain J1) (HHV7).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=57278;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RA Nicholas J.;
CC -1- FUNCTION: PRESUMED VIRION PROTEIN; POSSIBLE ROLE IN DNA
CC PACKAGING.
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL6,
CC EBV-1 56, EBV BBF1, HCMV UL104, AND VZV 54.
CC -----
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CC -----
DR EMBL: U43400; AAC54737.1; -
DR InterPro: IPR002660; Herpes_UL6.

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DR Pfam: PF01763; Herpes_Ub6; 1.
 DR PRODOM: PD003210; Herpes_Ub6; 1.
 SQ SEQUENCE 640 AA; 74538 MW; 4021A6E1B453B63 CRC64;
 Query Match 83.9%; Score 26; DB 1; Length 640;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SATSLAD 7
 Db 220 SATSLAD 226
 RESULT 15
 Z148_MOUSE STANDARD; PRT; 794 AA.
 ID Z148_MOUSE
 AC 061624; P97475;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Zinc finger protein 148 (Zinc finger DNA binding protein 89)
 DE (Transcription factor ZBP-89) (G-rich box-binding protein) (beta
 DE enolase repressor factor 1) (Transcription factor BRCOL1).
 GN ZNF148 OR ZFP148 OR ZBP89.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=Limb;
 RX MEDLINE=98079087; PubMed=9417107;
 RA Passaniti R., Anton A., Barbieri G., Rubino P., Melchionna R.,
 RA Cosu G., Fico S., Giallongo A.;
 RA "Negative regulation of beta enolase gene transcription in embryonic
 RT muscle is dependent upon a zinc finger factor that binds to the G-rich
 RT box within the muscle-specific enhancer."
 RL J. Biol. Chem. 273:484-494(1998).
 RN [2]
 RP SEQUENCE OF 26-794 FROM N.A.
 RX MEDLINE=97184139; PubMed=9030551;
 RA Hasegawa T., Takeuchi A., Miyashi O., Isobe K.-I., de Crombrughe B.;
 RT "Cloning and characterization of a transcription factor that binds to
 RT the proximal promoters of the two mouse type I collagen genes."
 RL J. Biol. Chem. 272:4915-4923(1997).
 CC -1- FUNCTION: INVOLVED IN TRANSCRIPTIONAL REGULATION. REPRESENTS THE
 CC TRANSCRIPTION OF A NUMBER OF GENES INCLUDING GASTRIN, STROMELYSIN
 CC AND ENOLASE. BINDS TO THE G-RICH BOX IN THE ENHANCER REGION OF
 CC THESE GENES.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.
 CC -----
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 CC -----
 DR EMBL: X98096; CAA66725.1; -;
 DR EMBL: U80078; AAB38507.1; -;
 DR HSSP: P08047; ISP2.
 DR MCD: MGI:133234; Zfp148.
 DR InterPro: IPR000822; Znf_C2H2.
 DR Pfam: PF00096; zf-C2H2; 4.
 DR PRINTS: PR00048; ZINC_FINGER.
 DR PRODOM: PD000003; Znf_C2H2; 1.
 DR SMART: SM00355; Znf_C2H2; 4.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 4.
 DR Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;

KW Nuclear protein; Repet.; Repressor.
 FT DOMAIN 171 278 ZINC-FINGERS.
 FT ZN_FING 171 193 C2H2-TYPE.
 FT ZN_FING 199 221 C2H2-TYPE.
 FT ZN_FING 227 249 C2H2-TYPE.
 FT ZN_FING 255 278 C2H2-TYPE.
 FT CONFLICT 283 283 K -> N (IN REF. 2).
 FT CONFLICT 314 314 K -> P (IN REF. 2).
 FT CONFLICT 319 319 K -> Q (IN REF. 2).
 SQ SEQUENCE 794 AA; 88751 MW; 4CB1C2A1822703FD CRC64;
 Query Match 83.9%; Score 26; DB 1; Length 794;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SATSLAD 7
 Db 698 SATSLAD 704
 Search completed: February 25, 2003, 10:37:28
 Job time : 3.6183 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 : Search time 1.77333 seconds
(without alignments)
813.344 Million cell updates/sec

Title: US-09-743-482A-4

Sequence: 1 SATSLAD 7

Scoring table: BLAST62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	1106	3 Q9USN5	Q9USN5 schizosacch
2	29	93.5	473	16 Q823P8	Q823P8 salmone
3	29	93.5	701	5 Q9GNT5	Q9GNT5 leishmania
4	28	90.3	66	16 Q9S2N5	Q9S2N5 streptomyce
5	28	90.3	140	16 Q98DG5	Q98DG5 rhizobium 1
6	28	90.3	144	16 Q98DH7	Q98DH7 rhizobium 1
7	28	90.3	185	16 Q8UHU5	Q8UHU5 agrobacteri
8	28	90.3	391	5 Q95YQ3	Q95YQ3 proteus mir
9	28	90.3	433	2 Q94847	Q94847 leishmania
10	28	90.3	433	16 Q25321	Q25321 helicobacte
11	28	90.3	433	16 Q9ZLN2	Q9ZLN2 helicobacte
12	28	90.3	522	4 Q96DN1	Q96DN1 homo sapien
13	28	90.3	563	10 Q9RCR1	Q9RCR1 populus bal
14	28	90.3	563	10 Q94KC2	Q94KC2 populus tre
15	28	90.3	703	3 Q74438	Q74438 schizosacch

17	28	90.3	742	5 Q965M4	Q965M4 caenorhabdi
18	28	90.3	772	4 Q96JG9	Q96JG9 homo sapien
19	28	90.3	851	16 Q9AC38	Q9AC38 caulobacter
20	28	90.3	1148	5 Q9V6P8	Q9V6P8 drosophila
21	28	90.3	1215	16 P96937	P96937 mycobacteri
22	28	90.3	1398	16 Q8VKH0	Q8VKH0 mycobacteri
23	27	87.1	75	16 Q8XAD5	Q8XAD5 escherichia
24	27	87.1	120	2 Q8RMB0	Q8RMB0 legionella
25	27	87.1	120	2 Q8RMA9	Q8RMA9 legionella
26	27	87.1	120	2 Q8RMA2	Q8RMA2 legionella
27	27	87.1	211	16 Q8ZQ04	Q8ZQ04 salmonella
28	27	87.1	211	16 Q8Z714	Q8Z714 salmonella
29	27	87.1	217	16 Q8XEW7	Q8XEW7 salmonella
30	27	87.1	231	10 Q9ZMS9	Q9ZMS9 arabidopsis
31	27	87.1	236	16 Q8X8G3	Q8X8G3 escherichia
32	27	87.1	353	5 Q9XZT7	Q9XZT7 leishmania
33	27	87.1	375	16 Q9ADJ2	Q9ADJ2 streptomyce
34	27	87.1	430	16 Q31703	Q31703 bacillus su
35	27	87.1	471	10 Q9M4R4	Q9M4R4 elaeis guin
36	27	87.1	532	10 Q94AC4	Q94AC4 arabidopsis
37	27	87.1	553	10 Q82252	Q82252 arabidopsis
38	27	87.1	554	6 Q95K39	Q95K39 macaca fasc
39	27	87.1	578	16 P95194	P95194 mycobacteri
40	27	87.1	583	3 Q97EJ1	Q97EJ1 schizosacch
41	27	87.1	616	2 Q50407	Q50407 mycobacteri
42	27	87.1	621	4 Q96MC4	Q96MC4 homo sapien
43	27	87.1	674	16 Q98F52	Q98F52 rhizobium 1
44	27	87.1	709	5 Q16729	Q16729 caenorhabdi
45	27	87.1	757	2 Q05992	Q05992 alcaligenes

ALIGNMENTS

RESULT 1

ID Q9USN5 PRELIMINARY: PRT: 1106 AA.

AC Q9USN5; 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE NAD-specific glutamate dehydrogenase.

GN SPOC132.04C.

OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972H-7.

RA Lyne M., Rajandream M.A., Barrell B.G., Aert R., Volckaert G.;

RL Submitted (OCF-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL121807; CAB58131.1; -

DR InterPro:IPR001625; GLFV_Dh.

DR Pfam: PF02028; GLFV_dehydrog_N; 1.

DR Pfam: PF02812; GLFV_dehydrog_N; 1.

DR Pfam: PF02812; GLFV_dehydrog_N; 1.

DR Pfam: PF02812; GLFV_dehydrog_N; 1.

Q965M4	caenorhabdi
Q96JG9	homo sapien
Q9AC38	caulobacter
Q9V6P8	drosophila
P96937	mycobacteri
Q8VKH0	mycobacteri
Q8XAD5	escherichia
Q8RMB0	legionella
Q8RMA9	legionella
Q8RMA2	legionella
Q8ZQ04	salmonella
Q8Z714	salmonella
Q8XEW7	salmonella
Q9ZMS9	arabidopsis
Q8X8G3	escherichia
Q9XZT7	leishmania
Q9ADJ2	streptomyce
Q31703	bacillus su
Q9M4R4	elaeis guin
Q94AC4	arabidopsis
Q82252	arabidopsis
Q95K39	macaca fasc
P95194	mycobacteri
Q97EJ1	schizosacch
Q50407	mycobacteri
Q96MC4	homo sapien
Q98F52	rhizobium 1
Q16729	caenorhabdi
Q05992	alcaligenes

Query Match 100.0%; Score 31; DB 3; Length 1106;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
DB 507 SATSLAD 513

RESULT 2
Q823P8 PRELIMINARY: PRT: 473 AA.
AC Q823P8;
DT 01-MAR-2002 (Tremblrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DT Putative exported protein.
 GN STY3343.
 OS *Salmonella typhi*.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Salmonella*.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Fellwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skellon J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 DR EMBL: A1627277; CAD03000.1;
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 473 AA; 55423 MW; 0DAD748F3A1B9PF CRC64;

Query Match 93.5%; Score 29; DB 16; Length 473;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
 Db 182 SATSLAD 188

RESULT 3
 ID 09GN15 PRELIMINARY; PRT; 701 AA.
 AC 09GN15;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 GN L3836.7.
 OS *Leishmania major*.
 CC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Myler P.J., Sisk E., Cawthra J., Handley F., Vogt C., Robertson L.,
 RA McDonagh P., Stuart K.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC011016; AAG34192.1;
 SQ SEQUENCE 701 AA; 73861 MW; EA1BC5ECF031966 CRC64;

Query Match 93.5%; Score 29; DB 5; Length 701;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
 Db 9 SATSLAD 15

RESULT 4
 ID 09S2N5 PRELIMINARY; PRT; 66 AA.
 AC 09S2N5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Hypothetical protein SCO2108.
 GN SCO2108 OR SC6E10.02.
 OS Streptomyces coelicolor.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K., Harris D.;
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA James K.D., Parkhill J., Barrall B.G., Rajandream M.A.;
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denaplatte D., Eichner A., Cullum J.,
 RA Kinsht H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hildreth J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL109661; CAB51956.1;
 DR InterPro: IPR003749; Tris.
 DR Pfam: PF02597; DUF170; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 66 AA; 6570 MW; E237269156D6F4EE CRC64;

Query Match 90.3%; Score 28; DB 16; Length 66;
 Best Local Similarity 85.7%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
 Db 47 SATSLAD 53

RESULT 5
 ID 09BDG5 PRELIMINARY; PRT; 140 AA.
 AC 09BDG5;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Large conductance mechanosensitive channel.
 GN MUR4713.
 OS *Rhizobium loti* (Mesorhizobium loti).
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

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RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL: AP003004; BAB51306.1; -.
DR InterPro: IPR001185; MS_channel.
DR Pfam: PF01741; MscL. 1.
DR PRINTS: PR01264; MECHCHANNEL.
DR ProDom: PD007253; MS_channel. 1.
DR TIGRFAMs: TIGR00220; mscL. 1.
KW Complete proteome.
SQ SEQUENCE 140 AA; 15086 MW; 24F05D204D47C240 CRC64;

OY 1 SATSLAD 7
Db 64 NATSLAD 70

Query Match 90.3%; Score 28; DB 16; Length 140;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
O98DH7 PRELIMINARY; PRT; 144 AA.
ID O98DH7
AC O98DH7
DT 01-OCT-2001 (TREMblrel. 18, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Mechanosensitive channel.
GN ML4699.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF30309; PubMed=11214968;
RX MEDLINE=21082930;
RA Kaneke T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL: AP003004; BAB51294.1; -.
DR InterPro: IPR001185; MS_channel.
DR Pfam: PF01741; MscL. 1.
DR PRINTS: PR01264; MECHCHANNEL.
DR ProDom: PD007253; MS_channel. 1.
DR TIGRFAMs: TIGR00220; mscL. 1.
KW Complete proteome.
SQ SEQUENCE 144 AA; 15570 MW; 7DE765C2638B3B54 CRC64;

Query Match 90.3%; Score 28; DB 16; Length 144;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
Db 69 NATSLAD 75

RESULT 7
O8UH05 PRELIMINARY; PRT; 185 AA.
ID O8UH05
AC O8UH05;
DT 01-JUN-2002 (TREMblrel. 21, Created)

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DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical protein Atu0584.
GN AT00584 OR AGR_C1032.
OC Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyce D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
RA Raymond C., Rouse G., Saenphimachak G., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quirello B., Goldman B.S., Cao Y., Askenzi M., Halling C., Mullin L.,
RA Houmel K., Gordon J., Vaudin M., Iatchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL: AE009027; AAL41601.1; ALT_INIT.
DR EMBL: AE007992; AAK86395.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 185 AA; 19783 MW; 6AD9D8697BB7F29D CRC64;

Query Match 90.3%; Score 28; DB 16; Length 185;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
Db 37 NATSLAD 43

RESULT 8
O8VPB0 PRELIMINARY; PRT; 214 AA.
ID O8VPB0
AC O8VPB0;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Regulatory protein AcrR.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A.
RA Visalli M.A., Murphy E., Projan S.J., Bradford P.A.;
RT "Acr multidrug efflux homolog is associated with reduced levels of
RT susceptibility to GAR-936 in Proteus mirabilis."
RL EMBL: AY061647; AAL32124.1; -.
DR InterPro: IPR001647; HTH_Tetr.
DR Pfam: PF00440; tetr. 1.
DR PRINTS: PR00455; HTHTEETR.
DR PROSITE: PS01081; HTH_TETR_FAMILY; UNKNOWN_1.

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SO SEQUENCE 214 AA; 24630 MW; 1A619F0ADF60CF16 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 214;
Best Local Similarity 85.7%; Pred. NO. 97;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
:|||||:
Db 30 SATSLAD 36

RESULT 9

OY95Y03 PRELIMINARY; PRT; 391 AA.
AC O95Y03;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical predicted protein LM15-1.64, unknown function.
GN LM15-1.64.
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
RN Submitted (AUG-2001) to the EMBL/GenBank/DDay databases.
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RT Smith D.E.;
RL "A physical map of the Leishmania major Friedlin genome.";
DR EMBL: AL160371; CAC59898.1;
SQ SEQUENCE 391 AA; 42630 MW; 71CC65CF296BD34 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 391;
Best Local Similarity 85.7%; Pred. NO. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
:|||||:
Db 3 SATSVAD 9

RESULT 10

P94847 PRELIMINARY; PRT; 433 AA.
AC P94847;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAY-2002 (TREMBlrel. 20, Last annotation update)
DE 48 kDa antigen.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HP921023;
RA MEDLINE=99386867; PubMed=10456921;
Hocking D., Webb E., Radcliff F., Rochel L., Taylor S., Pinczower G.,
Kapulas C., Braley H., Lee A., Doidge C.;
RT "Isolation of recombinant protective Helicobacter pylori antigens.";
RL Infect. Immun. 67:4713-4719(1999).
DR EMBL: U86607; A847275.1;
DR InterPro: IPR004089; Chntaxis_transd.
DR Pfam: PF00015; MCPsignal; 1.
DR SMART: SM00283; MA; 1.
SQ SEQUENCE, 433 AA; 48361 MW; 557188FA65101D19 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 433;
Best Local Similarity 85.7%; Pred. NO. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
:|||||:
Db 175 NATSLAD 181

RESULT 11

O25321 PRELIMINARY; PRT; 433 AA.
AC O25321;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hemolysin secretion protein precursor (HYLB).
GN HP0599.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kervavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weldman J.M., Fujii C., Bowman C., Matthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter pylori.";
RL Nature 388:539-547(1997).
DR EMBL: AE000573; AAD07662.1;
DR TIGR: HP0599;
DR InterPro: IPR004089; Chntaxis_transd.
DR Pfam: PF00015; MCPsignal; 1.
DR SMART: SM00283; MA; 1.
RW Hypothetical protein; Complete proteome.
SQ SEQUENCE 433 AA; 48361 MW; 3153A9D52D3A746E CRC64;

Query Match 90.3%; Score 28; DB 16; Length 433;
Best Local Similarity 85.7%; Pred. NO. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
:|||||:
Db 175 NATSLAD 181

RESULT 12

O9ZLN2 PRELIMINARY; PRT; 433 AA.
AC O9ZLN2;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Melhyl-accepting chemotaxis protein (MCP).
GN JH0546.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Molt D.T., King B.L., Brown E.D., Doidge P.C.,

RA Smith D.R., Noonan B., Guild B.C., deJonghe B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.,
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen *Helicobacter pylori*.";
 RL Nature 397:176-180(1999).
 DR EMBL: AE001487; AAD06131.1; -.
 DR InterPro: IPR004089; Chmtaxis_transd.
 DR InterPro: IPR004090; Me_Chmtaxis.
 DR Pfam: PF00015; MCPsignal; 1.
 DR PRINTS: PR00260; CHEMTRNSDCR.
 DR SMART: SM00283; MA; 1.
 KW Complete proteome.
 SQ SEQUENCE 433 AA; 48383 MW; 32736F842CA6479A CRC64;

Query Match 90.3%; Score 28; DB 16; Length 433;
 Best Local Similarity 85.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
 DB 175 SATSLAD 181

RESULT 13

O96DN1 PRELIMINARY; PRT; 522 AA.
 AC O96DN1;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE CDNA FLJ33082 fis, clone OCBF200231, weakly similar to phospholipase
 DE A2 inhibitor subunit B precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Nihomiyu K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
 RA Furuya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
 RA Katsuma N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Ota T., Makamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
 RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H.,
 RA Murakawa K., Kanemori Y., Takahashi-Fujii A., Oshima A., Sugiyama A.,
 RA Kawakami B., Suzuki Y., Sugano S., Negahari K., Masuno Y., Nagai K.,
 RA Isogai T.,
 RT "NEO human cDNA sequencing project."
 RL Submitted (OCF-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AK056644; BAB71240.1; -.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000372; LRR_Nterm.
 DR Pfam: PF00560; LRR; 9.
 DR Pfam: PF01462; LRRNT; 1.
 DR SMART: SM00013; LRRNT; 1.
 SQ SEQUENCE 522 AA; 58628 MW; 73000472E124245C CRC64;

Query Match 90.3%; Score 28; DB 4; Length 522;
 Best Local Similarity 85.7%; Pred. No. 2.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
 DB 390 SATSLAD 396

RESULT 14
 O9F081 PRELIMINARY; PRT; 563 AA.
 AC O9F081;

DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-JUN-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Polyphenol oxidase.
 OS Populus balsamifera subsp. trichocarpa x Populus deltoides.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_Taxid=3695;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20438222; PubMed=10982443;
 RA Constabel C.P., Yip L., Patton J.J., Christopher M.E.,
 RT "Polyphenol oxidase from hybrid poplar. Cloning and expression in
 RT response to wounding and herbivory."
 RL Plant Physiol. 124:285-296(2000).
 DR EMBL: AF261611; AAG21983.1; -.
 DR InterPro: IPR002227; Tyrosinase.
 DR Pfam: PF00264; Tyrosinase; 1.
 DR PRINTS: PR00092; TYROSINASE.
 DR PROSITE: PS00497; TYROSINASE_1; 1.
 DR PROSITE: PS00498; TYROSINASE_2; 1.
 SQ SEQUENCE 563 AA; 64016 MW; A5B0DC2AED27D9BF CRC64;

Query Match 90.3%; Score 28; DB 10; Length 563;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
 DB 56 SATSLAD 62

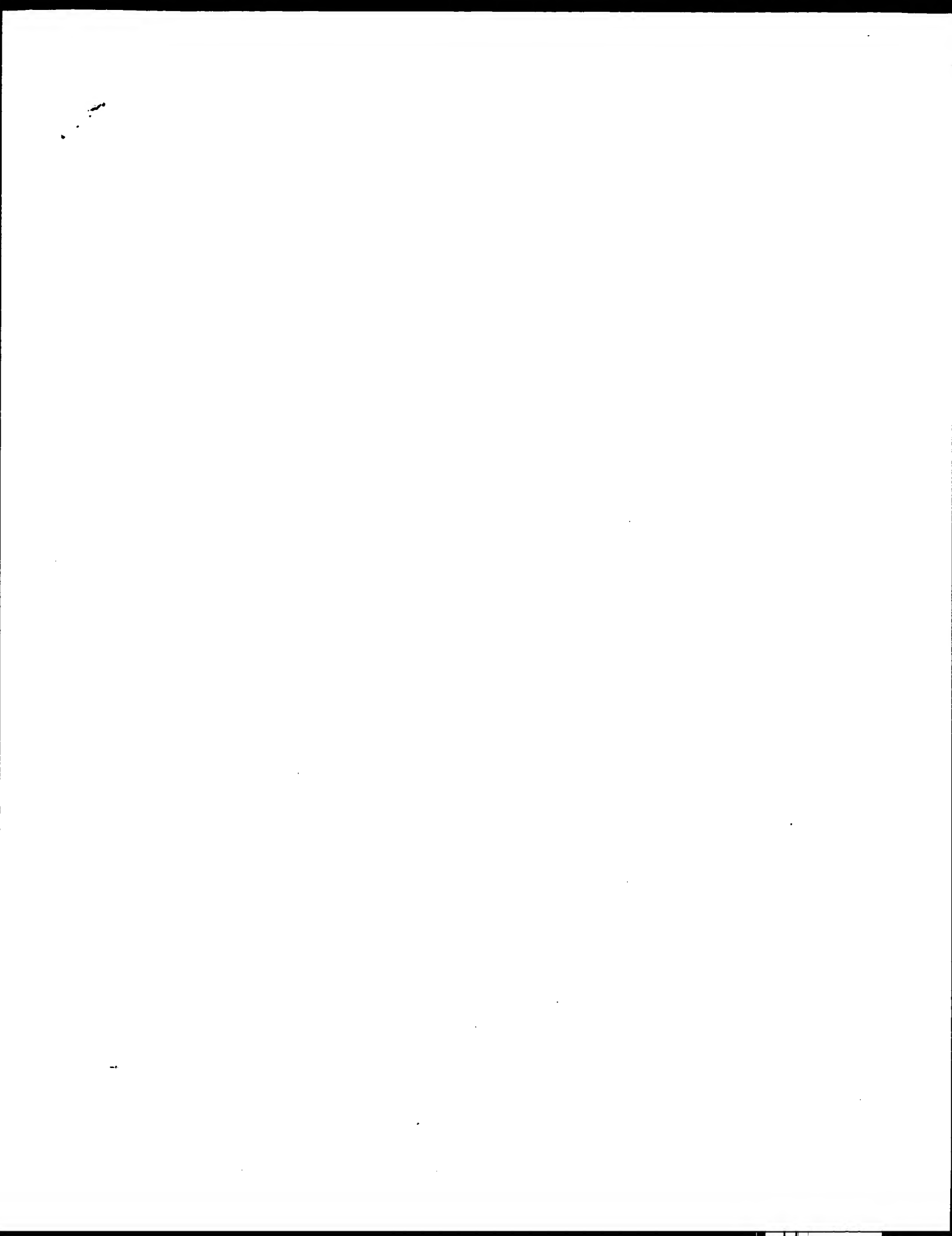
RESULT 15

O94KC2 PRELIMINARY; PRT; 563 AA.
 AC O94KC2;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Polyphenol oxidase.
 OS Populus tremuloides (Quaking aspen).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_Taxid=3693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haruta M., Pedersen J.A., Constabel C.P.,
 RT "Polyphenol oxidase and Herbivore Defense in Trembling Aspen (Populus
 RT tremuloides): cDNA Cloning, Expression, and Potential Substrates."
 RL Physiol. Plantarum 0:0-0(2001).
 DR EMBL: AF368291; AAK53414.1; -.
 DR InterPro: IPR002227; Tyrosinase.
 DR Pfam: PF00264; Tyrosinase; 1.
 DR PROSITE: PS00497; TYROSINASE_1; UNKNOWN_1.
 DR PROSITE: PS00498; TYROSINASE_2; UNKNOWN_1.
 SQ SEQUENCE 563 AA; 64461 MW; EEP601CE74B5DF4 CRC64;

Query Match 90.3%; Score 28; DB 10; Length 563;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
 DB 56 SATSLAD 62

Search completed: February 25, 2003, 10:36:28
 Job time : 4.77333 secs



XX	RESULT 1
XX	AAV78320
ID	AAV78320 standard; Protein; 7 AA.
XX	
AC	AAV78320;
XX	
DT	04-MAY-2000 (first entry)
XX	
DE	Anti-zeta chain antibody 2-B-5 VL-region CDR2 protein sequence.
XX	
KW	Anti-zeta chain antibody 2-B-5; rat; human zeta chain; immunisation;
KW	complementary determining region; CDR; autoimmune disease; cytostatic;
KW	immune deficiency; T-cell malignancy; infectious disease; antiviral;
XX	immunosuppressive; antimicrobial; immune response modulator; NK-cell.
OS	Rattus norvegicus.
XX	
PN	WO200003016-A1.
XX	
FD	20-JAN-2000.
XX	
PF	09-JUL-1999; 99WO-EP04838.
XX	
PR	10-JUL-1998; 98EP-0112867.
XX	
PA	(CONN-) CONNEX GMBH.
XX	
FI	Reiter C;
XX	
XX	
DR	WPI: 2000-160926/14.
XX	N-PSDB: AA288318.
PT	New oligonucleotide, polypeptide, antibody useful for treating

PT autoimmune disease, immune deficiencies, T-cell malignancies and
 PT infectious diseases -
 PS
 XX
 Claim 10: Fig 7; 79pp: English.

CC The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is
 CC encoded by (I), is obtained by immunising a rat with jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,
 CC infectious diseases and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC or viral infections. The antibody, and fragments of it, can be useful for
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC treatment of NK-cell derived malignancies. It can also be useful for the
 CC determination of zeta-chain or eta-chain expression on NK-cells,
 CC T-lymphocytes or their precursors. The present sequence represents the
 CC CDR2 of the VL-region of the anti-zeta-chain antibody 2-B-5, produced
 CC by rats from the present invention.

SQ Sequence 7 AA:
 Query Match 100.0%; Score 31; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
 ID AAY78326 standard; Protein: 107 AA.
 AC AAY78326;
 DT 04-MAY-2000 (first entry)
 DE Anti-zeta-chain antibody 2-B-5 VL-region protein sequence.
 XX
 XX Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
 KW complementary determining region; CDR: autoimmune disease; cytostatic;
 KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
 KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.
 XX
 OS Rattus norvegicus.
 PN WO200003016-A1.
 PD 20-JAN-2000.
 XX
 PD 09-JUL-1999; 99WO-EP04838.
 PF
 XX 10-JUL-1998; 98EP-0112867.
 PR
 XX (CONN-) CONNEX GMBH.
 PA
 XX Reiter C;
 PI
 XX WPI: 2000-160926/14.
 DR N-PSDB: AA288324.
 DR
 XX New oligonucleotide, polypeptide, antibody useful for treating
 PT autoimmune disease, immune deficiencies, T-cell malignancies and
 PT infectious diseases -
 PS
 XX Claim 9; Fig 7; 79pp: English.

CC The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is
 CC encoded by (I), is obtained by immunising a rat with jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,
 CC infectious diseases and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC or viral infections. The antibody, and fragments of it, can be useful for
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC treatment of NK-cell derived malignancies. It can also be useful for the
 CC determination of zeta-chain or eta-chain expression on NK-cells,
 CC T-lymphocytes or their precursors. The present sequence represents the
 CC VL-region of the anti-zeta-chain antibody 2-B-5, produced by rats from
 CC the present invention.

SQ Sequence 107 AA:
 Query Match 100.0%; Score 31; DB 21; Length 107;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
 ID AAY78328 standard; Protein: 532 AA.
 AC AAY78328;
 DT 04-MAY-2000 (first entry)
 DE Bispecific anti-zeta-chain/anti-EPCAM antibody protein sequence.
 XX
 XX Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
 KW complementary determining region; CDR: autoimmune disease; cytostatic;
 KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
 KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.
 XX
 OS Rattus norvegicus.
 OS Synthetic.
 PN WO200003016-A1.
 PD 20-JAN-2000.
 XX
 PD 09-JUL-1999; 99WO-EP04838.
 PF
 XX 10-JUL-1998; 98EP-0112867.
 PR
 XX (CONN-) CONNEX GMBH.
 PA
 XX Reiter C;
 PI
 XX WPI: 2000-160926/14.
 DR N-PSDB: AA288358.
 DR
 XX New oligonucleotide, polypeptide, antibody useful for treating
 PT autoimmune disease, immune deficiencies, T-cell malignancies and
 PT infectious diseases -
 PS
 XX Example 9; Page 74-76; 79pp: English.

CC The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is

PT antibody - useful for prodn. of artificial antibodies
 XX
 PS Claim 2; Page 20; 42pp; English.
 CC This sequence represents the variable heavy chain region of an
 CC anti-human influenza A type virus antibody. The antibody recognises the
 CC stem region of the haemagglutinin (HA) molecule of the H1N1 and H2N2
 CC subtypes of human influenza A type virus, and shows neutralisation
 CC activity against these two subtypes. The antibody shows no recognition
 CC of the H3N2 subtype. The DNA encoding this sequence and the variable
 CC heavy chain coding sequence (see AAT04159) are useful in the production
 CC of artificial antibodies and antigen-binding polypeptides. These
 CC artificial antibodies and polypeptides are useful in the diagnosis and
 CC treatment of human influenza. As the antibodies recognise the stem
 CC region of the HA molecule, the influenza virus will be recognised even if
 CC the HA molecule changes. This provides an advantage over current
 CC vaccines, as the virus periodically alters its HA molecule.
 SQ Sequence 98 AA;
 Query Match 90.3%; Score 28; DB 16; Length 98;
 Best Local Similarity 85.7%; Pred. No. 45;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SATSLAD 7
 :|||||
 DB 50 AATSLAD 56
 RESULT 6
 AAR36720
 ID AAR36720 standard; Protein; 104 AA.
 XX
 AC AAR36720;
 XX
 DT 03-SEP-1993 (first entry)
 XX
 DE c23.5 VL.
 XX
 KW Polymerase chain reaction; amplify; PCR; antibody; primer: c23.5;
 KW light; heavy; chain; monoclonal; variable; region; kappa; IgG2a;
 KW pbluescript1Kst+; E. coli; insulin; endorphin; oncogene; bacteria;
 KM virus.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Region
 FT /Label= CDR1
 FT 25..34
 FT Region
 FT /Label= CDR2
 FT 50..56
 FT Region
 FT /Label= CDR3
 FT 89..97
 FT
 XX
 PN WO9309247-A.
 XX
 PD 13-MAY-1993.
 XX
 PF 06-NOV-1992; 92WO-US09576.
 XX
 PR 08-NOV-1991; 91US-0789344.
 XX
 PA (IGEN-) IGEN INC.
 XX
 PI Paul S;
 XX
 DR WPI: 1993-167710/20.
 DR N-PSDB: AAO36720.
 XX
 PT Catalyzing chemical reaction of polypeptide - using polypeptide
 PT antigen elicited catalytic monoclonal antibody
 XX
 PS Disclosure; Page 24; 50pp; English.

XX
 CC This sequence represents the light (L) chain variable region of the
 CC monoclonal antibody (MAb) c23.5. The DNA encoding this sequence was
 CC produced using the primers given in AAO41251-53. These primers were
 CC based on consensus sequences found in L-chain (kappa). The L-chain
 CC variable (V) region was cloned into a pBluescript1Kst+ vector and
 CC used to transform E. coli. Isolated plasmids were then sequenced.
 CC The H-chain V region was cloned and sequenced in a similar manner.
 CC The MAb c23.5 may be used for catalyzing reactions of insulin,
 CC endorphins, oncogene products, bacterial or viral proteins etc.
 SQ Sequence 104 AA;
 Query Match 90.3%; Score 28; DB 14; Length 104;
 Best Local Similarity 85.7%; Pred. No. 48;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SATSLAD 7
 :|||||
 DB 50 AATSLAD 56
 RESULT 7
 AAY52761
 ID AAY52761 standard; Protein; 107 AA.
 XX
 AC AAY52761;
 XX
 DT 26-JAN-2000 (first entry)
 XX
 DE Anti-tissue factor mouse monoclonal antibody ATR-2 L chain V region.
 XX
 KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
 KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
 KW disseminated intravascular coagulation; immunogenicity; chimeric.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN WO9951743-A1.
 XX
 PD 14-OCT-1999.
 XX
 PF 02-APR-1999; 99WO-JP01768.
 XX
 PR 03-APR-1998; 98JP-0091850.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Sato K, Adachi H, Yabuta N;
 XX
 DR WPI: 1999-620204/53.
 DR N-PSDB: AA233012.
 XX
 PT Humanised antibody recognizing human tissue factor, used for treatment
 PT of disseminated intravascular coagulation
 XX
 PS Claim 5; Page 279-280; 291pp; Japanese.
 XX
 CC The present invention describes chimeric antibody (Ab) heavy (H) chains
 CC containing the variable region of the H chain of a mouse monoclonal Ab
 CC recognising human tissue factor (hrf) and the constant region of the H
 CC chain of a human Ab. The variable region is one of six specified
 CC sequences (which are the H chain variable regions from mouse monoclonal
 CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)
 CC chains containing the variable region of the L chain of a mouse
 CC monoclonal Ab recognising human tissue factor (hrf) and the constant
 CC region of the L chain of a human Ab, the variable region being one of six
 CC specified sequences (which are the L chain variable regions from mouse
 CC monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for
 CC the treatment and prevention of thrombotic disease, especially of
 CC disseminated intravascular coagulation (DIC). The humanised antibody has
 CC the high hrf binding activity of the mouse monoclonal antibody but

CC greatly reduced immunogenicity. AA233001 to AA233091 and Y527007 to
CC AA52767 represent sequences used in the exemplification of the present
CC invention.

XX Sequence 107 AA;

QY Query Match 90.3%; Score 28; DB 20; Length 107;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 SATSLAD 7
50 AATSLAD 56

RESULT 8
AA52762
ID AA52762 standard; Protein; 107 AA.

XX AC AA52762;

XX DT 26-JAN-2000 (first entry)

XX DE Anti-tissue factor mouse monoclonal antibody ATR-3 L chain V region.

XX KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;

XX KM ATR-2; ATR-3; ATR-4; ATR-5; ATR-6; thrombotic disease; DIC;
XX diseminated intravascular coagulation; immunogenicity; chimeric.

XX OS Synthetic.

XX OS Mus sp.

XX PN WO9951743-A1.

XX PD 14-OCT-1999.

XX PF 02-APR-1999; 99WO-JP01768.

XX PR 03-APR-1998; 98JP-0091850.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Sato K, Adachi H, Yabuta N;

XX DR WPI: 1999-620204/53.

XX DR N-PSDB; AA233013.

XX PT Humanised antibody recognizing human tissue factor, used for treatment
XX of disseminated intravascular coagulation

XX PS Claim 5; Page 280; 291pp; Japanese.

XX CC The present invention describes chimeric antibody (Ab) heavy (H) chains
XX containing the variable region of the H chain of a mouse monoclonal Ab
XX recognising human tissue factor (hrf) and the constant region of the H
XX chain of a human Ab. The variable region is one of six specified
XX sequences (which are the H chain variable regions from mouse monoclonal
XX Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)
XX chains containing the variable region of the L chain of a mouse
XX monoclonal Ab recognising human tissue factor (hrf) and the constant
XX region of the L chain of a human Ab, the variable region being one of six
XX specified sequences (which are the L chain variable regions from mouse
XX monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for
XX the treatment and prevention of thrombotic disease, especially of
XX disseminated intravascular coagulation (DIC). The humanised antibody has
XX the high hrf binding activity of the mouse monoclonal antibody but
XX greatly reduced immunogenicity. AA233001 to AA233091 and Y527007 to
XX AA52767 represent sequences used in the exemplification of the present
XX invention.

XX Sequence 107 AA;

Query Match 90.3%; Score 28; DB 20; Length 107;

Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
50 AATSLAD 56

RESULT 9
AAO20094
ID AAO20094 standard; Protein; 108 AA.

XX AC AAO20094;

XX DT 12-JUN-2002 (first entry)

XX DE Protein encoded by a 324nt DNA sequence of the invention.

XX KM Mouse monoclonal antibody; murine; surface antigen pres1 epitope;
XX hepatitis B virus.

XX OS Unidentified.

XX PN KR99008647-A.

XX PD 05-FEB-1999.

XX PF 02-JUL-1997; 97KR-0030694.

XX PR 02-JUL-1997; 97KR-0030694.

XX PA (KORE-) KOREA RES INST CHEM TECHNOLOGY.

XX PI Hong HJ, Ryoo CJ;

XX DR WPI: 2000-168375/15.

XX DR N-PSDB; AAK99183.

XX PT Changeable region of mouse monoclonal antibody recognizing surface
XX antigen pres1 epitope of hepatitis B virus and gene

XX PS Disclosure; Page 11; 14pp; Korean.

XX CC The invention relates to a changeable region of mouse monoclonal antibody
XX recognising surface antigen pres1 epitope of hepatitis B virus and gene.

XX CC This sequence relates to a protein encoded by a 324nt DNA of the
XX invention.

XX Sequence 108 AA;

QY Query Match 90.3%; Score 28; DB 21; Length 108;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
50 AATSLAD 56

RESULT 10
AAE12046
ID AAE12046 standard; Protein; 109 AA.

XX AC AAE12046;

XX DT 18-DEC-2001 (first entry)

XX DE Murine anti-TF antibody 5G6 variable light chain (VL) domain.

XX KM Murine tissue factor; TF; thrombotic disorder; variable light chain;
XX VL; anticoagulant; thrombolytic; cytostatic; antibacterial; vasotropic;
XX immunosuppressive; cerebroprotective; vaccine; thrombosis; septicemia;
XX Tumour; metastasis; arteriosclerosis; restenosis; angioplasty; stroke;

KW inflammation; adult respiratory distress syndrome; ARDS; hypotension;
 KW disseminated intravascular coagulopathy; DIC.
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 24..34 /label= CDR_H1
 FT Region 50..56 /label= CDR_H2
 FT Region 89..97 /label= CDR_H3
 FT Region /label= CDR_H3
 XX
 PN MO200170984-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 08-MAR-2001: 2001WO-US07501.
 XX
 PR 16-MAR-2000: 2000US-189775P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Kirchofer DK, Lowe DG, Presta LG;
 XX
 DR WPI: 2001-616406/71.
 XX
 PT Identifying anti-tissue factor antibodies for treating thrombotic
 PT disorders, comprises epitope mapping of anti-TF antibodies and
 PT selecting antibodies that bind to C-terminal macromolecular
 PT substrate-binding region of TF
 XX
 PS Claim 22: Fig 15; 75pp: English.
 XX
 CC The invention relates to a method for identifying anti-tissue factor
 CC (anti-TF) antibodies with enhanced anticoagulant potency. The method
 CC comprises subjecting a number of anti-TF antibodies to epitope mapping,
 CC and selecting the antibodies that bind to an epitope comprising at least
 CC a part of the C-terminal macromolecular substrate-binding region of
 CC tissue factor (TF). The method is useful for identifying anti-TF
 CC antibodies which are useful for blocking a TF-FVIIa associated process
 CC or event and for treating a TF-VIIa related disease or disorder
 CC e.g. thrombotic or coagulopathic disorder including deep venous
 CC thrombosis, arterial thrombosis, stroke, tumour, metastasis,
 CC thrombolysis, arteriosclerosis and restenosis following angioplasty,
 CC acute and chronic indications such as inflammation, septic shock,
 CC septicemia, hypotension, adult respiratory distress syndrome (ARDS) and
 CC disseminated intravascular coagulopathy (DIC). The present sequence is
 CC murine anti-TF antibody 566 variable light chain (VL) domain.
 CC
 XX
 SQ Sequence 109 AA;
 XX
 Query Match 90.3%; Score 28; DB 22; Length 109;
 Best Local Similarity 85.7%; Pred. No. 50;
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 ID AAM20162 standard; protein; 231 AA.
 XX
 AC AAM20162;
 XX
 DT 07-JUL-1997 (first entry)
 XX
 DE H. pylori inner membrane protein, 15824052.aa.
 XX
 KW Cytolysin; vaccine; prevention; infection; identification;
 KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;

KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope;
 KW inner membrane.
 XX
 OS Helicobacter pylori.
 XX
 PN WO9640893-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US09122.
 XX
 PR 01-APR-1996; 96US-0630405.
 PR 07-JUN-1995; 95US-0487032.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Berglundh OT, Smith D, Mellgaard BL;
 XX
 DR WPI: 1997-052306/05.
 DR N-PSDB: AAT67402.
 XX
 PT Helicobacter pylori nucleic acid sequences and related
 PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
 PT infection, and to detect Helicobacter
 XX
 PS Claim 56: Pages 379-380; 1481pp: English.
 XX
 CC The present sequence is a Helicobacter pylori inner membrane protein.
 CC The protein may be used in a vaccine to prevent or treat H. pylori
 CC infection or to identify H. pylori polypeptide binding compounds, useful
 CC as potential H. pylori life cycle activators or inhibitors. The genomic
 CC sequence of H. pylori (ATCC 55679) was determined from overlapping
 CC contigs generated by mechanically shearing the bacterial DNA. The
 CC sequences were analysed for ORF of at least 180 nucleotides, and the
 CC predicted coding regions defined by computer evaluation. To identify
 CC likely H. pylori antigens for vaccine development, the amino acid
 CC sequences predicted from various ORF were analysed for significant
 CC homology to other known or exported membrane proteins. Having identified
 CC and determined the sequences of interest, particular regions can be
 CC isolated from H. pylori by PCR amplification for recombinant polypeptide
 CC production, e.g. in E. coli hosts.
 CC
 XX
 SQ Sequence 231 AA;
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 Query Match 90.3%; Score 28; DB 18; Length 231;
 Best Local Similarity 85.7%; Pred. No. 11e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 DB 175 NATSLAD 181
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 AC AAR92829;
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 DT 09-MAY-1996 (first entry)
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 DE C179Fv-PP variable light chain sequence.
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 KW Antibody; human; influenza type A virus; H1N1; H2N2; H3N2; HA; diagnosis;
 KW haemagglutinin; variable light chain; therapy.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Protein 26..126
 FT Domain /note="variable light chain"
 FT /note="Fc binding domain-like structure"

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: February 25, 2003, 10:36:42 ; Search time 0.571667 seconds
(without alignments)
380.447 Million cell updates/sec

Title: US-09-743-482a-4

Perfect score: 31

Sequence: 1 SATSLAD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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- 14: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	28	90.3	433	8	US-08-945-038-6
3	28	90.3	522	9	US-09-992-598-278
4	28	90.3	522	9	US-09-989-293A-278
5	28	90.3	522	9	US-09-989-735-278
6	28	90.3	522	9	US-09-990-444-278
7	28	90.3	522	9	US-09-989-730-278
8	28	90.3	522	9	US-09-990-436-278
9	28	90.3	522	9	US-09-991-181-278
10	28	90.3	522	9	US-09-993-687-278
11	28	90.3	522	9	US-09-989-734-278
12	28	90.3	522	9	US-10-028-072-450
13	28	90.3	522	9	US-09-997-653-278
14	28	90.3	522	9	US-09-993-667-278
15	28	90.3	522	9	US-10-121-049-450
16	28	90.3	522	9	US-10-123-904-450
17	28	90.3	522	9	US-10-140-470-450
18	28	90.3	522	9	US-09-990-438-278
19	28	90.3	522	9	US-09-990-562-278

20	28	90.3	522	9	US-09-997-428-278	Sequence 278, App
21	28	90.3	522	9	US-09-997-666-278	Sequence 278, App
22	28	90.3	522	9	US-10-175-746-450	Sequence 450, App
23	28	90.3	522	9	US-10-176-918-450	Sequence 450, App
24	28	90.3	522	9	US-10-176-921-450	Sequence 450, App
25	28	90.3	522	9	US-10-227-884-158	Sequence 158, App
26	28	90.3	522	9	US-09-990-711-278	Sequence 278, App
27	28	90.3	522	9	US-10-137-865-450	Sequence 450, App
28	28	90.3	522	9	US-10-140-474-450	Sequence 450, App
29	28	90.3	522	10	US-09-989-722-278	Sequence 278, App
30	28	90.3	522	10	US-09-989-723-278	Sequence 278, App
31	28	90.3	522	10	US-09-989-727-278	Sequence 278, App
32	28	90.3	522	10	US-09-989-727-278	Sequence 278, App
33	28	90.3	522	10	US-09-989-731-278	Sequence 278, App
34	28	90.3	522	10	US-09-989-732-278	Sequence 278, App
35	28	90.3	522	10	US-09-991-073-278	Sequence 278, App
36	28	90.3	522	10	US-09-990-442-278	Sequence 278, App
37	28	90.3	522	10	US-09-991-163-278	Sequence 278, App
38	28	90.3	522	10	US-09-993-604-278	Sequence 278, App
39	28	90.3	522	10	US-09-990-456-278	Sequence 278, App
40	28	90.3	522	10	US-09-989-721-278	Sequence 278, App
41	27	87.1	143	10	US-09-864-761-34585	Sequence 34585, A
42	27	87.1	143	10	US-09-864-761-34587	Sequence 34587, A
43	27	87.1	236	10	US-09-741-669-381	Sequence 381, App
44	27	87.1	561	9	US-10-078-770-154	Sequence 154, App
45	27	87.1	827	9	US-10-171-384-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-971-536-69
Sequence 69, Application US/09971536
Patent No. US20020159976A1
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Havukkala, Ilkka
APPLICANT: Bloksberg, Leonard
APPLICANT: Lubbers, Mark
APPLICANT: Dekker, James
APPLICANT: Christensson, Anna
APPLICANT: Holland, Ross
APPLICANT: O'Toole, Paul
APPLICANT: Reid, Julian
TITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and Meth
FILE OF INVENTION: Using Them
FILE REFERENCE: 1043C2
CURRENT APPLICATION NUMBER: US/09/971,536
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: PCT/NZ01/00160
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 69
LENGTH: 1463
TYPE: PRT
ORGANISM: Lactobacillus rhamnosus
US-09-971-536-69

Query Match 100.0%; Score 31; DB 9; Length 1463;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SATSLAD 7
Db 1349 SATSLAD 1355

RESULT 2
US-08-945-038-6
Sequence 6, Application US/08945038
Patent No. US20020146423A1
GENERAL INFORMATION:
APPLICANT: Doldge, Christopher V.
APPLICANT: Lee, Adrian
APPLICANT: Radcliffe, Fiona J.
APPLICANT: Hocking, Diana M.
APPLICANT: Webb, Elizabeth A.
TITLE OF INVENTION: PROTECTIVE HELICOBACTER ANTIGENS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,038
FILING DATE: 23-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00225
FILING DATE: 19-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P42575
FILING DATE: 21-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P43931
FILING DATE: 03-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P47565
FILING DATE: 16-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-945-038-6
Query Match 90.3%; Score 28; DB 8; Length 433;
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Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 175 NATSLAD 181
RESULT 3
US-09-992-598-278
Sequence 278, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavitt, Ivor J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-09

Query Match 90.3%; Score 28; DB 9; Length 522;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 390 SATTLAD 396

RESULT 4
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; Sequence 278, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Geiber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavito, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 90.3%; Score 28; DB 9; Length 522;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
Db 390 SATTLAD 396

RESULT 5
; Sequence 278, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C61
;; CURRENT APPLICATION NUMBER: US/09/989,735
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/091978
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 90.3% Score 28: DB 9: Length 522:
Best Local Similarity 85.7% Pred. No. 60:
Matches 6: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 SATSLAD 7
DB 390 SATSLAD 396

RESULT 6
US-09-990-444-278

; Sequence 278, Application US/09990444
; Publication No. US20020193300A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gelber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumes, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/091560
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 90.38; Score 28; DB 9; Length 522;
Best Local Similarity 85.78; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 SATSLAD 7
Db 390 SATSLAD 396

RESULT 7
US-09-989-730-278
Sequence 278, Application US/09989730
Publication No. US20020197674A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C69
CURRENT APPLICATION NUMBER: US/09/989,730
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
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PRIOR APPLICATION NUMBER: 60/089600
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PRIOR APPLICATION NUMBER: 60/089653
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PRIOR APPLICATION NUMBER: 60/089801
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PRIOR APPLICATION NUMBER: 60/090694
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PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 90.3%; Score 28; DB 9; Length 522;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
DB 390 SATTLAD 396

RESULT 8
US-09-990-436-278
Sequence 278, Application US/09990436
Publication No. US20020198148A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PC14
CURRENT APPLICATION NUMBER: US/09/990.436
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945	PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910	PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106	PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607	PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609	PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759	PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827	PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021	PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025	PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026	PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028	PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029	PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030	PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033	PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088655	PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824	PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/088876	PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105	PRIOR FILING DATE: 1998-06-12
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PRIOR APPLICATION NUMBER: 60/089514	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538	PRIOR FILING DATE: 1998-06-17

1	PRIOR FILING DATE: 1998-06-17
2	PRIOR APPLICATION NUMBER: 60/089358
3	PRIOR FILING DATE: 1998-06-17
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5	PRIOR FILING DATE: 1998-06-17
6	PRIOR APPLICATION NUMBER: 60/089600
7	PRIOR FILING DATE: 1998-06-17
8	PRIOR APPLICATION NUMBER: 60/089653
9	PRIOR FILING DATE: 1998-06-17
10	PRIOR APPLICATION NUMBER: 60/089801
11	PRIOR FILING DATE: 1998-06-18
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13	PRIOR FILING DATE: 1998-06-18
14	PRIOR APPLICATION NUMBER: 60/089947
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16	PRIOR APPLICATION NUMBER: 60/089948
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19	PRIOR FILING DATE: 1998-06-19
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21	PRIOR FILING DATE: 1998-06-22
22	PRIOR APPLICATION NUMBER: 60/090026
23	PRIOR FILING DATE: 1998-06-23
24	PRIOR APPLICATION NUMBER: 60/090345
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26	PRIOR APPLICATION NUMBER: 60/090355
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28	PRIOR APPLICATION NUMBER: 60/090429
29	PRIOR FILING DATE: 1998-06-24
30	PRIOR APPLICATION NUMBER: 60/090431
31	PRIOR FILING DATE: 1998-06-24
32	PRIOR APPLICATION NUMBER: 60/090435
33	PRIOR FILING DATE: 1998-06-24
34	PRIOR APPLICATION NUMBER: 60/090444
35	PRIOR FILING DATE: 1998-06-24
36	PRIOR APPLICATION NUMBER: 60/090445
37	PRIOR FILING DATE: 1998-06-24
38	PRIOR APPLICATION NUMBER: 60/090472
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48	PRIOR APPLICATION NUMBER: 60/090676
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56	PRIOR APPLICATION NUMBER: 60/090695
57	PRIOR FILING DATE: 1998-06-25
58	PRIOR APPLICATION NUMBER: 60/090696
59	PRIOR FILING DATE: 1998-06-25
60	PRIOR APPLICATION NUMBER: 60/090862
61	PRIOR FILING DATE: 1998-06-26
62	PRIOR APPLICATION NUMBER: 60/090863
63	PRIOR FILING DATE: 1998-06-26
64	PRIOR APPLICATION NUMBER: 60/091366
65	PRIOR FILING DATE: 1998-07-01
66	PRIOR APPLICATION NUMBER: 60/091478
67	PRIOR FILING DATE: 1998-07-02
68	PRIOR APPLICATION NUMBER: 60/091544
69	PRIOR FILING DATE: 1998-07-01

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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 90.3%; Score 28; DB 9; Length 522;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
Db 390 SATTLAD 396

RESULT 9
US-09-991-181-278
Sequence 278, Application US/09991181
Publication No. US20020197615A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C53
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US/09/991,181
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-28
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PRIOR APPLICATION NUMBER: 60/089653
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978

PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
Query Match 90.3%; Score 28; DB 9; Length 522;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Caps 0;
QY 1 SATSLAD 7
DB 390 SATSLAD 396
RESULT 10
US-09-993-687-278
Sequence 278, Application US/09993687
Publication No. US20020198149A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C1
CURRENT APPLICATION NUMBER: US/09/993,687
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/083322
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PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02

90.38; Score 28; DB 9; Length 522;

Best Local Similarity 85.7% Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7

Db 390 SATTLAD 396

RESULT 11

US-09-989-734-278
; Sequence 278, Application US/09989734
; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC64
; CURRENT APPLICATION NUMBER: US/09/989,734
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 90.3%, Score 28; DB 9; Length 522;

Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
DB 390 SATTLAD 396

RESULT 12
US-10-028-072-450
Sequence 450, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
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;; PRIOR FILING DATE: 1998-07-07

Query Match 90.3%; Score 28; DB 9; Length 522;

Best Local Similarity 85.7%; Pred. No. 60;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SATSLAD 7
||:|
Db 390 SATSLAD 396

RESULT 13

US-09-997-653-278

; Sequence 278; Application US/09997653

; Publication No. US20030008297A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Garber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goodard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C38
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 90.3% Score 28; DB 9; Length 522;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
DB 390 SATSLAD 396

RESULT 14
US-09-993-667-278
Sequence 278, Application US/09993667
Publication No. US20030022187A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavito, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C4
CURRENT APPLICATION NUMBER: US/09/993,667
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-09

Query Match          90.3%; Score 28; DB 9; Length 522;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SATSLAD 7
Db      390 SATTLAD 396

RESULT 15
US-10-121-049-450
Sequence 450, Application US/10121049
Publication No. US200302239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K

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APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 450
LENGTH: 522
TYPE: PRT
ORGANISM: Homo Sapien
US-10-121-049-450

Query Match 90.3%; Score 28; DB 9; Length 522;
Best Local Similarity 85.7%; Pred. NO. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 390 SATTLAD 396

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Job time : 1.57167 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 0.761667 seconds
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Title: US-09-743-482a-4

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Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	28	87.1	7	2	US-08-053-451B-69
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7	28	87.1	107	2	US-08-480-434-73
8	28	87.1	107	2	US-08-053-451B-73
9	28	87.1	107	2	US-08-053-451B-174
10	28	87.1	138	2	US-08-480-434-63
11	28	87.1	138	2	US-08-053-451B-63
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15	28	87.1	132	4	US-08-818-112-67
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29	26	83.9	518	4	US-09-620-412C-333	Sequence 333, App
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31	26	83.9	525	4	US-09-620-412C-196	Sequence 196, App
32	26	83.9	583	4	US-09-620-412C-353	Sequence 353, App
33	26	83.9	585	4	US-09-620-412C-337	Sequence 337, App
34	26	83.9	618	2	US-08-912-129A-54	Sequence 54, App
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36	26	83.9	631	4	US-09-620-412C-325	Sequence 325, App
37	26	83.9	646	4	US-09-620-412C-317	Sequence 317, App
38	26	83.9	654	4	US-09-620-412C-341	Sequence 341, App
39	26	83.9	683	4	US-09-620-412C-357	Sequence 357, App
40	26	83.9	691	4	US-09-620-412C-313	Sequence 313, App
41	26	83.9	700	4	US-09-620-412C-345	Sequence 345, App
42	26	83.9	715	4	US-09-620-412C-321	Sequence 321, App
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ALIGNMENTS

RESULT 1
US-08-401-908-2
Sequence 2, Application US/08401908
Patent No. 5684146
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: A DNA WHICH CODES FOR THE VARIABLE REGION OF
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,908
FILING DATE: March 10, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-9850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 98
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-401-908-2
Query Match 90.3%; Score 28; DB 1; Length 98;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;
Qy 1 SATSLAD 7

Db 50 ATSLAD 56

RESULT 2
US-07-789-344A-8

Sequence 8, Application US/07789344A

Patent No. 5318897

GENERAL INFORMATION:

APPLICANT: Sughir, Paul

TITLE OF INVENTION: MONOCLONAL ANTIBODY AND ANTIBODY

TITLE OF INVENTION: COMPONENTS ELICITED TO A POLYPEPTIDE ANTIGEN

TITLE OF INVENTION: GROUND STATE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford

ADDRESSEE: c/o Barry Evans

STREET: 530 Fifth Avenue

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/789,344A

FILING DATE: 08-NOV-1991

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Evans, Barry

REGISTRATION NUMBER: 22,802

REFERENCE/DOCKET NUMBER: 370068-3500

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 104 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-07-789-344A-8

Query Match

Best Local Similarity 90.3%; Score 28; DB 1; Length 104;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSLAD 7

Db 50 ATSLAD 56

RESULT 3
US-08-480-434-69

Sequence 69, Application US/08480434

Patent No. 5811248

GENERAL INFORMATION:

APPLICANT: Charles C. Dillow, et al.

TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,

TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

US-08-480-434-69

Query Match

Best Local Similarity 85.7%; Score 28; DB 1; Length 104;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 50 ATSLAD 56

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,434

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Albert P. Halluin

REGISTRATION NUMBER: 25,227

REFERENCE/DOCKET NUMBER: 7606-053

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 854-3660

TELEFAX: (415) 854-3694

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: N

ANTI-SENSE: N

US-08-480-434-69

Query Match

Best Local Similarity 87.1%; Score 27; DB 2; Length 7;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATSLAD 7

Db 2 ATSLAD 7

RESULT 4
US-08-480-434-77

Sequence 77, Application US/08480434

Patent No. 5811248

GENERAL INFORMATION:

APPLICANT: Charles C. Dillow, et al.

TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,

TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,434

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Albert P. Halluin

REGISTRATION NUMBER: 25,227

REFERENCE/DOCKET NUMBER: 7606-053

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 854-3660

TELEFAX: (415) 854-3694

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

US-08-480-434-77

Query Match

Best Local Similarity 100.0%; Score 27; DB 2; Length 7;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATSLAD 7

Db 2 ATSLAD 7

TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-480-434-77

Query Match 87.1%; Score 27; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATSLAD 7
Db 2 ATSLAD 7

RESULT 5
US-08-053-451B-69
Sequence 69, Application US/08053451B
Patent No. 5955584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Diltow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halliuh, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-69
Query Match 87.1%; Score 27; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2 ATSLAD 7
RESULT 6
US-08-053-451B-77
Sequence 77, Application US/08053451B

Patent No. 5955584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Diltow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halliuh, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-77

Query Match 87.1%; Score 27; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATSLAD 7
Db 2 ATSLAD 7

RESULT 7
US-08-480-434-73
Sequence 73, Application US/08480434
Patent No. 5811248
GENERAL INFORMATION:
APPLICANT: Charles C. Diltow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
NUMBER OF SEQUENCES: 88
TITLE OF INVENTION: ANTIBODIES THEREOF, AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-JUN-1995
CLASSIFICATION: 433
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-480-434-73

Query Match 87.1%; Score 27; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSLAD 7
DB 51 ATSLAD 56

RESULT 8
US-08-053-451B-73
Sequence 73, Application US/08053451B
Patent No. 5955584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Diltow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-73

Query Match 87.1%; Score 27; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSLAD 7
DB 51 ATSLAD 56

RESULT 9
US-08-053-451B-174
Sequence 174, Application US/08053451B
Patent No. 5955584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Diltow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-053-451B-174

Query Match 87.1%; Score 27; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATSLAD 7
DB 51 ATSLAD 56

RESULT 10
US-08-480-434-63
Sequence 63, Application US/08480434
Patent No. 5811248
GENERAL INFORMATION:
APPLICANT: Charles C. Diltow, et al.

;; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
;; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
;; NUMBER OF SEQUENCES: 88
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/480,434
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Albert P. Halluin
;; REGISTRATION NUMBER: 25,227
;; REFERENCE/DOCKET NUMBER: 7606-053
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 854-3694
;; TELEFAX: (415) 854-3660
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 63:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 138 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: N
;; ANTI-SENSE: N
;; US-08-480-434-63

Query Match 87.1%; Score 27; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATSLAD 7
Db 71 ATSLAD 76

RESULT 11
US-08-053-451B-63
; Sequence 63, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Diltow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993

;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Halluin, Albert P.
;; REGISTRATION NUMBER: 25,227
;; REFERENCE/DOCKET NUMBER: 7606-033-999
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-854-3660
;; TELEFAX: 415-854-3694
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 63:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 138 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA
;; HYPOTHETICAL: N
;; ANTI-SENSE: N
;; US-08-053-451B-63

Query Match 87.1%; Score 27; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATSLAD 7
Db 71 ATSLAD 76

RESULT 12
US-08-818-112-66
; Sequence 66, Application US/08818112
; Patent No. 6280969
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, David C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedavick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,112
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-818-112-66

Query Match

Best Local Similarity 83.9%; Score 26; DB 4; Length 132;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7

DB 91 SATAMAD 97

RESULT 13

US-09-605-785-819

Sequence 819, Application US/09605785

Patent No. 6321716

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitchell, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqi

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Derrick

APPLICANT: Li, Samuel

APPLICANT: Wang, Aljun

APPLICANT: Skelky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.427C16

CURRENT APPLICATION NUMBER: US/09/605,785

CURRENT FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 835

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 819

LENGTH: 132

TYPE: PRT

ORGANISM: Homo sapien

US-09-605-785-819

Query Match

Best Local Similarity 83.9%; Score 26; DB 4; Length 132;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7

DB 91 SATAMAD 97

RESULT 14

US-08-818-111-67

Sequence 67, Application US/08818111

Patent No. 6338852

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skelky, Yasir A.W.

APPLICANT: Dillon, Davin C.

APPLICANT: Campos-Neto, Antonia

APPLICANT: Houghton, Raymond

APPLICANT: Vedvick, Thomas S.

APPLICANT: Twardzik, Daniel R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 148

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/818,111

FILING DATE: 13-MAR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Makl, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.417C6

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-818-111-67

Query Match

Best Local Similarity 83.9%; Score 26; DB 4; Length 132;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7

DB 91 SATAMAD 97

RESULT 15

US-09-056-556-66

Sequence 66, Application US/09056556

Patent No. 6350456

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skelky, Yasir A.W.

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND

NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,556

FILING DATE: 07-APR-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Makl, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.457

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
us-09-056-556-66

Query Match 83.9%; Score 26; DB 4; Length 132;
Best Local Similarity 71.4%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SATSLAD 7
|||:|
Db 91 SATAMAD 97

Search completed: February 25, 2003, 10:38:40
Job time : 1.78167 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 0.795 Seconds
(without alignments)

469.543 Million cell updates/sec

Title: US-09-743-482A-6

Perfect score: 49
Sequence: 1 LQRTSNPNT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	71.4	261	Y4ZC_RHISN	P55730 rhizobium s
2	35	71.4	414	YLPD_CAEEL	P34384 caenorhabdi
3	35	71.4	839	YNEI_YEAST	P53959 saccharomyc
4	34	69.4	704	LIPM_NEIMA	P57037 neisseria m
5	34	69.4	794	LIPM_NEIMA	005013 neisseria m
6	33	67.3	313	KI12_YEAST	P34253 saccharomyc
7	33	67.3	477	ISCI_YEAST	P40015 saccharomyc
8	33	67.3	585	ATKA_THIAC	P57685 thermoplasm
9	33	67.3	687	VIVA_VIBCH	Q00964 vibrio chol
10	33	67.3	759	YDEP_ECOLI	P75561 escherichia
11	33	67.3	1186	CEAA_BACTS	Q45710 bacillus th
12	33	67.3	1980	MY9B_RAT	Q63358 rattus norv
13	33	67.3	2114	MY9B_MOUSE	Q09y06 mus musculu
14	32	65.3	140	GRFA_VACCV	P01136 vaccinia vi
15	32	65.3	142	GRFA_VACCV	P20494 vaccinia vi
16	32	65.3	165	DSBE_CHRVI	Q64676 chromatiu
17	32	65.3	245	CTRA_BOVIN	P00766 bos taurus
18	32	65.3	331	RBSR_HAATN	P44329 haemophilus
19	32	65.3	435	KI14_YEAST	P22841 saccharomyc
20	32	65.3	504	C6A9_DROME	Q27594 drosophila
21	32	65.3	504	C6A9_DROME	Q27594 drosophila
22	32	65.3	2199	DPOE_SCHPO	P81754 schizosacch
23	32	65.3	201	CLP2_PSEAE	Q9hyt9 pseudomonas
24	31	63.3	216	YUKI_YERRU	O67970 yersinia ru
25	31	63.3	218	Y279_MTCRN	P75368 mycoplasma
26	31	63.3	224	Y209_LISMO	P33381 listeria mo
27	31	63.3	224	Y241_LISIN	Q92166 listeria in
28	31	63.3	266	NANH_BACFR	P31206 bacteroides
29	31	63.3	285	FLB2_TREHY	P50160 treponema h
30	31	63.3	317	ISPH_YERPE	P58680 yersinia pe
31	31	63.3	332	IPAD_SHIFL	Q03947 shigella dy
32	31	63.3	332	IPAD_SHIFL	P18013 shigella fl
33	31	63.3	346	TBCC_HUMAN	Q15814 homo sapien

34	31	63.3	351	1	HEM2_RHOCA
35	31	63.3	353	1	HEM2_RHILLO
36	31	63.3	463	1	DAID_YERPE
37	31	63.3	473	1	MAIR_YEAST
38	31	63.3	477	1	FES_FSVST
39	31	63.3	500	1	C912_ARATH
40	31	63.3	502	1	YE10_YEAST
41	31	63.3	534	1	VL1_HPV41
42	31	63.3	609	1	FES_FSVCA
43	31	63.3	657	1	YGG6_YEAST
44	31	63.3	722	1	Z219_HUMAN
45	31	63.3	744	1	TRM2_HUMAN

ALIGNMENTS

RESULT 1	Y4ZC_RHISN	STANDARD:	PRT:	261 AA.
ID	Y4ZC_RHISN			
AC	P55730;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	Hypothetical 28.3 kDa protein Y4ZC.			
GN	Y4ZC.			
OS	Rhizobium sp. (strain NGR234).			
OG	Plasmid sym pNGR234a.			
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
OC	Rhizobiaceae; Rhizobium.			
OX	NCBI_TaxID=394;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97305956; PubMed=9163424;			
RA	Friedberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,			
RA	Perrel X.;			
RT	"Molecular basis of symbiosis between Rhizobium and legumes.";			
RL	Nature 387:394-401(1997).			
CC	-1 SIMILARITY: TO P.SYRINGAE (PV. PHASCOLICOLA) AVIRULENCE PROTEIN			
CC	AVRPH3.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; AE000109; AAB91961.1; -			
KW	Hypothetical protein; Plasmid.			
SO	SEQUENCE 261 AA; 28349 MW; 52939C1919DFEC43 CRC64;			
Query Match 71.4%; Score 35; DB 1; Length 261;				
Best Local Similarity 100.0%; Pred. NO. 11;				
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	3 RYSNPN 8			
DB	243 RYSNPN 248			
RESULT 2				
ID	YLPD_CAEEL	STANDARD:	PRT:	414 AA.
AC	P34384;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Hypothetical protein F02A9.4b in chromosome III.			
GN	F02A9.4.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;			

```

OC Rhadidae; Peloderinae; Caenorrhadidae.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Johnson L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Lareille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP REVISIONS.
RA Durbin R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: a (AC P34385) and b (shown
CC here); may be produced by alternative splicing.
CC -----
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CC -----
DR EMBL: Z19555; CAAT9619.1; -
DR PIR: S28312; S28312.
DR Wormpep: F02A9.4b; CE20652.
KW Hypothetical protein; Alternative splicing.
SQ SEQUENCE 414 AA; 46765 MW; 1EFD5BA193D14368 CRC64;

Query Match
Best Local Similarity 71.4%; Score 35; DB 1; Length 414;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQRTSNPN 8
DB 312 LERYSOBN 319

RESULT 3
YNEI_YEAST STANDARD; PRT; 839 AA.
ID YNEI_YEAST
AC P53959;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Hypothetical 97.0 kDa protein in YIP3-TFC5 intergenic region.
GN YNL041C OR N2675.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,
RA Hilbert H., Moestl D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: SOME. S.POMBE SPBC776.10C.
CC -----
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CC -----
DR EMBL: Z71317; CA95908.1; -
DR SGD: S0004986; YNL041C.
KW Hypothetical protein.
SQ SEQUENCE 839 AA; 96975 MW; 6484A40F999AD787 CRC64;

Query Match
Best Local Similarity 71.4%; Score 35; DB 1; Length 839;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQRTSNPN 8
DB 50 LQRTSNPN 57

RESULT 4
LIPM_NEIMA STANDARD; PRT; 704 AA.
ID LIPM_NEIMA
AC P57037;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Capsule polysaccharide modification protein LipA.
GN LIPA OR NMA0186.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65639;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Z2491 / Serogroup A / Serotype 4A;
RA MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrett B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RL Nature 404:502-506(2000).
CC -1- FUNCTION: INVOLVED IN THE PHOSPHOLIPID MODIFICATION OF THE
CC CAPSULAR POLYSACCHARIDE. A STRONG REQUIREMENT FOR ITS
CC TRANSLOCATION TO THE CELL SURFACE.
CC CC CAPSULAR POLYSACCHARIDE. INNER MEMBRANE-ASSOCIATED (CYTOPLASMIC
CC SIDE) (PROBABLE).
CC -----
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CC -----
DR EMBL: AL162752; CAB83501.1; -
DR KW Inner membrane; Polysaccharide transport; Transport;
KW Complete proteome.
SQ SEQUENCE 704 AA; 79565 MW; 2E1C5DE65D9BB61 CRC64;

Query Match
Best Local Similarity 69.4%; Score 34; DB 1; Length 704;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 RYSNPN 9
DB 322 RYLNTM 328

RESULT 5

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LIPM_NEfMB
 ID LIPM_NEfMB STANDARD: PRT: 704 AA.
 AC Q05013;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Capsule polysaccharide modification protein 11pA.
 GN LIPM OR NMB0082.
 OS *Neisseria meningitidis* (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.
 OX NCBI_TaxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / Serogroup B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwin M.L., Debey R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Ciecko A., Parksey D.S., Blair E., Citron H., Clark E.B.,
 RA Colton M.D., Ulteback T.R., Knout H., Qin H., Vamathevan J.,
 RA Gill J., Scarlato V., Maignan V., Pizsa M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain
 MC58.";
 RL Science 287:1809-1815(2000).
 RN [2]
 RP SEQUENCE OF 184-704 FROM N.A.
 RC STRAIN=B1940 / Serogroup B;
 RX MEDLINE=93316845; PubMed=8326861;
 RA Frosch M., Mueller A.;
 RT "Phospholipid substitution of capsular polysaccharides and mechanisms
 of capsule formation in *Neisseria meningitidis*.";
 RL Mol. Microbiol. 8:483-493(1993).
 CC -1- FUNCTION: INVOLVED IN THE PHOSPHOLIPID MODIFICATION OF THE
 CAPSULAR POLYSACCHARIDE, A STRONG REQUIREMENT FOR ITS
 TRANSPORT TO THE CELL SURFACE.
 CC -1- SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED (CYTOPLASMIC
 SIDE) (PROBABLE).
 CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION
 566 ONWARD DUE TO A FRAMESHIFT.
 CC -----
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 CC -----
 DR EMBL: AF002367; AAF40546.1; -;
 DR EMBL: Z133995; -; NOT_ANNOTATED_CDS.
 DR PIR: S28077; S28077.
 DR PIR: S32879; S32879.
 DR TIGR: NMB0082; -;
 KM Inner membrane: Polysaccharide transport; Transport;
 KM Complete proteome.
 FT CONFLICT 238 H -> N (IN REF. 1).
 FT CONFLICT 253 V -> I (IN REF. 1).
 FT CONFLICT 294 EINK -> KIDS (IN REF. 1).
 FT CONFLICT 306 T -> P (IN REF. 1).
 FT CONFLICT 316 A -> R (IN REF. 1).
 FT CONFLICT 331 A -> R (IN REF. 1).
 FT CONFLICT 331 R -> G (IN REF. 1).
 FT CONFLICT 390 S -> G (IN REF. 1).
 FT CONFLICT 449 T -> A (IN REF. 1).
 FT CONFLICT 456 T -> A (IN REF. 1).
 FT CONFLICT 462 Y -> H (IN REF. 1).
 SQ SEQUENCE 704 AA; 79605 MW; 2909C40642CD326A CRC64;
 Query Match 69.4%; Score 34; DB 1; Length 704;
 Best Local Similarity 85.7%; Pred. No. 52;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RYSNPNT 9
 Db 322 RYLNPN 328
 RESULT 6
 ID KTI2_YEAST STANDARD: PRT: 313 AA.
 AC P34253;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE KTI12 protein.
 GN KTI12 OR YKL10C OR YKL500 OR YKL446.
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=9434141; PubMed=8065362;
 RA Butler A.R., White J.H., Follawyo Y., Edlin A., Gardiner D.,
 RA Stark M.J.R.;
 RT "Two *Saccharomyces cerevisiae* genes which control sensitivity to GI
 arrest induced by *Kluyveromyces fragilis* toxin.";
 RL Mol. Cell. Biol. 14:6306-6316(1994).
 RN [2]
 RP SEQUENCE OF 1-75 FROM N.A.
 RC MEDLINE=94152173; PubMed=8109175;
 RA Cheret G., Pallier C., Valens M., Daignan-Fornier B., Fukuhara H.,
 RA Bolotin-Fukuhara M., Sor F.;
 RT "The DNA sequence analysis of the HAP4-LAP4 region on chromosome XI
 of *Saccharomyces cerevisiae* suggests the presence of a second
 aspartate aminotransferase gene in yeast.";
 RL Yeast 9:1259-1265(1993).
 RN [3]
 RP SEQUENCE OF 75-313 FROM N.A.
 RC MEDLINE=92221689; PubMed=1561835;
 RA Jacquier A., Legrain P., Dujon B.;
 RT "Sequence of a 10.7 kb segment of yeast chromosome XI identifies the
 RTI and the BAP1 loci and reveals one tRNA gene and several new open
 reading frames including homologs to RAD2 and kinases.";
 RL Yeast 8:121-132(1992).
 CC -1- FUNCTION: CAUSES RESISTANCE TO K. LACTIS TOXIN.
 CC -----
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 CC -----
 DR EMBL: X77511; CA54646.1; -;
 DR EMBL: X71133; CA54044.1; -;
 DR EMBL: S93804; AAB22001.1; -;
 DR EMBL: Z28110; CA81950.1; -;
 DR PIR: S37937; S37937.
 DR PIR: S47958; S47958.
 DR SGD: S0001593; KTI12.
 KM ATP-binding.
 FT NP-BIND 8 ATP (POTENTIAL).
 FT CONFLICT 15
 SQ SEQUENCE 313 AA; 35322 MW; 15A9534087A24A6 CRC64;
 Query Match 67.3%; Score 33; DB 1; Length 313;
 Best Local Similarity 55.6%; Pred. No. 34;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 7

ISCL_YEAST STANDARD: PRT: 477 AA.
AC P40015;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inositol phosphoglycerolipids phospholipase C (EC 3.1.4.-) (IPS
DE phospholipase C) (IPS-PLC) (Neutral sphingomyelinase) (N-Smase)
DE (nsmase).
OS ISCL OR YER019W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Arango R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Huntke-Smith S.,
RA Hyman R., Kayser A., Komp C., Laskari D., Law H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W.;
RA Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RL [2]
RN CHARACTERIZATION.
RP MEDLINE=20564359; PubMed=11006294;
RX Sawal H., Okamoto Y., Luberto C., Mao C., Bielawska A., Domae N.,
RA Hannun Y.A.;
RT "Identification of ISCL (YER019W) as inositol phosphoglycerolipid
RT phospholipase C in Saccharomyces cerevisiae.";
RL J. Biol. Chem. 275:39793-39798(2000).
CC -I- FUNCTION: Responsible for the hydrolysis of the
CC phosphoglycerolipids (IPs), inositol phosphoglyceramide (IPG),
CC mannosylinositol phosphoglyceramide (MIPG), and mannosylinositol
CC phosphoglyceramide (MIP2C). Also active on sphingomyelin, but
CC this activity is probably not physiologically relevant.
CC -I- COFACTOR: Magnesium.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: BELONGS TO THE NEUTRAL SPHINGOMYELINASE FAMILY.
CC -----
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CC -----
DR EMBL: U18778; AAB64552.1; -;
DR SGD: S0000821; ISCL;
DR InterPro: IPR005135; Exo_endo_phos.
DR Pfam: PF03372; Exo_endo_phos.1.
KW Hydrolase; Magnesium; Transmembrane.
FT TRANSMEM 369 417
FT TRANSMEM 425 449
FT METAL 100 100
FT SITE 233
FT FT
FT FT
SQ ACT_SITE 334 334
SEQUENCE 477 AA: 53940 MW; 0670FD303FEB8EFF CRC64;

Query Match 67.3%; Score 33; DB 1; Length 477;
Best Local Similarity 77.8%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LORYSNPT 9
DB 368 LORYSNPT 376

RESULT 8

ATRA_THEAC STANDARD: PRT: 585 AA.
AC P57685;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium-transporting ATPase A chain (EC 3.6.3.12) (Potassium-
DE translocating ATPase A chain) (ATP phosphohydrolase [potassium-
DE transporting] A chain) (Potassium binding and translocating subunit
DE A).
OS KDP A OR TAI310.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasmata.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Granel W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frisuman D., Stocker S., Lupas A.N., Baumelster W.;
RT "The genome sequence of the thermophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513(2000).
CC -I- FUNCTION: ONE OF THE COMPONENTS OF THE HIGH-AFFINITY ATP-DRIVEN
CC POTASSIUM TRANSPORT (OR KDP) SYSTEM, WHICH CATALYZES THE
CC HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF HYDROGEN AND
CC POTASSIUM IONS (BY SIMILARITY).
CC -I- CATALYTIC ACTIVITY: ATP + H(2)O + K(+) (Out) = ADP + phosphate +
CC K(+) (In).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -I- SIMILARITY: BELONGS TO THE KDP A FAMILY.
CC -----
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CC -----
DR EMBL: AL45067; CAC12431.1; -;
DR InterPro: IPR004623; K_ATPaseA.
DR TrEMBL: TIGR00680; kdpA.1.
KW Hydrolase; Transport; Potassium transport; Transmembrane;
KW Complete proteome.
FT TRANSMEM 23 43
FT TRANSMEM 85 105
FT TRANSMEM 152 172
FT TRANSMEM 194 214
FT TRANSMEM 275 295
FT TRANSMEM 307 327
FT TRANSMEM 345 365
FT TRANSMEM 368 388
FT TRANSMEM 397 417
FT TRANSMEM 444 464
FT TRANSMEM 502 522
FT TRANSMEM 547 567
FT FT
SQ SEQUENCE 585 AA: 64844 MW; F18BFA4D64125400 CRC64;

Query Match 67.3%; Score 33; DB 1; Length 585;
Best Local Similarity 85.7%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LORYSNP 7
DB 136 LORYSNP 142
VUIA_VIBCH STANDARD: PRT: 687 AA.

AC 00964; 093000.
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Vibriobactin receptor precursor.
 GN VTUA OR VC2211.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Classical Ogawa 395 / ATCC 39541 / Serotype O1;
 RX MEDLINE=92276356; PubMed=1317381;
 RA Butleron J.R., Stoeber J.A., Payne S.M., Calderwood S.B.;
 RT "Cloning, sequencing, and transcriptional regulation of *vib*, the gene encoding the ferric vibriobactin receptor of *Vibrio cholerae*.";
 RL J. Bacteriol. 174:3729-3738(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Classical Ogawa 395 / ATCC 39541 / Serotype O1;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolenko M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McInzberg L., Ustehack T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.";
 RL Nature 406:477-483(2000).
 CC -1- FUNCTION: RECEPTOR FOR FERRIC VIBRIOBACTIN.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -1- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
 CC -----
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 CC -----
 DR EMBL: AF030977; AAB86828.1; -
 DR EMBL: AE004293; AAF95355.1; -
 DR PIR: A11905; A41905.
 DR TIGR: VC2211; -
 DR InterPro: IPR000531; TONB_boxC.
 DR Pfam: PF00593; TONB_boxC; 1.
 DR PROSITE: PS00430; TONB-DEPENDENT_REC_1; FALSE.NEG.
 KW Signal; Receptor; TonB box; Outer membrane; Transport; Iron transport; Complete proteome.
 KM FT CHAIN 1 37
 FT SIGNAL 38 687
 SQ SEQUENCE 687 AA; 76413 MW; 2CB4FA9BBAD1AF87 CRC64;
 Query Match 67.3%; Score 33; DB 1; Length 687;
 Best Local Similarity 71.4%; Pred. No. 80;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 RYSNPNT 9
 Db 332 RYTNPN 338

RESULT 10
 YDEP_ECOLI STANDARD; PRT; 759 AA.
 ID YDEP_ECOLI

AC P77561; P78160;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein ydeP.
 GN YDEP OR B1501.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakabe G., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
 RA Sempel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
 RA Takenoko K., Takeuchi Y., Wada C., Yamamoto Y., Horikuchi T.;
 RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 CC -----
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 CC -----
 DR EMBL: AE000247; AAC74574.1; -
 DR EMBL: D90792; BAA15174.1; -
 DR EMBL: D90793; BAA15182.1; -
 DR Ecogene: EG13798; ydeP.
 DR InterPro: IPR001467; Prok_Mboxred.
 DR Pfam: PF00384; molybdopterin; 2.
 KW Hypothetical protein; Complete proteome.
 KM SQ SEQUENCE 759 AA; 83494 MW; 4DE7C14068B66DD CRC64;
 Query Match 67.3%; Score 33; DB 1; Length 759;
 Best Local Similarity 75.0%; Pred. No. 89;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQSYSDPN 8
 Db 138 LQSYSDPN 145

RESULT 11
 CEAA_BACTS STANDARD; PRT; 1186 AA.
 ID CEAA_BACTS
 AC 045710;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidial crystal protein cryIIAa (insecticidal delta-endotoxin
 DE CryIIA(a)) (Crystalline entomocidal protoxin) (132 kDa crystal
 DE protein).
 GN CRY14AA OR CRYXIVA(A).
 OS *Bacillus thuringiensis* (subsp. *soltis*).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

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OX NCBI_TaxID=29340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL B-18674 / PS80J1;
RA Payne J.M., Narva K.E.;
RT "Novel Bacillus thuringiensis toxins active against corn rootworm
  larvae."
RL Patent number WO9416079, 21-JUL-1994.
CC -1- FUNCTION: PROMOTES COLLOIDSMORPHIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF INSECTS.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOREILATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U03955; AAA21516.1;
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
DR Toxin: Sporulation.
SQ SEQUENCE 1186 AA; 131694 MW; EF4B1BAE2CB9487 CRC64;

Query Match
Best Local Similarity 67.3%; Score 33; DB 1; Length 1186;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 RYSNPNT 9
DB 587 RYANPMS 593

RESULT 12
MY9B_RAT STANDARD; PRT; 1980 AA.
AC 063358;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin IXb (Unconventional myosin-9b).
GN MY9B OR MYR5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain stem, and spinal cord;
RA MEDLIN=95188874; PubMed=7882973;
RA Reinhard J., Scheel A.A., Diekmann D., Hall A., Ruppert C.,
RA Baehler M.;
RT "A novel type of myosin implicated in signalling by rho family
  GTPases."
RL EMD J. 14:697-704(1995).
CC -1- FUNCTION: UNCONVENTIONAL MYOSIN SERVE IN INTRACELLULAR MOVEMENTS.
CC MAY BE INVOLVED IN THE REMODELING OF THE ACTIN CYTOSKELETON. BINDS
CC ACTIN WITH HIGH AFFINITY BOTH IN THE ABSENCE AND PRESENCE OF ATP
CC AND ITS MECHANOCHEMICAL ACTIVITY IS INHIBITED BY CALCIUM IONS.
CC ALSO ACTS AS A GTPASE ACTIVATING PROTEIN ON RHO.
CC -1- SUBCELLULAR LOCATION: IN UNDIFFERENTIATED CELLS COLOCALIZES WITH
CC F-ACTIN IN THE CELL PERIPHERY WHILE IN DIFFERENTIATED CELLS ITS
CC LOCALIZATION IS CYTOPLASMIC WITH THE HIGHEST LEVELS IN THE
CC PERINUCLEAR REGION (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN TESTIS, LUNG, THYMUS, BRAIN,

```

```

CC LIVER, AND SPLEEN.
CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC -1- SIMILARITY: CONTAINS 4 IQ DOMAINS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X77609; CA54700.1;
DR HSSP: P08799; IAMD.
DR InterPro: IPR002219; DAG_PE_bind.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR000159; RA_domain.
DR InterPro: IPR000198; RhogAP.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00063; myosin_head; 2.
DR Pfam: PF00130; DAG_PE_bind; 1.
DR Pfam: PF00612; IQ; 4.
DR Pfam: PF00620; RhogAP; 1.
DR Pfam: PF00788; RA; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRODOM: PD000355; myosin_head; 2.
DR SMART: SM00109; C1; 1.
DR SMART: SM00015; IQ; 3.
DR SMART: SM00242; MYSC; 1.
DR SMART: SM00314; RA; 1.
DR SMART: SM00324; RhogAP; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS50096; IQ; 3.
KW Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;
KW Cytoskeleton; Coiled coil; GTPase activation; Phorbol-ester binding;
KW Zinc.
FT DOMAIN 1 940 HEAD OR MOTOR DOMAIN.
FT FT 941 1045 NECK OR REGULATORY DOMAIN.
FT FT 1046 1980 TAIL.
FT DOMAIN 1841 1861 COILED COIL (POTENTIAL).
FT DOMAIN 1918 1948 COILED COIL (POTENTIAL).
FT DOMAIN 845 856 ACTIN-BINDING.
FT DOMAIN 958 978 IQ 1.
FT DOMAIN 981 1001 IQ 2.
FT DOMAIN 1002 1024 IQ 3.
FT DOMAIN 1025 1054 IQ 4.
FT DOMAIN 1593 1641 PHORBOL-ESTER AND DAG BINDING.
FT FT 1673 1822 RHO-GAP.
FT NP_BIND 239 246 ATP (POTENTIAL).
SQ SEQUENCE 1980 AA; 225035 MW; D79FEC4DFAE0C05 CRC64;

Query Match
Best Local Similarity 67.3%; Score 33; DB 1; Length 1980;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LORSNPNT 9
DB 1273 IORQHPT 1281

RESULT 13
MY9B_MOUSE STANDARD; PRT; 2114 AA.
AC 090106; 090107; 090108; 090109;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin IXb (Unconventional myosin-9b).
GN MY9B OR MYR5.

```


FT	DOMAIN	1562	1592		COILED COIL (POTENTIAL).
FT	DOMAIN	1839	1859		COILED COIL (POTENTIAL).
FT	DOMAIN	1915	1945		COILED COIL (POTENTIAL).
FT	DOMAIN	844	855		ACTIN-BINDING.
FT	DOMAIN	957	977		IO 1.
FT	DOMAIN	979	1000		IO 2.
FT	DOMAIN	1001	1023		IO 3.
FT	DOMAIN	1024	1053		IO 4.
FT	DOMAIN	1591	1639		PHOSHO-ESTER AND DAG BINDING.
FT	DOMAIN	1671	1820		RHO-GAP.
FT	NP-BIND	239	246		ATP (POTENTIAL).
FT	VARSPLIC	740	740		R -> RCTGGLFFSEFSELDVNAFEDIMAFYESR (IN ISOFORM 2).
FT	VARSPLIC	1875	1890		MISSING (IN ISOFORM 3).
FT	VARSPLIC	1977	2114		GPPALPCPSPLSPISPEAANAPRGAPTSTVYTRVKTPR RTPIPMANIKLPGLPLHLSWAPLDAEAVPVKREPPA RRQDDVHSVYIAPGADLPSSQTLLALDHDTITLPGTKRRYS D PPTCYCLPPSGQANG -> E (IN ISOFORM 3).
FT	VARLANT	1243	1243		L -> LEVSPVLPSSL (ONLY IN STRAIN C57BL/6; CONTAINS AN IN-FRAME 3 BP IMPERFECT DUPLICATION).
FT	VARLANT	1243	1243		A -> P.
FT	VARIANT	2083	2083		
FT	SEQUENCE	2114 AA;	238632 MW;	D774D4B1B278045 CRC64;	
SQ	Query Match		Best Local Similarity	67.3%;	Score 33; DB 1; Length 2114;
	Matches	5; Conservative	55.6%;	Pred. No. 2.7e+02;	Mismatches 1; Indels 0; Gaps 0;
OY	1 LORNSNPT	9			
DB	1271 IORYHPDT	1279			
RESULT 14					
ID	GFRA_VACCV				
NC	P01136;	STANDARD:	PRT:	140 AA.	
DN	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	01-FEB-1996 (Rel. 33, Last annotation update)				
DE	Growth factor.				
GN	CIIR.				
OS	Vaccinia virus (Strain WR).				
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;				
CC	Orthopoxvirus.				
OX	NCB1_FtaxID=10254;				
RN	{1}				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83059924; PubMed=7143577;				
RA	Venkatesan S., Garshowitz A., Moss B.;				
RT	"Complete nucleotide sequences of two adjacent early vaccinia virus genes located within the inverted terminal repetition."				
RL	J. Virol. 44:637-646(1982).				
CC	- i SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.				
CC	-----				
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CC	-----				
DR	EMBL: J02421.. NOT_ANNOTATED_CDS.				
DR	PIR: A01391; WWVZ9.				
DR	HSSP: P01132; IA3P.				
DR	InterPro: IPRO00561; EGF-like.				
DR	InterPro: IPRO01336; EGF_1.				
DR	Pfam: PF00008; EGF_1.				
DR	PRINTS: PRO0009; EGFTGP.				
DR	SMART: SMO0181; EGF_1.				
DR	PROSITE: PS00022; EGF_1; 1.				
DR	PROSITE: PS01186; EGF_2; 1.				

KW EGF-like domain; Growth factor; Glycoprotein.
 FT DOMAIN 41 81 EGF-LIKE.
 FT DISULFID 45 58 BY SIMILARITY.
 FT DISULFID 53 69 BY SIMILARITY.
 FT DISULFID 71 80 BY SIMILARITY.
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 140 AA: 15524 MW: F47C814309BDC6F CRC64:

Query Match Best Local Similarity 65.3%; Score 32; DB 1; Length 140;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ORYSNPNT 9
 DB 89 ORSENPT 96

RESULT 15

GFPA_VACC STANDARD; PRT; 142 AA.

AC P20494; 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Growth factor.

CN C11R.

OS Vaccinia virus (strain Copenhagen).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OX NCBI_TaxID=10249;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91021027; PubMed=2219722;

RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,

RA Paoletti E.;

RT "The complete DNA sequence of vaccinia virus.";

RL Virology 179:247-266(1990).

RN [2]

RP COMPLETE GENOME.

RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,

RA Paoletti E.;

RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";

RL Virology 179:517-563(1990).

CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

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CC -----

DR EMBL: M35027; AAA47985.1; -

DR PIR: C42503; MMV23C.

DR HSSP: P01132; 1A3P.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR001336; EGF_1.

DR Pfam: PF00008; EGF_1.

DR PRINTS: PR00009; EGF1GF.

DR SMART: SM00181; EGF_1.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01166; EGF_2; 1.

KW EGF-like domain; Growth factor; Glycoprotein.

FT DOMAIN 41 81 EGF-LIKE.

FT DISULFID 45 58 BY SIMILARITY.

FT DISULFID 53 69 BY SIMILARITY.

FT DISULFID 71 80 BY SIMILARITY.

FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 142 AA: 15777 MW: 60A6A33CC61C2E66 CRC64;

Query Match Best Local Similarity 65.3%; Score 32; DB 1; Length 142;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ORYSNPNT 9
 DB 89 ORSENPT 96

Search completed: February 25, 2003, 10:37:30
 Job time : 2.795 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 1.14 Seconds
(without alignments)
756.956 Million cell updates/sec

Title: US-09-743-482a-6

Perfect score: 49

Sequence: 1 LQRYSNPRT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_73:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	79.6	271	2 F69442	hypothetical prote
2	39	79.6	340	2 A83401	hypothetical prote
3	37	75.5	2215	2 T16871	hypothetical prote
4	36	73.5	276	2 E90553	hypothetical prote
5	35	71.4	113	2 E33936	ig heavy chain V r
6	35	71.4	322	2 D89785	hypothetical prote
7	35	71.4	414	2 D88547	protein F02A9.4b (
8	35	71.4	434	2 S28312	hypothetical prote
9	35	71.4	568	1 S44904	ZK652.9 protein -
10	35	71.4	760	2 I51720	probable DNA helic
11	35	71.4	839	2 S62963	hypothetical prote
12	34	69.4	267	2 T23361	hypothetical prote
13	34	69.4	290	2 T05009	hypothetical prote
14	34	69.4	400	2 S32879	lipa protein - Nel
15	34	69.4	487	2 G90496	transporter (impor
16	34	69.4	510	2 AD3623	glutamate/gamma-am
17	34	69.4	537	2 T27612	hypothetical prote
18	34	69.4	704	2 D81240	capsule polysaccha
19	34	69.4	704	2 D81240	capsule polysaccha
20	34	69.4	1004	2 S51133	transposase Tn4652
21	34	69.4	248	2 A85432	probable MADS-box
22	33	67.3	313	2 S37937	KTI12 protein - ye
23	33	67.3	345	2 T29261	hypothetical prote
24	33	67.3	454	2 T08280	hypothetical prote
25	33	67.3	454	2 A84162	hypothetical prote
26	33	67.3	468	2 B84166	hypothetical prote
27	33	67.3	477	2 S50477	conserved hypothet
28	33	67.3	520	2 E90304	conserved hypothet
29	33	67.3	687	2 A41905	ferric vibriobacti

30	33	67.3	759	2 B90892	probable oxidoredu
31	33	67.3	759	2 G85725	probable oxidoredu
32	33	67.3	759	2 H64903	hypothetical prote
33	33	67.3	1098	2 J03209	helicase homolog 9
34	33	67.3	1133	2 J70665	helicase II-like p
35	33	67.3	1186	2 T18210	delta endotoxin -
36	33	67.3	1778	2 J70382	apolipoprotein B -
37	33	67.3	1980	2 S54307	myosin heavy chain
38	33	67.3	2629	2 I45569	apolipoprotein B -
39	32	65.3	125	2 H95149	hypothetical prote
40	32	65.3	125	2 G98017	hypothetical prote
41	32	65.3	140	1 MWV29	growth factor - va
42	32	65.3	142	1 MWV23C	growth factor - va
43	32	65.3	195	2 B90065	hypothetical prote
44	32	65.3	227	2 E70935	probable lppm prot
45	32	65.3	245	1 KYB0A	chymotrypsin (EC 3

ALIGNMENTS

RESULT 1

F69442 hypothetical protein AF1543 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_rev150n 05-Dec-1997 #text_change 20-Jun-2000

C:Accession: F69442

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod

., Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E

Nature 390, 364-370, 1997

A:Authors: Uitterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kalne, B.P.; Sykes,

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; PMID:98049343; PMID:9389475

A:Accession: F69442

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-271 <KLE>

A:Cross-references: GB:AE000996; GB:AE000782; NID:92689319; PIDN:AMB89714.1; PID:9264

C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1420

Query Match

Best Local Similarity 79.6%; Score 39; DB 2; Length 271;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRYSNPRT 9

DB 223 QRYSNPRT 230

RESULT 2

A83401

hypothetical protein PA1954 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_rev150n 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: A83401

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; I

., Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pe

A:Reference number: A82950; PMID:20437337; PMID:10984043

A:Accession: A83401

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-340 <STO>

A:Cross-references: GB:AE004622; GB:AE004091; NID:99947948; PIDN:AA05342.1; GSPDB:GN

C:Genetics:

A:Experimental source: strain PA01

A:Gene: PA1954

Query Match

Best Local Similarity 79.6%; Score 39; DB 2; Length 340;

Best Local Similarity 77.8%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQRYSNPNT 9
| | | | |
Db 127 LNMYSNPNT 135

RESULT 3

T16871

hypothetical protein T13H2.4 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000

A:Accession: T16871

R:WU, X.

Submitted to the EMBL Data Library, October 1995

A:Description: The sequence of *C. elegans* cosmid T13H2.

A:Reference number: 218593

A:Accession: T16871

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2215 <WUX>

A:Cross-references: EMBL:U95653; NID:91049397; PID:91049401; PIDN:AA852495.1; GSPDB:GN00

A:Experimental source: strain Bristol N2; clone T13H2

C:Genetics:

A:Gene: CESP:T13H2.4

A:Map position: X

A:Insertion: 112/2; 136/1; 167/1; 196/1; 649/1; 696/1; 757/1; 850/1; 882/1; 985/1; 1046/1;

Query Match

Best Local Similarity 75.5%; Score 37; DB 2; Length 2215;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQRYSNPNT 9
| | | | |
Db 1347 LQRYSEPOT 1355

RESULT 4

P90553

hypothetical protein MYPV_3340 [Imported] - *Mycoplasma pulmonis* (strain UAB CTIP)C:Species: *Mycoplasma pulmonis*

C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001

A:Accession: P90553

R:Chambaud, I.; Helli, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A:Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulm*

A:Reference number: A99512; MUID:21267165; PMID:11353084

A:Accession: P90553

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-276 <KUR>

A:Cross-references: GB:AL445566; PID:g14089748; PIDN:CAC13507.1; GSPDB:GN00153

A:Experimental source: strain UAB CTIP

C:Genetics:

A:Gene: MYPV_3340

A:Genetic code: SGC3

Query Match
Best Local Similarity 73.5%; Score 36; DB 2; Length 276;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQRYSNPNT 8
| | | | |
Db 41 LKRYKNPN 48

RESULT 5

E33936

Ig heavy chain V region (VM13) - mouse (fragment)

C:Species: *mus musculus* (house mouse)

C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 23-Jul-1999

C:Accession: E33936

R:Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.

Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989

A:Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin 9

A:Reference number: A33936; MUID:89282831; PMID:2471975

A:Accession: E33936

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <MEP>

A:Cross-references: GB:J04578; NID:9623178; PIDN:AA60438.1; PID:9623180

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 71.4%; Score 35; DB 2; Length 113;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSNPNT 9
| | | | |
Db 46 YSNPNT 51

RESULT 6

D89785

hypothetical protein SA0217 [Imported] - *Staphylococcus aureus* (strain N315)C:Species: *Staphylococcus aureus*

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

A:Accession: D89785

R:Kurita, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cul, L.; O

ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: D89785

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-322 <KUR>

A:Cross-references: GB:BA000018; PID:g13700140; PIDN:BA841439.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: SA0217

Query Match
Best Local Similarity 71.4%; Score 35; DB 2; Length 322;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSNPNT 9
| | | | |
Db 159 YSNPNT 164

RESULT 7

D88547

protein F02A9.4b [Imported] - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001

A:Accession: D88547

R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating blo

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_

A:Accession: D88547

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-414 <STO>

A:Cross-references: GB:chr_III; PIDN:CAA79619.1; PID:93875449; GSPDB:GN00021; CESP:FO

C:Genetics:

A:Gene: F02A9.4b

A:Map position: 3

C:Superfamily: *Caenorhabditis elegans* hypothetical protein F02A9.4

Query Match 71.4%; Score 35; DB 2; Length 414;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQRYSNPN 8
Db 312 LERYSQPN 319

RESULT 8

528312
hypothetical protein F02A9.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 04-Mar-2000

C:Accession: 528312

R:Berks, M.
submitted to the EMBL Data Library, December 1992

A:Reference number: S28296

A:Accession: 528312

A:Molecule type: DNA

A:Residues: 1-434 <BER>

A:Cross-references: EMBL:Z19555; NID:96705; PID:96710

C:Genetics:

A:Introns: 5/2; 30/3; 113/1; 179/1; 261/2; 374/3

C:Superfamily: Caenorhabditis elegans hypothetical protein F02A9.4

Query Match 71.4%; Score 35; DB 2; Length 434;
Best Local Similarity 75.0%; Pred. No. 47;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQRYSNPN 8
Db 274 LERYSQPN 281

RESULT 9

544904

ZK652.9 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 23-Mar-2001

C:Accession: 544904

R:Du, Z.

submitted to the EMBL Data Library, May 1993

A:Description: Sequence of the C. elegans cosmid ZK652.

A:Reference number: S44618

A:Accession: 544904

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-568 <DU2>

A:Cross-references: EMBL:L14429; NID:9289765; PID:9289770

C:Genetics:

A:Introns: 57/1; 144/3; 236/1; 259/2; 285/3; 314/2; 365/2; 529/2

C:Superfamily: ZK652.9 protein; bioc homology

F:96-203/Domain: bioc homology <BIOC>

Query Match 71.4%; Score 35; DB 1; Length 568;
Best Local Similarity 62.5%; Pred. No. 62;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQRYSNPN 8
Db 414 VERTNPN 421

RESULT 10

151720

Probable DNA helicase ERCC2/XPD - southern platyfish

C:Species: Xiphophorus maculatus (southern platyfish)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Feb-2001

C:Accession: 151720; A56748

R:Walter, R.B.; Harless, J.; Svensson, R.T.; Kallman, K.D.; Morizot, D.C.; Nairn, R.S.

Genomics 10; 1083-1086, 1991

A:Title: Linkage assignment of a DNA sequence (ERCC2L1) homologous to a human DNA rep

A:Reference number: 151720; MUID:92009912; PMID:1680795

A:Accession: 151720

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-760 <MAL>

A:Cross-references: EMBL:U17896; NID:9604370; PIDN:AAA85822.1; PID:9604371

R:Coletta, L.D.; Rolig, R.L.; Fossey, S.; Morizot, D.C.; Nairn, R.S.; Walter, R.B.

Genomics 26; 70-76, 1995

A:Title: Characterization of the Xiphophorus fish (teleostei: poeciliidae) ERCC2/XPD

A:Reference number: A56748; MUID:95301295; PMID:7782088

A:Accession: A56748

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-760 <COR>

A:Cross-references: GB:U17896; NID:9604370; PIDN:AAA85822.1; PID:9604371

C:Genetics:

A:Gene: ERCC2/XPD

A:Introns: 2/2; 35/3; 61/3; 82/3; 120/3; 159/3; 198/3; 240/1; 272/2; 317/1; 373/2; 41

C:Keywords: ATP; nucleotide binding; P-loop

F:42-49/Region: nucleotide-binding motif A (P-loop)

F:230-235/Region: nucleotide-binding motif B

F:234-237/Region: DEAH motif

Query Match 71.4%; Score 35; DB 2; Length 760;
Best Local Similarity 85.7%; Pred. No. 83;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 QRYSNPN 8
Db 145 QRHSNPN 151

RESULT 11

S62963

hypothetical protein YNL041c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein N2675

C:Species: Saccharomyces cerevisiae

C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002

C:Accession: S62963

R:Submittedhoelt, A.; Floeth, M.; Fritz, C.; Heuss-Nelitzel, D.; Hilbert, H.; Moestl, D.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S62944

A:Accession: S62963

A:Molecule type: DNA

A:Residues: 1-839 <DUB>

A:Cross-references: EMBL:Z71317; NID:91301893; PID:e239673; PID:91301894; GSPDB:GN000

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:TF12; MIPS:YNL041C

A:Cross-references: SGD:S0004986

A:Map position: 14L

Query Match 71.4%; Score 35; DB 2; Length 839;
Best Local Similarity 87.5%; Pred. No. 92;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQRYSNPN 8
Db 50 LQRYSNPN 57

RESULT 12

T23361

hypothetical protein K06B4.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000

C:Accession: T23361

R:Lloyd, C.

submitted to the EMBL Data Library, December 1996

A:Reference number: Z19732

A:Accession: T23361

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-267 <WIL>
 A:Cross-references: EMBL:Z83233; PIDN:CA805757.1; GSPDB:GN00023; CESP:K06B4.9
 A:Experimental source: clone K06B4
 C:Genetics:
 A:Gene: CESP:K06B4.9
 A:Map position: 5
 A:Introns: 13/3: 67/2: 116/2
 C:Superfamily: Caenorhabditis elegans hypothetical protein K06B4.9

Query Match 69.4%; Score 34; DB 2; Length 267;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QRYSNPNT 9
 : : : : :
 Db 113 QLFNPNT 120

RESULT 13

T05009
 hypothetical protein T19P19.110 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
 C:Accession: T05009
 R:Bevan, M.; Montfort, A.; Casacuberta, E.; Puigdomenech, P.; Hohnleisel, J.; Mewes, H.W.;
 submitted to the Protein Sequence Database, April 1998
 A:Reference number: 215394
 A:Accession: T05009
 A:Molecule type: DNA
 A:Residues: 1-290 <BEV>
 A:Cross-references: EMBL:AL022605
 A:Experimental source: cultivar Columbia; BAC clone T19P19
 C:Genetics:
 A:Map position: 4
 A:Note: T19P19.110

Query Match 69.4%; Score 34; DB 2; Length 290;
 Best Local Similarity 62.5%; Pred. No. 49;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQRYSNPN 8
 : : : : :
 Db 203 IQQYQNPNT 210

RESULT 14

S32879
 l1pa protein - Neisseria meningitidis
 C:Species: Neisseria meningitidis
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
 C:Accession: S32879; S28077
 R:Frosch, M.; Mueller, A.
 MOL. Microbiol. 8, 483-493, 1993
 A:Title: Phospholipid substitution of capsular polysaccharides and mechanisms of capsule
 A:Reference number: S32879; MUID:93316845; PMID:8326861
 A:Accession: S32879
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-400 <FRO>
 A:Cross-references: EMBL:Z13995
 C:Genetics:
 A:Gene: l1pa

Query Match 69.4%; Score 34; DB 2; Length 400;
 Best Local Similarity 85.7%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 RYSNPNT 9
 * : : : : :
 Db 140 RYLNPNNT 146

RESULT 15

G90496
 transporter (imported) - Sulfolobus solfataricus
 C:Species: Sulfolobus solfataricus
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
 C:Accession: G90496
 R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awaize, M.J.; Ch
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder
 arett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
 submitted to Genbank, April 2001
 A:Description: Sulfolobus solfataricus complete genome.
 A:Reference number: A99139
 A:Accession: G90496
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1487 <KUR>
 A:Cross-references: GB:AE006641; NID:g13816553; PIDN:AAK43230.1; GSPDB:GN00155
 C:Genetics:
 A:Gene: SS03129

Query Match 69.4%; Score 34; DB 2; Length 487;
 Best Local Similarity 71.4%; Pred. No. 83;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 RYSNPNT 9
 : : : : :
 Db 190 KYTNPNNT 196

Search completed: February 25, 2003, 10:33:52
 Job time : 4.14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:58 ; Search time 2.28 Seconds
(without alignments)
813.344 Million cell updates/sec

Title: US-09-743-482A-6

Perfect score: 49

Sequence: 1 LQRXSNPNT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp-phage:*

10: sp-plant:*

11: sp-rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	79.6	271	17 028729	028729 archaeoglob
2	39	79.6	340	16 0912F0	0912F0 pseudomonas
3	39	79.6	743	5 0958R9	0958R9 drosophila
4	39	79.6	1346	5 09V6J8	09V6J8 drosophila
5	38	77.6	428	16 09A202	09A202 streptococ
6	37	75.5	1702	5 08WQC8	08WQC8 caenorhabd
7	36	73.5	175	10 09W724	09W724 arabidopsis
8	36	73.5	179	10 09LJX2	09LJX2 arabidopsis
9	36	73.5	276	16 096QW7	096QW7 mycoplasma
10	36	73.5	582	5 076214	076214 schistosoma
11	36	73.5	582	5 09VTF3	09VTF3 schistosoma
12	35.5	72.4	552	5 09VEQ0	09VEQ0 drosophila
13	35	71.4	71	7 08SPD6	08SPD6 salvelinus
14	35	71.4	263	10 093X25	093X25 plasmu sativ
15	35	71.4	322	16 095WZ8	095WZ8 staphylococ
16	35	71.4	340	5 095PW5	095PW5 caenorhabd

ALIGNMENTS

17	35	71.4	512	5 0879C4	0879C4 drosophila
18	35	71.4	563	12 08V6K1	08V6K1 halovirus h
19	35	71.4	739	12 08V7T7	08V7T7 tt virus. o
20	35	71.4	760	13 0819A1	0819A1 xiphophorus
21	35	71.4	1469	5 0961D9	0961D9 drosophila
22	34	69.4	85	11 0912R6	0912R6 ratius nov
23	34	69.4	267	5 045662	045662 caenorhabd
24	34	69.4	290	10 065659	065659 arabidopsis
25	34	69.4	323	10 08S177	08S177 oryza sativ
26	34	69.4	324	4 096G79	096G79 homo sapien
27	34	69.4	324	11 09D321	09D321 mus musculu
28	34	69.4	324	11 09D0A7	09D0A7 mus musculu
29	34	69.4	324	11 0912R7	0912R7 ratius nov
30	34	69.4	325	11 099JX8	099JX8 mus musculu
31	34	69.4	365	3 09UV71	09UV71 candida alb
32	34	69.4	390	2 093MLO	093MLO lactobacill
33	34	69.4	394	17 08T035	08T035 methanosarc
34	34	69.4	411	2 032743	032743 lactobacill
35	34	69.4	462	11 08VED6	08VED6 mus musculu
36	34	69.4	471	2 08RK23	08RK23 pseudomonas
37	34	69.4	475	16 09CN34	09CN34 pasteurella
38	34	69.4	487	17 097U91	097U91 sulfolobus
39	34	69.4	492	2 093UT1	093UT1 neisseria m
40	34	69.4	505	5 018274	018274 caenorhabd
41	34	69.4	510	16 08VBJ1	08VBJ1 bruceella me
42	34	69.4	545	5 09NEK9	09NEK9 caenorhabd
43	34	69.4	680	16 08XRJ8	08XRJ8 ralsionia s
44	34	69.4	696	2 085455	085455 pasteurella
45	34	69.4	696	2 09RP69	09RP69 pasteurella

RESULT 1

ID 028729 PRELIMINARY: PRT; 271 AA.

AC 028729;

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Hypothetical protein AF1543.

GN AF1543.

OS Archaeoglobus fulgidus.

OC Archaea: Euryarchaeota: Archaeoglobi: Archaeoglobales;

OC Archaeoglobaceae; Archaeoglobus.

OX NCBI_TaxID=2234;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE=98049343; PubMed=9389475;

RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Ketchum K.A., Dodson R.J., Gwin M., Hickey E.K., Peterson J.D.,

RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyripides N.C.,

RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glöckl A., Zhou L.,

RA Overbeek R., Cocayne J.D., Weidman J.F., McDonald L., Utterback T.,

RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,

RA Sedow P.W., d'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

RA Venter J.C.;

RT "The complete genome sequence of the hyperthermophilic, sulphate-

RT reducing archaeon Archaeoglobus fulgidus.";

RL Nature 390:364-370(1997).

DR EMBL: AF000996; AAB89714.1; .

DR TIGR: AF1543; .

DR InterPro: IPR001330; Premyltrans.

DR InterPro: IPR000169; SHProl_acsite.

DR Pfam: PF00432; Premyltrans; 3.

DR PROSITE: PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.

KW Hypothetical protein: Complete proteome.

SQ SEQUENCE 271 AA; 31009 MW; 9ADP0208FDE658F CRC64;

Query Match 79.6%; Score 39; DB 17; Length 271;
Best Local Similarity 87.5%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ORYSNPNT 9
DB 223 ORYSNPNT 230

RESULT 2

ID 0912FO PRELIMINARY; PRT; 340 AA.
AC 0912FO;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Hypothetical protein PA1954.
GN PA1954.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01.
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Plam X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V., an
RT Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunity pathogen.
RL Nature 406:959-964 (2000).
DR EMBL: AE004622; AAC05342.1;
KM Hypothetical protein: Complete proteome.
SO SEQUENCE 340 AA; 33893 MW; CBA3675651FAC248 CRC64;

Query Match 79.6%; Score 39; DB 16; Length 340;
Best Local Similarity 77.8%; Pred. No. 9.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LORYSNPNT 9
DB 127 LNNYSNPNT 135

RESULT 3
O95RK9 PRELIMINARY; PRT; 743 AA.
AC 095RK9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE LD222566.
GN CAP-G OR CG13327 OR CG17054.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Fatfan D., Frise E., George R.,
RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacle J., Paragans V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Ceiniker S.,
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY061306; AAL28854.1;

DR FLYBase: FBgn0033795; Cap-G.
SO SEQUENCE 743 AA; 85380 MW; F3E5DF1355CA9188 CRC64;

Query Match 79.6%; Score 39; DB 5; Length 743;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LORYSNPNT 9
DB 377 LKRYNPNT 385

RESULT 4

ID 09V6J8 PRELIMINARY; PRT; 1346 AA.
AC 09V6J8; 09V6J9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CG17054 protein.
GN CAP-G OR CG13327 OR CG17054.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burlis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegyam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasok P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostrel A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003819; AAF58425.2;
DR FLYBase: FBgn0033795; Cap-G.
KM Hypothetical protein.
SO SEQUENCE 1346 AA; 153344 MW; 127103AB4C8DD5F CRC64;

Query Match 79.6%; Score 39; DB 5; Length 1346;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQRYSNPNT 9
DB 787 LKRYENPNT 795

RESULT 5

O9A202 PRELIMINARY; PRT; 428 AA.
AC O9A202;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical protein SPY0012.
GN SPY0012.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SE370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferrerli J.J., Moshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006472; AAK3154.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 428 AA; 48848 MW; F88716EE4C847F46 CRC64;

Query Match 77.6%; Score 38; DB 16; Length 428;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQRYSNPNT 8
DB 198 LQRYNPN 205

RESULT 6

O8MOC8 PRELIMINARY; PRT; 1702 AA.
AC O8MOC8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical 190.6 kDa protein.
GN T13H2.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99065613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Wu X.;
RL "The sequence of C. elegans cosmid T13H2.";
RN Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U39653; AAL56623.1; -;
KW Hypothetical protein.
SQ SEQUENCE 1702 AA; 190617 MW; 1F5CAC942100FEB5 CRC64;

Query Match 75.5%; Score 37; DB 5; Length 1702;
Best Local Similarity 77.8%; Pred. No. 13e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LQRYSNPNT 9
DB 834 LQRYSEPOT 842

RESULT 7

O9M724 PRELIMINARY; PRT; 175 AA.
AC O9M724;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE M2M20.2 protein.
GN M2M20.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III p1.M2M20 genomic sequence.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC023838; AAF34827.1; -;
SQ SEQUENCE 175 AA; 19040 MW; 243A41728006E472 CRC64;

Query Match 73.5%; Score 36; DB 10; Length 175;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QRYSNPNT 9
DB 84 QHYONPNT 91

RESULT 8

O9LUX2 PRELIMINARY; PRT; 179 AA.
AC O9LUX2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE G01AAV34827.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;

RX MEDLINE-20363099; PubMed-10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
 RT TAC and BAC clones."
 RL DNA Res. 7:217-221(2000).
 DR EMBL: AF000385; BAB01417.1;
 SQ SEQUENCE 179 AA; 19541 MW; 070273BCB1279F8D CRC64;

Query Match 73.5%; Score 36; DB 10; Length 179;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QRSNPT 9
 1 1 1 1 1 1
 DB 88 QHYONPT 95

RESULT 9
 O98QM7 PRELIMINARY; PRT; 276 AA.

AC O98QM7;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DE Hypothetical protein MYPU_3340.

OS Mycoplasma pulmonis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.

OX NCBI_TaxID=2107;
 RN 1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=UAB CTIP;
 RX MEDLINE-21267165; PubMed-11353084;
 RA Chambaud I., Helling R., Ferris S., Barbe V., Samson D., Galisson F.,
 RA Moszer I., Dybvig K., Wroblewski H., Viart A., Rocha E.P.C.,
 RA Blanchard A.;
 RT "The complete genome sequence of the murine respiratory pathogen
 RT Mycoplasma pulmonis."
 RL Nucleic Acids Res. 29:2145-2153(2001).

DR EMBL: AL45564; CAC13507.1;
 DR Mypulist; MYPU_3340;
 KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 276 AA; 33481 MW; CAB11F4429FE2858 CRC64;

Query Match 73.5%; Score 36; DB 16; Length 276;
 Best Local Similarity 75.0%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LORVSNP 8
 1 1 1 1 1 1
 DB 41 LKRYKNP 48

RESULT 10
 O76214 PRELIMINARY; PRT; 582 AA.

AC O76214;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Calcium-binding protein Sj66 precursor.

OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
 OC Schistosomatoidae; Schistosomatidae; Schistosoma.

OX NCBI_TaxID=6182;
 RN 11)

RP SEQUENCE FROM N.A.
 RC STRAIN=PHILIPPINE;
 RX MEDLINE-99143763; PubMed-9989218;
 RA Hooker C.W., Brindley P.J.;

RT "Cloning of a cDNA encoding Sjirv1, a Schistosoma japonicum calcium-

binding protein similar to calnexin, and expression of the recombinant
 protein in Escherichia coli";
 RT Biochim. Biophys. Acta 1429:331-341(1999).

RL EMBL: AF025955; AAC3883.1;
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; Calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 1.

FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 582 CALCIUM-BINDING PROTEIN SJ66.
 SQ SEQUENCE 582 AA; 66028 MW; AA2CF3138B7C738D CRC64;

Query Match 73.5%; Score 36; DB 5; Length 582;
 Best Local Similarity 85.7%; Pred. No. 66;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 RYSNPT 9
 1 1 1 1 1 1
 DB 183 RYKNPT 189

RESULT 11
 O9TVF3 PRELIMINARY; PRT; 582 AA.

AC O9TVF3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Calcium-binding protein Sj66.

OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
 OC Schistosomatoidae; Schistosomatidae; Schistosoma.

OX NCBI_TaxID=6182;
 RN 11)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHINESE;
 RX MEDLINE-99143763; PubMed-9989218;
 RA Hooker C.W., Brindley P.J.;

RT "Cloning of a cDNA encoding Sjirv1, a Schistosoma japonicum calcium-
 RT binding protein similar to calnexin, and expression of the recombinant
 RT protein in Escherichia coli."
 RL Biochim. Biophys. Acta 1429:331-341(1999).

DR EMBL: AF030342; AAC62193.1;
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; Calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 1.
 SQ SEQUENCE 582 AA; 66027 MW; 79E3CE047F6B821 CRC64;

Query Match 73.5%; Score 36; DB 5; Length 582;
 Best Local Similarity 85.7%; Pred. No. 66;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 RYSNPT 9
 1 1 1 1 1 1
 DB 183 RYKNPT 189

RESULT 12
 O9VE00 PRELIMINARY; PRT; 552 AA.

AC O9VE00;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE CG3534 protein (LUD23605P).

GN CG3534.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanoside P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.-H., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champs M., Pfeiffer B.D.,
 RA Wan K.H., Doyle G., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigwan C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,
 RA Klamm B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacler J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sidon-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrstkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Sequence 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Flise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacler J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AE003715; AAF55371.1; -;
 DR EMBL: AY058530; AAL13759.1; -;
 DR FLYBase: FBgn0038463; CG3534.
 DR InterPro: IPR000577; FGGY_Kin.
 DR Pfam: PF02782; FGGY_1.
 DR SEQUENCE 552 AA; 61154 MW; 336B58B1A4FB7868 CRC64;

Query Match 72.4%; Score 35.5; DB 5; Length 552;
 Best Local Similarity 56.2%; Pred. No. 79;
 Matches 9; Conservative 0; Mismatches 0; Indels 7; Gaps 1;

OY 1 LORY-----SNPNT 9
 |||||
 DB 537 LORYREMARKVLSNPNT 552

RESULT 13
 O8SPD6 PRELIMINARY; PRT; 71 AA.
 AC O8SPD6;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE MHC class II antigen beta 1 (Fragment).
 GN SANA-DABI.
 OS Salvelinus namaycush (lake trout).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
 OC NCBI_TaxID=8040;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reimer T., Noakes M.A., Phillips R.;
 RT "MHC class II alleles in lake trout."
 RT Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF455262; AAL78327.1; -;
 FT NON_TER
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 71 AA; 8047 MW; 3A4F964670698356 CRC64;

Query Match 71.4%; Score 35; DB 7; Length 71;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LORYSNPNT 9
 |||||
 DB 52 LERYCKPNT 60

RESULT 14
 O93X25 PRELIMINARY; PRT; 263 AA.
 AC O93X25;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE 2-Cys peroxidoxin.
 OS Pisum sativum (Garden pea).
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eudicots I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OC NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF;
 RA Bernier-Villamor L.;
 RL Thesis (2001). Department of Bioquimica,
 RL Biologia Celular y Molecular de plantas,
 RL Estacion Experimental del Zaidin (CSIC), Granada, Spain.
 DR EMBL: AJ315851; CAC48323.1; -;
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 DR SEQUENCE 263 AA; 28864 MW; 195B62833258A16 CRC64;

Query Match 71.4%; Score 35; DB 10; Length 263;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSNPNT 9
 |||||
 DB 12 YSNPNT 17

RESULT 15
 O99WZ8 PRELIMINARY; PRT; 322 AA.
 AC O99WZ8;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE Hypothetical protein SAV0225.
 GN SAV0225 OR SA0217.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 OX NCBI_TaxID=158878, 158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshida K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 DR EMBL: AP003358; BAB56387.1; -
 DR EMBL: AP003129; BAB41459.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 322 AA; 36948 MW; 361920F382FDF32D CRC64;

Query Match

71.4%; Score 35; DB 16; Length 322;

Best Local Similarity 100.0%; Pred. No. 56;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSNPNT 9
 |||||

Db 159 YSNPNT 164

Search completed: February 25, 2003, 10:36:30
 Job time : 4.28 secs

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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:28:57 : Search time 2.97 seconds
(without alignments)
403.790 Million cell updates/sec

Title: US-09-743-482a-6
Perfect score: 49
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Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 14: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT:*
- 15: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT:*
- 16: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1995.DAT:*
- 17: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1996.DAT:*
- 18: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1997.DAT:*
- 19: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	21	AAV78321
2	49	100.0	107	21	AAV78326
3	49	100.0	532	21	AAV78328
4	39	79.6	1346	22	ABB65153
5	38	77.6	428	23	ABP27989
6	35.5	72.4	552	22	ABB71235
7	35	71.4	235	21	AA845275
8	35	71.4	283	18	AA889755
9	34	69.4	229	23	AA017235
10	34	69.4	303	22	AAW78596

11	34	69.4	317	20	AA888667
12	34	69.4	317	22	ABB50434
13	34	69.4	324	22	AAE04905
14	34	69.4	324	22	AA831674
15	34	69.4	324	23	AA017236
16	34	69.4	324	23	ABB90407
17	34	69.4	395	22	AB812029
18	34	69.4	395	22	AAW79580
19	34	69.4	1000	22	ABB62399
20	34	69.4	1026	22	ABB70604
21	33	67.3	47	22	AAU14752
22	33	67.3	56	20	AAV02522
23	33	67.3	56	20	AAV02525
24	33	67.3	56	20	AAV02496
25	33	67.3	76	22	AAU14776
26	33	67.3	104	23	ABP32060
27	33	67.3	112	19	AAW98457
28	33	67.3	139	22	ABG03688
29	33	67.3	236	21	AA824291
30	33	67.3	236	21	AA843464
31	33	67.3	240	20	AAV02472
32	33	67.3	240	22	AA846005
33	33	67.3	240	22	AA846006
34	33	67.3	240	22	AA846007
35	33	67.3	240	22	AA846008
36	33	67.3	240	22	AA846038
37	33	67.3	248	21	AA824290
38	33	67.3	248	21	AA843463
39	33	67.3	248	23	AAU92988
40	33	67.3	260	21	AA843462
41	33	67.3	261	23	AA824289
42	33	67.3	281	23	AA017825
43	33	67.3	353	22	ABB52558
44	33	67.3	404	22	AAE01421
45	33	67.3	487	22	ABG11400

ALIGNMENTS

RESULT 1
AAV78321
ID AAV78321 standard; Protein; 9 AA.
XX
AC AAV78321;
XX
DT 04-MAY-2000 (first entry)
XX
DE Anti-zeta-chain antibody 2-B-5 VL-region CDR3 protein sequence.
XX
XX Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; Immunisation;
XX complementary determining region; CDR; autoimmune disease; cytotoxic;
XX immune deficiency; T-cell malignancy; infectious disease; antiviral;
XX immunosuppressive; antimicrobial; Immune response modulator; NK-cell.
XX
XX Rattus norvegicus.
XX
XX WO200003016-A1.
XX
XX 20-JAN-2000.
XX
XX 09-JUL-1999; 99MO-EP04838.
XX
XX 10-JUL-1998; 98EP-0112867.
XX
XX (CONN-) CONNEX GMBH.
XX
XX Reiter C;
XX
XX WPI: 2000-160926/14.
XX N-FSDB; AA288319.
XX
XX New oligonucleotide, polypeptide, antibody useful for treating
PT

Secreted protein e
Human secreted pro
Human transporter
Amino acid sequenc
Human secreted pro
Human polypeptide
Human secreted pro
Human protein SEQ
Drosophila melanog
Drosophila melanog
Novel bone marrow
Clone selected aft
Clone selected aft
Clone selected aft
Novel bone marrow
Human ORF033 prot
H. pylori GHP0 669
Novel human diagno
Arabidopsis thalia
Arabidopsis thalia
A single chain ant
Human MUC-1 scfv c
Human MUC-1 scfv c
Human MUC-1 scfv c
Human MUC-1 scfv c
Human TF anti-Idio
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Sponge okadaic aci
Escherichia coli P
Human gene 7 encod
Novel human diagno

PT autoimmune disease, immune deficiencies, T-cell malignancies and
 PT infectious diseases -
 XX
 PS Claim 10; Fig 7; 79pp; English.
 CC The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is
 CC encoded by (I), is obtained by immunising a rat with jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,
 CC infectious diseases and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC treatment of NK-cell derived malignancies. It can also be useful for the
 CC determination of zeta-chain or eta-chain expression on NK-cells,
 CC T-lymphocytes or their precursors. The present sequence represents the
 CC CDR3 of the VL-region of the anti-zeta-chain antibody 2-B-5, produced
 CC by rats from the present invention.
 CC
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 49; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQRYSNPNT 9
 ID AAY78326 standard; Protein; 107 AA.
 AC AAY78326;
 XX
 DT 04-MAY-2000 (first entry)
 DE Anti-zeta-chain antibody 2-B-5 VL-region protein sequence.
 XX
 KW Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
 KW complementary determining region; CDR; autoimmune disease; cytostatic;
 KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
 KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.
 XX
 OS Rattus norvegicus.
 XX
 PN WO200003016-A1.
 PD 20-JAN-2000.
 XX
 PF 09-JUL-1999; 99WO-EP04838.
 XX
 PR 10-JUL-1998; 98EP-0112867.
 XX
 PA (CONN-) CONNEX GMBH.
 XX
 PI Reiter C;
 XX
 DR WPI: 2000-160926/14.
 DR N-PSDB: AA288324.
 XX
 PT New oligonucleotide, polypeptide, antibody useful for treating
 PT autoimmune disease, immune deficiencies, T-cell malignancies and
 PT infectious diseases -
 PS Claim 9; Fig 7; 79pp; English.
 XX

CC The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is
 CC encoded by (I), is obtained by immunising a rat with jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,
 CC infectious diseases and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC or viral infections. The antibody, and fragments of it, can be useful for
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC treatment of NK-cell derived malignancies. It can also be useful for the
 CC determination of zeta-chain or eta-chain expression on NK-cells,
 CC T-lymphocytes or their precursors. The present sequence represents the
 CC VL-region of the anti-zeta-chain antibody 2-B-5, produced by rats from
 CC the present invention.
 CC
 SQ Sequence 107 AA;
 Query Match 100.0%; Score 49; DB 21; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQRYSNPNT 9
 ID AAY78328 standard; Protein; 532 AA.
 AC AAY78328;
 XX
 DT 04-MAY-2000 (first entry)
 DE Bispecific anti-zeta-chain/anti-EPICAM antibody protein sequence.
 XX
 KW Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
 KW complementary determining region; CDR; autoimmune disease; cytostatic;
 KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
 KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.
 XX
 OS Rattus norvegicus.
 OS Synthetic.
 XX
 PN WO200003016-A1.
 PD 20-JAN-2000.
 XX
 PF 09-JUL-1999; 99WO-EP04838.
 XX
 PR 10-JUL-1998; 98EP-0112867.
 XX
 PA (CONN-) CONNEX GMBH.
 XX
 PI Reiter C;
 XX
 DR WPI: 2000-160926/14.
 DR N-PSDB: AA288358.
 XX
 PT New oligonucleotide, polypeptide, antibody useful for treating
 PT autoimmune disease, immune deficiencies, T-cell malignancies and
 PT infectious diseases -
 PS Example 9; Page 74-76; 79pp; English.
 XX
 PS The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is

Query Match 77.6%; Score 38; DB 23; Length 428;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LORNSNP 8
11:1111
Db 198 LORNSNP 205

RESULT 6
ABB71235
ID ABB71235 standard; Protein: 552 AA.

XX ABB71235;
XX
XX 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 40497.

KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.

OS Drosophila melanogaster.

XX MO200171042-A2.

XX 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI: 2001-656860/75.

DR N-PDB; ABL15338.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -

PS Disclosure: SEQ ID NO 40497; 21pp + Sequence listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABR57737-ABR72072).

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 552 AA;

Query Match 72.4%; Score 35.5; DB 22; Length 552;
Best Local Similarity 56.2%; Pred. No. 3.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 7; Gaps 1;

OY 1 LORNSNP 9
1111111111
Db 537 LORNSNP 552

RESULT 7
AAB45275
ID AAB45275 standard; Protein: 235 AA.

XX AAB45275;
AC
XX 13-FEB-2001 (first entry)

DE Sequence #1 homologous to protein fragment of the invention.

KW Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticancer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.

XX Homo sapiens.

XX WO200063230-A2.

XX 26-OCT-2000.

PF 23-MAR-2000; 2000WO-US07677.

PR 26-MAR-1999; 99US-0126601.

PR 17-SEP-1999; 99US-0154373.

PR 14-JAN-2000; 2000US-0176064.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM, Komatsu G;

DR WPI: 2000-647515/62.

XX New nucleic acid molecules encoding 49 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -
XX Disclosure: Page 387-388; 402pp; English.

XX The present invention relates to the isolation of genes encoding
CC 49 human secreted proteins. The genes can be used to
CC generate fusion proteins by linking to the gene for the human
CC immunoglobulin G Fc portion for increasing the stability of
CC the fusion protein as compared to the human protein only. The genes and
CC proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated
CC from a range of human tissues disclosed in the specification. The
CC nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischemias; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections. The present sequence is a protein of the invention.

XX Sequence 235 AA;

Query Match 71.4%; Score 35; DB 21; Length 235;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LORNSNP 8
1111111111
Db 218 LORNSNP 225

RESULT 8
AAB89755
ID AAB89755 standard; Protein: 283 AA.

XX 16-MAR-1999 (first entry)
 XX
 XX
 DE Staphylococcus aureus protein SEQ ID #5203.
 XX
 XX Computer readable medium; vaccine; S.aureus infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome.
 XX
 OS Staphylococcus aureus.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 225..240
 FT /note="these residues represent a line of missing text
 FT in the sequence listing in the specification.
 FT They are included to maintain the residue
 FT numbering given in the specification for this
 FT protein sequence"
 XX
 XX EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 XX 07-JAN-1997: 97EP-0100117.
 XX
 XX 05-JAN-1996: 96US-0009861.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
 PI Rosen CA;
 PI
 XX WPI: 1997-374922/35.
 DR
 XX Polynucleotide(s) and proteins derived from Staphylococcus aureus
 PT stored on computer readable medium and used in the production of
 PT anti-S.aureus vaccines
 XX
 PS Claim 23: Page 3200-3201; 3271pp; English.
 XX
 CC This sequence represents a Staphylococcus aureus protein sequence of the
 CC invention. The DNA sequences encoding the S.aureus proteins are recorded
 CC on a computer readable medium, preferably selected from a floppy or hard
 CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
 CC Homology searches using the S.aureus DNA sequences allows putative
 CC functions to be assigned so that protein-encoding or regulatory regions
 CC of commercial, therapeutic or industrial importance can be obtained.
 CC Specifically, sequences which are likely to encode antigens have been
 CC identified and these polypeptides can be used in a vaccine composition
 CC against S.aureus infection. The polypeptides can also be used in a kit
 CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
 CC in numerous human diseases, including cellulitis, eyelid infections, food
 CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
 CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
 CC DNA sequences can be used for recombinant production of the polypeptides.
 CC The new DNA sequences (and their fragments) are useful as primers or
 CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
 CC contained on the computer readable medium.
 XX
 SQ Sequence 283 AA;
 XX
 OY Query Match 71.4%; Score 35; DB 18; Length 283;
 Best Local Similarity 100.0%; Pred. NO. 2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 4 YSNPNT 9
 |||||
 Db 159 YSNPNT 164

ID AA017235 standard; Protein: 229 AA.
 XX
 AC AA017235;
 XX
 DT 08-JUL-2002 (first entry)
 XX
 DE Human secreted protein homologous protein SEQ ID NO: 134.
 XX
 KW Human; secreted protein; gene therapy; cancer; immune disease;
 KW haemostatic disorder; hyperproliferative disorder; renal disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disease;
 KW infection; reproductive system disorder; immunosuppressive;
 KW antithrombotic; antipneumatic; antiproliferative; cytostatic; cardiant;
 KW vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
 KW virocid; fungicide; ophthalmological.
 XX
 OS Homo sapiens.
 XX
 PN WO200228877-A1.
 XX
 PD 11-APR-2002.
 XX
 XX 17-JAN-2001: 2001WO-0501432.
 XX
 XX 29-SEP-2000: 2000US-236326P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;
 PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M,
 PI Ni J;
 PI
 XX WPI: 2002-340092/37.
 DR
 XX Isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition
 PT
 XX
 PS Disclosure: Page 528-529; 538pp; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human secreted proteins. These can be used in the treatment of
 CC cancer, immune diseases, haemostatic disorders, hyperproliferative
 CC disorders, renal disorders, cardiovascular disorders, respiratory
 CC disorders, neurological diseases, infections and reproductive system
 CC disorders. The present sequence is a protein showing homology to a
 CC protein of the invention.
 XX
 SQ Sequence 229 AA;
 XX
 OY Query Match 69.4%; Score 34; DB 23; Length 229;
 Best Local Similarity 66.7%; Pred. NO. 2.5e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 XX
 OY 1 LORYSNPNT 9
 |||||
 Db 126 LORYMDPST 134

RESULT 10
 AAM78596
 ID AAM78596 standard; Protein: 303 AA.
 XX
 AC AAM78596;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 1258.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX

OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang Y.T., Liu C., Drmanac R.T., Asundi V., Zhou P., Xu C., Cao Y., Ma Y.;
PI Zhao Q.A., Wang D., Wang J., Zhang J., Ren F., Chen R., Wang ZW;
PI Xue A.J., Yang Y., Wejhrman T., Goodrich R.
XX
DR WPI: 2001-476283/51.
DR N-PSDB: AAK51729.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 3520-3521; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoietic regulatory
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAW80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 303 AA:

Query Match 69.4%; Score 34; DB 22; Length 303;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LORRYNPST 9
| | | | : | : |
DB 85 LQRYMDPST 93

RESULT 11
AAW88667
ID AAW88667 standard; protein; 317 AA.
XX
AC AAW88667;
XX
DT 01-MAR-1999 (first entry)
XX
DE Secreted protein encoded by gene 134 clone HAIBP9.
XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal;
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX

KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9854963-A2.
XX
PD 10-DEC-1998.
XX
PF 04-JUN-1998; 98WO-US11422.
XX
PR 18-DEC-1997; 97US-0070923.
PR 06-JUN-1997; 97US-0048877.
PR 06-JUN-1997; 97US-0048881.
PR 06-JUN-1997; 97US-0048884.
PR 06-JUN-1997; 97US-0048893.
PR 06-JUN-1997; 97US-0048896.
PR 06-JUN-1997; 97US-0048899.
PR 06-JUN-1997; 97US-0048915.
PR 06-JUN-1997; 97US-0048949.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048972.
PR 06-JUN-1997; 97US-0049020.
PR 06-JUN-1997; 97US-0049375.
PR 06-JUN-1997; 97US-0057628.
PR 05-SEP-1997; 97US-0057635.
PR 05-SEP-1997; 97US-0057644.
PR 05-SEP-1997; 97US-0057647.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057661.
PR 05-SEP-1997; 97US-0057667.
PR 05-SEP-1997; 97US-0057761.
PR 05-SEP-1997; 97US-0057764.
PR 05-SEP-1997; 97US-0057770.
PR 05-SEP-1997; 97US-0057775.
PR 05-SEP-1997; 97US-0057778.
PR 06-JUN-1997; 97US-0048875.
PR 06-JUN-1997; 97US-0048878.
PR 06-JUN-1997; 97US-0048882.
PR 06-JUN-1997; 97US-0048885.
PR 06-JUN-1997; 97US-0048894.
PR 06-JUN-1997; 97US-0048897.
PR 06-JUN-1997; 97US-0048900.
PR 06-JUN-1997; 97US-0048916.
PR 06-JUN-1997; 97US-0048962.
PR 06-JUN-1997; 97US-0048970.
PR 06-JUN-1997; 97US-0048974.
PR 06-JUN-1997; 97US-0049373.
PR 05-SEP-1997; 97US-0057629.
PR 05-SEP-1997; 97US-0057642.
PR 05-SEP-1997; 97US-0057645.
PR 05-SEP-1997; 97US-0057648.
PR 05-SEP-1997; 97US-0057651.
PR 05-SEP-1997; 97US-0057662.
PR 05-SEP-1997; 97US-0057668.
PR 05-SEP-1997; 97US-0057762.
PR 05-SEP-1997; 97US-0057765.
PR 05-SEP-1997; 97US-0057771.
PR 05-SEP-1997; 97US-0057776.
PR 06-JUN-1997; 97US-0048876.
PR 06-JUN-1997; 97US-0048880.
PR 06-JUN-1997; 97US-0048883.
PR 06-JUN-1997; 97US-0048892.
PR 06-JUN-1997; 97US-0048895.
PR 06-JUN-1997; 97US-0048898.
PR 06-JUN-1997; 97US-0048901.
PR 06-JUN-1997; 97US-0048917.
PR 06-JUN-1997; 97US-0048963.
PR 06-JUN-1997; 97US-0048971.
PR 06-JUN-1997; 97US-0049019.
PR 05-SEP-1997; 97US-0049374.
PR 05-SEP-1997; 97US-0057627.

PR 05-SEP-1997; 97US-0057634.
PR 05-SEP-1997; 97US-0057643.
PR 05-SEP-1997; 97US-0057646.
PR 05-SEP-1997; 97US-0057649.
PR 05-SEP-1997; 97US-0057654.
PR 05-SEP-1997; 97US-0057666.
PR 05-SEP-1997; 97US-0057760.
PR 05-SEP-1997; 97US-0057763.
PR 05-SEP-1997; 97US-0057769.
PR 05-SEP-1997; 97US-0057774.
PR 05-SEP-1997; 97US-0057777.
XX (HUMA-) HUMAN GENOME SCI INC.
PI Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA;
PI Fan P, Feng P, Ferrie AM, Fischer CL, Florence C;
PI Florence K, Greene JM, Hu J, Kyaw H, Lafleur DM;
PI Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM;
PI Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
XX WPI: 1999-059865/05.
DR N-PSDB: AAV84544.
XX
XX New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 11: Page 551-552; 772pp: English.
XX
XX The invention relates to nucleic acid sequences (AAV84411 to AAV84633)
CC encoding human secreted proteins (AAW88534 to AAW88756). The secreted
CC protein gene sequences are deposited with the ATCC under deposit numbers
CC ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
CC 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
CC cells comprising recombinant vectors containing the nucleic acid
CC sequences are used for the recombinant production of the secreted
CC proteins. The polynucleotide and amino acid sequences are useful for are
CC useful for preventing, treating or ameliorating medical conditions e.g.
CC by protein or gene therapy. Pathological conditions can be also
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the polynucleotides, based on
CC which tissues they are most highly expressed in, and include developing
CC products for the diagnosis or treatment of cancer, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC restenosis, prostate diseases, obesity, disorders involving osteoclasts
CC such as osteoporosis, arthritis or malignancies, diseases of testes,
CC lung or thymus, digestive/endocrine disorders, infections and AIDS. The
CC polypeptides are also useful for identifying their binding partners.
CC The present sequence represents human secreted protein (see descriptor
CC line for gene number and clone identification).
XX
XX Sequence 317 AA:
SQ
Query Match 69.4%; Score 34; DB 20; Length 317;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LORYSNPNT 9
Db 99 LQRYMDPST 107
||||:|:|
RESULT 12
ABBS0434
ID ABBS0434 standard; Protein: 317 AA.
XX
AC ABBS0434;
XX
XX
DT 07-FEB-2002 (first entry)

XX
DE Human secreted protein encoded by gene 134 SEQ ID NO:382.
XX
XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
XX dermatological; immunosuppressive; anti-inflammatory; immunostimulant;
XX cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological;
XX neuroprotective; nootropic; anticonvulsant; antialzheimer's; vulnery;
XX antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
XX multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
XX human immunodeficiency virus; hyperproliferative disorder; wound healing;
XX Gaucher's disease; cardiovascular disease; Schmitz syndrome; chemotaxis;
XX Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;
XX corneal graft neovascularisation; diabetic retinopathy; regeneration;
XX neurological disorder; Huntington's chorea; Alzheimer's disease;
XX Parkinson's disease; infectious disease; chromosome 5.
XX
XX Homo sapiens.
XX
XX WO200162891-A2.
XX
XX 30-AUG-2001.
XX
XX 21-FEB-2001; 2001WO-US05614.
XX
XX 24-FEB-2000; 2000US-184836P.
XX
XX 29-MAR-2000; 2000US-193170P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ni J, Ebner R, Lafleur DM, Moore PA, Olsen HS, Rosen CA;
XX Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
XX Florence C, Hu J, Kyaw H, Fischer CL, Ferrie AM, Fan P;
XX Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;
XX Zeng Z, Greene JM;
XX
XX WPI: 2001-625724/72.
XX
XX N-PSDB: ABA83327.
XX
XX Nucleic acids encoding 207 human secreted polypeptides, useful for
XX preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
XX disease and diabetic retinopathy -
XX
XX Claim 11: Page 1153-1154; 1533pp: English.
XX
XX ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
XX proteins (I) and polynucleotide (II) sequences (I) and (II) have various
XX activities based on the tissues and cells the genes are expressed in.
XX Example of these activities include: immunomodulatory; antisclerotic;
XX dermatological; immunosuppressive; anti-inflammatory; immunostimulant;
XX anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological;
XX neuroprotective; nootropic; anticonvulsant; antialzheimer's; vascular;
XX antiparkinsonian; antimicrobial; and vulnery. (I) and (II) can be used
XX in gene therapy and vaccine production. (I) and (II) can be used in the
XX prevention, diagnosis and treatment of immune disorders (e.g. multiple
XX sclerosis, systemic lupus erythematosus and human immunodeficiency virus
XX (HIV) infections), hyperproliferative disorders (e.g. cancers and
XX Gaucher's disease), cardiovascular diseases (e.g. Schmitz syndrome,
XX Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
XX disorders (e.g. corneal graft neovascularisation and diabetic
XX retinopathy), neurological disorders (e.g. Huntington's chorea,
XX Alzheimer's disease and Parkinson's disease), infectious diseases and/or
XX for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to
XX ABA83193 and ABB50300 represent sequences used in the exemplification of
XX the present invention.
XX
XX Sequence 317 AA:
SQ
Query Match 69.4%; Score 34; DB 22; Length 317;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LORYSNPNT 9
||||:|:|

DB 99 LQRYMDPST 107

RESULT 13
AAE04905
ID AAE04905 standard; Protein: 324 AA.
XX
AC AAE04905;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human transporter and ion channel-18 (TRICH-18) protein.

Human: transporter and ion channel-18; TRICH-18; cystic fibrosis; mood;
KW gene therapy; amyotrophic lateral sclerosis; amnesia; bipolar disorder;
KW hypertension; angina; neurological disorder; asthma; bipolar disorder;
KW dementia; depression; Alzheimer's disease; epilepsy; vaccine; arrhythmia;
KW Pick's disease; ischemic cerebrovascular disease; AIDS; anxiety; stroke;
KW Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy;
KW demyelinating disease; mental disorder; schizophrenia; polymyositis;
KW muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease;
KW dermatomyositis; diabetes mellitus; immunological disorder; psoriasis;
KW rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus;
KW sickle cell anemia; Wilson's disease; infertility; Cushing's disease;
KW scleroderma; pulmonary artery stenosis; neutropenia; Addison's disease;
KW malabsorption syndrome; hypercholesterolemia; cancer.

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 145..163
FT /label= Transmembrane_domain
FT Domain 302..319
FT /label= Transmembrane_domain

WO200146258-A2.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000MO-US35095.
XX
PR 23-DEC-1999; 99US-0172000.
PR 14-JAN-2000; 2000US-0176083.
PR 21-JAN-2000; 2000US-0177332.
PR 28-JAN-2000; 2000US-0178572.
PR 02-FEB-2000; 2000US-0179758.
PR 10-FEB-2000; 2000US-0181625.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Baughn MR, Burford N, Au-Young J, Lu DM, Yang J, Reddy R, Lal P;
PI Hillman JL, Azimzai Y, Yue H, Nguyen DB, Yao MG, Gandhi AR;
PI Tang YT, Khan FA;
XX
DR WPI: 2001-418042/44.
DR N-PSDB: AAD09569.
XX
PT Novel human transporter and ion channel proteins useful for treating
PT and preventing transport, neurological, muscle and immunological
PT disorders -
XX
PS Claim 1; Page 130-131; 160pp; English.

The present sequence is transporter and ion channel-18 (TRICH-18)
CC protein. TRICH is used as vaccine. TRICH is useful for treating a disease
CC or condition associated with decreased expression of functional TRICH,
CC such as transport disorder including amyotrophic lateral sclerosis,
CC cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth
CC disease, Duchenne muscular dystrophy, angina and hypertension,
CC neurological disorders including Alzheimer's disease, amnesia, bipolar
CC disorder, dementia, depression, epilepsy, ischemic cerebrovascular
CC disease, stroke, cerebral neoplasms, Pick's disease, Huntington's
CC disease and Parkinson's disease, demyelinating diseases, mental disorders

CC including mood, anxiety, schizophrenia and seasonal affective disorder,
CC muscle disorder including cardiomyopathy, myocarditis, polymyositis,
CC dermatomyositis, arrhythmias and asthma and immunological disorders
CC including AIDS, adult respiratory distress syndrome (ARDS), allergies,
CC anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's
CC syndrome, systemic lupus erythematosus and other diseases including
CC sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary
CC artery stenosis, Grave's disease, Cushing's disease, Addison's disease,
CC glucose-galactose malabsorption syndrome, hypercholesterolemia, cancers
CC psoriasis and viral, bacterial, fungal, helminthic and protozoal
CC infections. TRICH DNA is useful in gene therapy and in diagnostic
CC purposes.

SQ Sequence 324 AA:
XX
OY 1 LQRYMDPST 9
DB 106 LQRYMDPST 114

Query Match 69.4%; Score 34; DB 22; Length 324;
Best Local Similarity 66.7%; Pred. No. 3.0e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 14
AAB31674
ID AAB31674 standard; Protein: 324 AA.
XX
AC AAB31674;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of a human protein having a hydrophobic domain.
XX
KW Human: hydrophobic protein; secretory protein; membrane protein; sepsis;
KW tumour inhibition; immune deficiency; autoimmune disorder; anemia; burn;
KW infectious disease; cancer; ulcer; periodontal disease; coagulation;
KW Parkinson's disease; fertility; immune response; thrombosis.
XX
OS Homo sapiens.
XX
PN WO200104297-A2.
XX
PD 18-JAN-2001.
XX
PF 16-JUN-2000; 2000MO-JP03942.
XX
PR 08-JUL-1999; 99JP-0194359.
XX
PA (SAGA-) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
XX
PI Kato S, Kimura T;
XX
DR WPI: 2001-103081/11.
DR N-PSDB: AAF25164, AAF25174.
XX
PT Isolated human proteins and polynucleotides are used in research and
PT have activities including cell proliferation/differentiation activity,
PT immune stimulating activity and receptor/ligand activity -
XX
PS Claim 1; Page 99-101; 151pp; English.

The present sequence represents a human protein with hydrophobic domains.
CC The protein possesses a hydrophobic domain and so is a secretory protein
CC or a membrane protein. The protein is used as an antigen to prepare
CC antibodies. The polynucleotide sequence is useful as a source of probes
CC for genetic diagnosis. It is also useful for producing the protein
CC in large quantities and for gene therapy. The eukaryotic cells are
CC used for detecting the receptors or ligands corresponding to the protein and
CC for detecting small novel pharmaceuticals. The antibodies are also used
CC for detection, quantification and purification of the proteins. Both the
CC protein and polynucleotide may be used in research or as nutritional

CC sources or supplements. The protein may have cytokine and cell
 CC proliferation/differentiation activity, immune stimulating or suppressing
 CC activity, hematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity and tumour inhibition activity. It may therefore may be used to
 CC treat immune deficiencies resulting from autoimmune disorders or
 CC infectious diseases, cancer, sepsis, anaemias, burns and ulcers,
 CC periodontal disease, Parkinson's disease, induce fertility, improve
 CC immune response and enhance coagulation or inhibit thrombosis.

XX Sequence 324 AA:

Query Match 69.4%; Score 34; DB 23; Length 324;

Best Local Similarity 66.7%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQRYSNPNT 9

Db 106 LQRYMDPST 114

RESULT 15

AA017236 AAO17236 standard; Protein: 324 AA.

AC AAO17236:

DT 08-JUL-2002 (first entry)

DE Human secreted protein homologous protein SEQ ID NO: 135.

KM Human; secreted protein; gene therapy; cancer; immune disease;
 KM haemostatic disorder; hyperproliferative disorder; renal disorder;
 KM cardiovascular disorder; respiratory disorder; neurological disease;
 KM infection; reproductive system disorder; immunosuppressive;
 KM anaphylactic; antirheumatic; antiproliferative; cytostatic; cardiac;
 KM vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
 KM virocidic; fungicide; ophthalmological.

OS Homo sapiens.

PN WO200228877-A1.

PD 11-APR-2002.

PE 17-JAN-2001: 2001WO-US01432.

PR 29-SEP-2000: 2000US-236326P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;
 PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fliscella M;
 PI NI J;

DR WPI: 2002-340092/37.

XX Isolated nucleic acid molecule encoding a human secreted protein is

PT used in preventing, treating or ameliorating a medical condition.

PS Disclosure; Page 529-530; 538pp; English.

XX The present invention provides the protein and coding sequences of a
 CC number of human secreted proteins. These can be used in the treatment of
 CC cancer, immune diseases, haemostatic disorders, hyperproliferative
 CC disorders, renal disorders, cardiovascular disorders, respiratory
 CC disorders, neurological diseases, infections and reproductive system
 CC disorders. The present sequence is a protein showing homology to a
 CC protein of the invention.

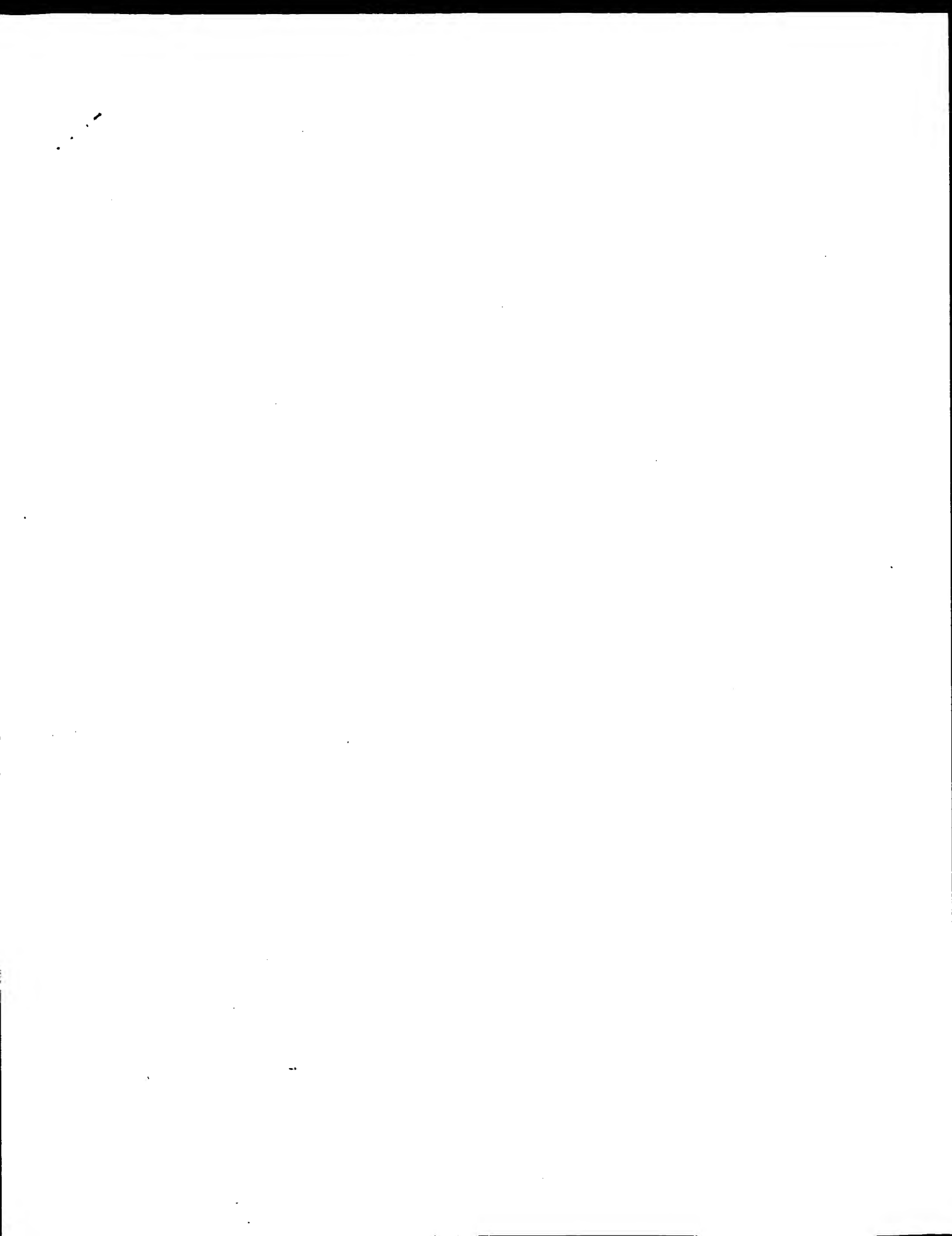
XX Sequence 324 AA:

Query Match 69.4%; Score 34; DB 23; Length 324;
 Best Local Similarity 66.7%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQRYSNPNT 9

Db 106 LQRYMDPST 114

Search completed: February 25, 2003, 10:32:28
 Job time : 4.97 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:32:42 ; Search time 13.995 Seconds
(without alignments)
114.619 Million cell updates/sec

Title: US-09-743-482A-6
Perfect score: 49
Sequence: 1 LORISNPNT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues
Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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20:	/cgn2_6/ptodata/1/paa/US104_COMB.pep.*
21:	/cgn2_6/ptodata/1/paa/US105_COMB.pep.*
22:	/cgn2_6/ptodata/1/paa/US106_COMB.pep.*
23:	/cgn2_6/ptodata/1/paa/US107_COMB.pep.*
24:	/cgn2_6/ptodata/1/paa/US108_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	9	US-09-743-482A-6	Sequence 6, Appl
2	49	100.0	107	US-09-743-482A-16	Sequence 16, Appl
3	49	100.0	532	US-09-743-482A-18	Sequence 18, Appl
4	39	79.6	339	US-09-252-991A-32096	Sequence 32096, A
5	39	79.6	1008	US-60-173-464-20881	Sequence 20881, A
6	39	79.6	1008	US-60-191-637-25364	Sequence 25364, A

7	39	79.6	1008	27	US-60-191-681-19973	Sequence 19973, A
8	39	79.6	1346	20	US-09-614-150-25251	Sequence 25251, A
9	36	73.5	95	21	US-09-733-089-23384	Sequence 23384, A
10	36	73.5	95	22	US-09-816-660-23384	Sequence 23384, A
11	36	73.5	112	21	US-09-791-537-62999	Sequence 62999, A
12	36	73.5	627	25	US-10-179-131-9095	Sequence 9095, Ap
13	36	73.5	910	21	US-09-733-089-19599	Sequence 19599, A
14	36	73.5	910	22	US-09-816-660-19599	Sequence 19599, A
15	35.5	72.4	116	16	US-09-270-767-40294	Sequence 40294, A
16	35.5	72.4	116	16	US-09-270-767-55510	Sequence 55510, A
17	35.5	72.4	116	16	US-09-270-8498-193034	Sequence 193034, A
18	35.5	72.4	552	20	US-09-614-150-40497	Sequence 40497, A
19	35.5	72.4	552	20	US-09-619-049-1389	Sequence 1389, Ap
20	35.5	72.4	552	21	US-09-791-537-124554	Sequence 124554, A
21	35.5	72.4	552	27	US-60-167-324-129	Sequence 129, App
22	35.5	72.4	552	27	US-60-171-627-2046	Sequence 2046, Ap
23	35.5	72.4	552	27	US-60-173-386-129	Sequence 129, App
24	35.5	72.4	552	27	US-60-175-871-147	Sequence 147, App
25	35.5	72.4	552	27	US-60-184-775-138	Sequence 138, App
26	35.5	72.4	552	27	US-60-191-637-40123	Sequence 40123, A
27	35.5	72.4	552	27	US-60-191-700-147	Sequence 147, App
28	35	71.4	94	21	US-09-791-537-34671	Sequence 34671, A
29	35	71.4	108	22	US-09-855-768-658	Sequence 658, App
30	35	71.4	113	21	US-09-791-537-54578	Sequence 54578, A
31	35	71.4	223	26	US-10-219-999-37248	Sequence 37248, A
32	35	71.4	223	27	US-60-324-109-23583	Sequence 23583, A
33	35	71.4	223	1	PCT-US00-07677-109	Sequence 109, App
34	35	71.4	283	11	US-08-781-986A-5203	Sequence 5203, Ap
35	35	71.4	283	13	US-08-956-171-5203	Sequence 5203, Ap
36	35	71.4	283	13	US-08-956-171B-5203	Sequence 5203, Ap
37	35	71.4	283	13	US-08-956-171C-5203	Sequence 5203, Ap
38	35	71.4	283	13	US-08-956-171D-5203	Sequence 5203, Ap
39	35	71.4	283	13	US-08-956-171E-5203	Sequence 5203, Ap
40	35	71.4	303	16	US-09-270-767-39800	Sequence 39800, A
41	35	71.4	303	16	US-09-270-767-55017	Sequence 55017, A
42	35	71.4	303	16	US-09-270-8498-191982	Sequence 191982, A
43	35	71.4	325	12	US-08-827-356-4312	Sequence 4312, Ap
44	35	71.4	325	20	US-09-611-529-7363	Sequence 7363, Ap
45	35	71.4	599	19	US-09-540-209B-6951	Sequence 6951, Ap

ALIGNMENTS

RESULT 1
US-09-743-482A-6
Sequence 6, Application US/09743482A
GENERAL INFORMATION:
APPLICANT: Comex GmbH
TITLE OF INVENTION: Immunological reagent specifically interacting with the
FILE REFERENCE: C1368BCT
CURRENT APPLICATION NUMBER: US/09/743,482A
CURRENT FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: EP 98 11 2867.1
PRIOR FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 9
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-743-482A-6

Query Match 100.0% Score 49; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LORISNPNT 9
DB 1 LORISNPNT 9

RESULT 2
US-09-743-482A-16
; Sequence 16, Application US/09743482A
; GENERAL INFORMATION:
; APPLICANT: Connex GmbH
; TITLE OF INVENTION: Immunological reagent specifically interacting with the
; TITLE OF INVENTION: extracellular domain of the human zeta chain
; FILE REFERENCE: C1368PCT
; CURRENT APPLICATION NUMBER: US/09/743,482A
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: EP 98 11 2867.1
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-743-482A-16

Query Match 100.0%; Score 49; DB 21; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LORYSNPT 9
Db 89 LORYSNPT 97

RESULT 3
US-09-743-482A-18
; Sequence 18, Application US/09743482A
; GENERAL INFORMATION:
; APPLICANT: Connex GmbH
; TITLE OF INVENTION: Immunological reagent specifically interacting with the
; TITLE OF INVENTION: extracellular domain of the human zeta chain
; FILE REFERENCE: C1368PCT
; CURRENT APPLICATION NUMBER: US/09/743,482A
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: EP 98 11 2867.1
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct of DNA encoding bispecific single chain
; OTHER INFORMATION: antibody comprising anti-zeta-chain/anti-EPCAM
; OTHER INFORMATION: domains.
US-09-743-482A-18

Query Match 100.0%; Score 49; DB 21; Length 532;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LORYSNPT 9
Db 108 LORYSNPT 116

RESULT 4
US-09-252-991A-32096
; Sequence 32096, Application US/09252991A
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32096
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32096

Query Match 79.6%; Score 39; DB 16; Length 339;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LORYSNPT 9
Db 126 LORYSNPT 134

RESULT 5
US-60-173-464-20881
; Sequence 20881, Application US/60173464
; GENERAL INFORMATION:
; APPLICANT: IL, Peter W.D.
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
; FILE REFERENCE: C1000173
; CURRENT APPLICATION NUMBER: US/60/173,464
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 30269
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20881
; LENGTH: 1008
; TYPE: PRT
; ORGANISM: Drosophila
US-60-173-464-20881

Query Match 79.6%; Score 39; DB 27; Length 1008;
Best Local Similarity 77.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LORYSNPT 9
Db 762 LORYSNPT 770

RESULT 6
US-60-191-637-25364
; Sequence 25364, Application US/60191637
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
; TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: C1000392
; CURRENT APPLICATION NUMBER: US/60/191,637
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 42660
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25364
; LENGTH: 1008
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-60-191-637-25364

Query Match 79.6%; Score 39; DB 27; Length 1008;
Best Local Similarity 77.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LORYSNPT 9
Db 111 LORYSNPT 111

Db 762 LKRYFNPT 770

RESULT 7

US-60-191-681-19973
; Sequence 19973, Application US/60191681
; GENERAL INFORMATION:
; APPLICANT: Li, Peter, W.D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
; TITLE OF INVENTION: USES THEREOF.
; FILE REFERENCE: c1000390
; CURRENT APPLICATION NUMBER: US/60/191,681
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 30973
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19973
; LENGTH: 1008
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-60-191-681-19973

Query Match

Best Local Similarity 77.6%; Score 39; DB 27; Length 1008;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LORYSNPT 9
1:11111111

Db 762 LKRYFNPT 770

RESULT 8

US-09-614-150-25251
; Sequence 25251, Application US/09614150
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: C1000728
; CURRENT APPLICATION NUMBER: US/09/614,150
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25251
; LENGTH: 1346
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-09-614-150-25251

Query Match

Best Local Similarity 77.8%; Score 39; DB 20; Length 1346;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LORYSNPT 9
1:11111111

Db 787 LKRYFNPT 795

RESULT 9

US-09-733-089-23384
; Sequence 23384, Application US/09733089
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Transcription In Plants
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23384
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-733-089-23384

Query Match

Best Local Similarity 73.5%; Score 36; DB 21; Length 95;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QRRSNPT 9
1:11111111

Db 34 RRRSNPT 41

RESULT 10

US-09-816-660-23384
; Sequence 23384, Application US/09816660
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Transcription In Plants
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/816,660
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/733,089
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER:) US 09/684,016
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23384
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-816-660-23384

Query Match

Best Local Similarity 73.5%; Score 36; DB 22; Length 95;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LORYSNPT 9
1:11111111

Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QRYSNPT 9
: : : : :
Db 34 RRHSNPT 41

RESULT 11
US-09-791-537-62999

; Sequence 62999, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 62999
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-62999

Query Match 73.5%; Score 36; DB 21; Length 112;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QRYSNPT 9
: : : : :
Db 92 QRYHNPT 99

RESULT 12
US-10-179-131-9095

; Sequence 9095, Application US/10179131
; GENERAL INFORMATION:
; APPLICANT: HARE, ROBERTA S.
; APPLICANT: SHAW, KAREN J.
; APPLICANT: SHIMER JR., GEORGE H.
; APPLICANT: KESSLER, MARCO
; APPLICANT: NOLLING, JORK
; APPLICANT: ZENG, QIANDONG
; APPLICANT: GREENE, JONATHAN R.
; TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC ACIDS AND POLYPEPTIDES,
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 2976-4031
; CURRENT APPLICATION NUMBER: US/10/179,131
; CURRENT FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 10194
; SEQ ID NO 9095
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-179-131-9095

Query Match 73.5%; Score 36; DB 25; Length 627;
Best Local Similarity 85.7%; Pred. No. 8.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 QRYSNPT 8
: : : : :
Db 503 RRISNPT 509

RESULT 13
US-09-733-089-19599
; Sequence 19599, Application US/09733089
; GENERAL INFORMATION:

; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Transcription In Plants
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 19599
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-733-089-19599

Query Match 73.5%; Score 36; DB 21; Length 910;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QRYSNPT 9
: : : : :
Db 31 RRHSNPT 38

RESULT 14
US-09-816-660-19599

; Sequence 19599, Application US/09816660
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Transcription In Plants
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/816,660
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/733,089
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER:)
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 19599
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-816-660-19599

Query Match 73.5%; Score 36; DB 22; Length 910;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

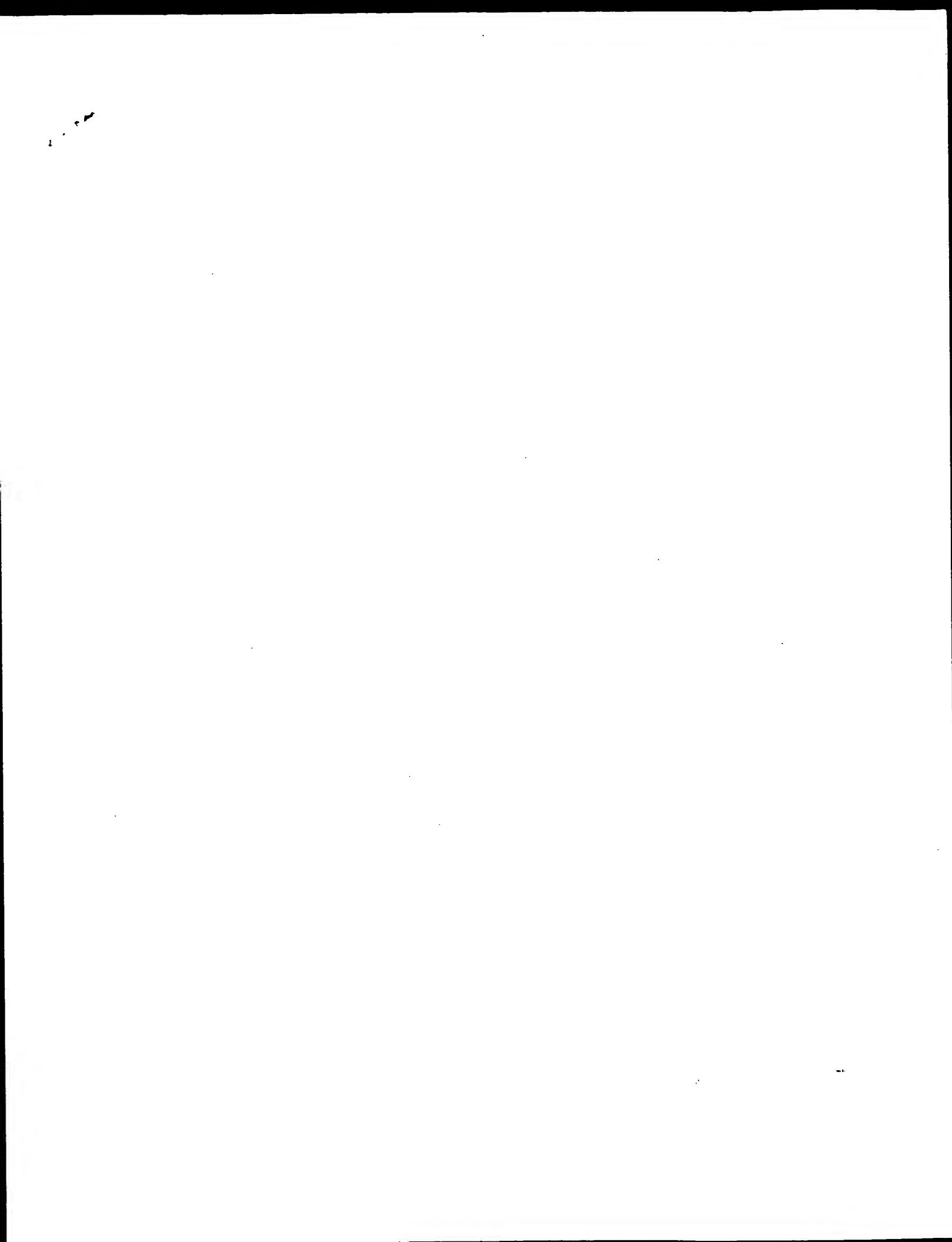
OY 2 QRYSNPT 9
: : : : :
Db 31 RRHSNPT 38

RESULT 15
US-09-270-767-40294
; Sequence 40294, Application US/09270767
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40294
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40294

Query Match 72.4% Score 35.5; DB 16; Length 116;
Best Local Similarity 56.2%; Pred No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 7; Gaps 1;

QY 1 LQRY-----SNPT 9
DB 86 LQRYREMARVLSNPNT 101

Search completed: February 25, 2003, 10:54:24
Job time : 15.995 secs



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OM protein - protein search, using sw model

Run on: February 25, 2003, 10:36:42 : Search time 0.735 Seconds

(Without alignments)
380.447 Million cell updates/sec

Title: US-09-743-482a-6

Perfect score: 49

Sequence: 1 LQRYSNPT 9

Scoring table: BIOSUM62

Searched: Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	67.3	9	US-09-968-561A-144	Sequence 144, App
2	33	67.3	9	US-09-968-561A-300	Sequence 300, App
3	33	67.3	9	US-09-968-561A-318	Sequence 318, App
4	33	67.3	9	US-09-968-561A-318	Sequence 318, App
5	33	67.3	112	US-09-895-913A-144	Sequence 144, App
6	33	67.3	240	US-09-968-561A-144	Sequence 2, App1
7	33	67.3	240	US-09-968-561A-144	Sequence 2, App1
8	31	63.3	106	US-09-764-864-1402	Sequence 1402, App
9	31	63.3	316	US-09-764-864-967	Sequence 967, App
10	31	63.3	363	US-09-797-464A-11	Sequence 11, App1
11	31	63.3	390	US-09-975-139-6	Sequence 6, App1
12	31	63.3	752	US-10-003-295-2	Sequence 2, App1
13	31	63.3	822	US-10-003-295-4	Sequence 2, App1
14	31	63.3	1404	US-09-944-849-8	Sequence 4, App1
15	30	61.2	141	US-09-867-550-1434	Sequence 1434, App
16	30	61.2	229	US-09-966-880A-36	Sequence 36, App1
17	30	61.2	237	US-10-040-805-3	Sequence 3, App1
18	30	61.2	237	US-10-056-884-4	Sequence 4, App1
19	30	61.2	323	US-09-815-242-10239	Sequence 10239, A

20	30	61.2	375	9	US-09-738-626-6846	Sequence 6846, App
21	30	61.2	432	10	US-09-977-653-6	Sequence 6, App1
22	30	61.2	475	10	US-09-738-363-8	Sequence 8, App1
23	30	61.2	475	10	US-09-977-653-2	Sequence 2, App1
24	30	61.2	475	10	US-09-977-653-4	Sequence 4, App1
25	30	61.2	810	9	US-09-712-363-281	Sequence 281, App
26	29.5	60.2	122	10	US-09-764-847-793	Sequence 793, App
27	29	59.2	9	10	US-09-968-561A-174	Sequence 174, App
28	29	59.2	9	10	US-09-192-854-98	Sequence 98, App1
29	29	59.2	123	10	US-09-753-436-86	Sequence 86, App1
30	29	59.2	138	10	US-09-753-436-78	Sequence 78, App1
31	29	59.2	162	9	US-09-928-457-42	Sequence 42, App1
32	29	59.2	179	9	US-09-738-626-5426	Sequence 5426, App
33	29	59.2	242	9	US-09-861-097-23	Sequence 23, App1
34	29	59.2	280	10	US-09-815-242-13182	Sequence 13182, A
35	29	59.2	321	10	US-09-925-297-685	Sequence 685, App
36	29	59.2	359	10	US-09-815-242-5116	Sequence 5116, App
37	29	59.2	396	10	US-09-765-272-16	Sequence 16, App1
38	29	59.2	511	9	US-10-121-032-21	Sequence 21, App1
39	29	59.2	512	9	US-10-121-032-26	Sequence 26, App1
40	29	59.2	570	10	US-09-815-242-10760	Sequence 10760, A
41	29	59.2	599	10	US-09-789-561-120	Sequence 120, App
42	29	59.2	673	9	US-10-090-455-7	Sequence 7, App1
43	29	59.2	685	9	US-10-029-180-82	Sequence 82, App1
44	29	59.2	694	9	US-09-738-626-3867	Sequence 3867, App
45	29	59.2	740	10	US-09-815-242-10876	Sequence 10876, A

ALIGNMENTS

RESULT 1
US-09-968-561A-144
Sequence 144, Application US/09968561A
Patent No. US20020164642A1
GENERAL INFORMATION:
APPLICANT: Minter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
FILE REFERENCE: 8039/10738
CURRENT APPLICATION NUMBER: US/09/968, 561A
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 144
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-144

Query Match 67.3%; Score 33; DB 9; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QRYSNPT 9
Db 2 QVSTPWT 9

RESULT 2
US-09-968-561A-300
Sequence 300, Application US/09968561A
Patent No. US20020164642A1

GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 300
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-300

Query Match
Best Local Similarity 67.3%; Score 33; DB 9; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QRYSNPNT 9
Db 1 1 1 1 1
2 QSYSTPNT 9

RESULT 3
US-09-968-561A-318
Sequence 318, Application US/09968561A
Patent No. US20020164642A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 318
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-318

Query Match
Best Local Similarity 67.3%; Score 33; DB 9; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QRYSNPNT 9
Db 1 1 1 1 1
2 QSYSTPNT 9

RESULT 4

US-09-192-854-84
Sequence 84, Application US/09192854
Patent No. US20020068276A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
PRIOR FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 84
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-192-854-84

Query Match
Best Local Similarity 67.3%; Score 33; DB 10; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QRYSNPNT 9
Db 1 1 1 1 1
2 QSYSTPNT 9

RESULT 5
US-09-895-913A-144
Sequence 144, Application US/09895913A
Patent No. US20020160456A1
GENERAL INFORMATION:
APPLICANT: Kleantous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020160456A1el Helicobacter Polypeptides in t
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/043002
CURRENT APPLICATION NUMBER: US/09/895,913A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 08/881,227
PRIOR FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 144
LENGTH: 112
TYPE: PRT
ORGANISM: Helicobacter pylori
US-09-895-913A-144

Query Match
Best Local Similarity 67.3%; Score 33; DB 9; Length 112;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LQRYSNPNT 9
Db 55 LKRIKPNPT 63

RESULT 6
US-09-968-561A-2
Sequence 2, Application US/09968561A
Patent No. US20020164642A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
FILE REFERENCE: 8039/1073B

```
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-2
```

```
Query Match
Best Local Similarity 67.3%; Score 33; DB 9; Length 240;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 2 QRYSNPNT 9
    1 1 1 1 1
Db 222 QSYSTPNT 229
```

```
RESULT 7
US-09-192-854-2
; Sequence 2, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-2
```

```
Query Match
Best Local Similarity 67.3%; Score 33; DB 10; Length 240;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 2 QRYSNPNT 9
    1 1 1 1 1
Db 222 QSYSTPNT 229
```

```
RESULT 8
US-09-764-864-1402
; Sequence 1402, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1402
```

```
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (85)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (96)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (98)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (106)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1402
```

```
Query Match
Best Local Similarity 63.3%; Score 31; DB 10; Length 106;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 LQRYSN 6
    1 1 1 1 1
Db 29 LQRYSN 34
```

```
RESULT 9
US-09-764-864-967
; Sequence 967, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 967
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-967
```

```
Query Match
Best Local Similarity 63.3%; Score 31; DB 10; Length 316;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 LQRYSN 6
    1 1 1 1 1
Db 29 LQRYSN 34
```

```
RESULT 10
US-09-797-464A-11
; Sequence 11, Application US/09797464A
; Publication No. US20030022807A1
; GENERAL INFORMATION:
; APPLICANT: Willing, Reinhard
; APPLICANT: Bjornvad, Mads Eskelund
; APPLICANT: Kauppinen, Markus Sakari
; APPLICANT: Schielein, Martin
; TITLE OF INVENTION: Family 5 xyloglucanases
; FILE REFERENCE: 6073.200-US
; CURRENT APPLICATION NUMBER: US/09/797,464A
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 363
; TYPE: PRT
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ORGANISM: Paenibacillus pabuli
US-09-797-464A-11

Query Match 63.3%; Score 31; DB 9; Length 363;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 YSNPNT 9
DB 156 YGNPNT 161

RESULT 11
US-09-975-139-6
Sequence 6, Application US/09975139
Patent No. US20020155460A1

GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
APPLICANT: Schellenberger, Volker
APPLICANT: Naki, Donald

APPLICANT: Morison, Thomas B.
TITLE OF INVENTION: INFORMATION RICH LIBRARIES

FILE REFERENCE: 23623-7060
CURRENT APPLICATION NUMBER: US/09/975,139
CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/239,476
PRIOR FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 390
TYPE: PRT

ORGANISM: Ochrobactrum anthropi
FEATURE:
OTHER INFORMATION: Ampc protein
US-09-975-139-6

Query Match 63.3%; Score 31; DB 9; Length 390;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QRYSNPN 8
DB 174 RRYSNPS 180

RESULT 12
US-10-003-295-2
Sequence 2, Application US/10003295
Patent No. US20020168741A1

GENERAL INFORMATION:
APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01183DIV

CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 752
TYPE: PRT

ORGANISM: Homo sapiens
US-10-003-295-2

Query Match 63.3%; Score 31; DB 9; Length 752;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQRYSNPN 8
DB 541 LKQYSHPN 548

RESULT 13
US-10-003-295-4

Sequence 4, Application US/10003295
Patent No. US20020168741A1
GENERAL INFORMATION:

APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01183DIV

CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 822
TYPE: PRT

ORGANISM: Homo sapiens
US-10-003-295-4

Query Match 63.3%; Score 31; DB 9; Length 822;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQRYSNPN 8
DB 611 LKQYSHPN 618

RESULT 14
US-09-944-849-8
Sequence 8, Application US/09944849
Patent No. US20020151487A1

GENERAL INFORMATION:
APPLICANT: Nickoloff, Brian
TITLE OF INVENTION: Miele, Lucio

TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND TREAT
TITLE OF INVENTION: MALIGNANT AND BENIGN SKIN DISORDERS BY MODULATING THE NOTCH P
FILE REFERENCE: 212583

CURRENT APPLICATION NUMBER: US/09/944,849
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,614

PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1

SEQ ID NO 8
LENGTH: 1404
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-944-849-8

Query Match 63.3%; Score 31; DB 10; Length 1404;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQRYSNPN 7
DB 1279 LRRYTNP 1285

RESULT 15
US-09-867-550-1434
Sequence 1434, Application US/09867550
Patent No. US20020082206A1

GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Mehrtan, Fuad

APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: NO. US20020082206A1el Polynucleotides from Atherogenic Cells a

;; TITLE OF INVENTION: Thereby
;; FILE REFERENCE: 21402-013 (Cura-313)
;; CURRENT APPLICATION NUMBER: US/09/867,550
;; CURRENT FILING DATE: 2001-09-20
;; PRIOR APPLICATION NUMBER: USSN 60/208,427
;; PRIOR FILING DATE: 2000-05-30
;; NUMBER OF SEQ ID NOS: 2125
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1434
;; LENGTH: 141
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-867-350-1434

Query Match 61.2%; Score 30; DB 10; Length 141;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSNPN 8
 |||||
Db 103 YSNPN 107

Search completed: February 25, 2003, 10:57:18
Job time : 0.735 secs

